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1 MNSNBNQRVIVIGAGLGGLS......MPMVTLSGQLVRDXIVADLQ 497
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                                                               ELGVETRIDAEVSETOKODGRACAVKLANGDVI.PADIVVSNMEVIPAMEKLIRSPASELK 300
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APPLICANT: BISOSCOWICZ, Patricia C.
APPLICANT: Cheng, Glong
APPLICANT: Cheng, Olong
APPLICANT: DiCosimo, Deana J.
APPLICANT: Molfas, Mattheos
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Odom, J. Martin
APPLICANT: Odom, J. Martin
APPLICANT: Odom, J. Martin
APPLICANT: Rouviere, Pierre E.
TITLE OF INVENTION: CAROTENDID PRODUCTION FROM A SINGLE CARBON SOURCE
FILE REFERENCE: CL1903 US NA
CURRENT APPLICANTON NUMBER: US/09/941, 947A
CURRENT APPLICANTON NUMBER: 60/229, 907
PRIOR FILING DATE: 2000-09-01
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CKTDPAQAPAGCELIKILPHIPHLDPDKLITAEDYSALRERVLVKLERMGLTDLRQHIVT
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Best Local Similarity 100.0%; Pred. No. 4.6e-251;
Matches 497; Conservative 0; Mismatches 0; Indels 0;
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ORGANISM: Methylomonas 16a
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      ILIMPHIFEALFTGAGROMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGP
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APPLICANT: Odom, James M
APPLICANT: Odom, James M
APPLICANT: Odom, James M
APPLICANT: Odom, James M
TITLE OF INVENTION: DENIRHIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: CL1596 US NA
CURRENT APPLICATION NUMBER: US/09/934,868
CURRENT PILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Microsoft Office 97
SEQ ID NO 28
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100.0%; Score 2598; DB 9;
Best Local Similarity 100.0%; Pred. No. 4.6e-251;
Matches 497; Conservative 0; Mismatches 0;
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Patent No. US20020137190A1
GENERAL INFORMATION:
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                                                               421 EEYWTPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 HTGARVDNIKTYQRRVTGVRLDTGEFVKADYIISNMEVIPTYKYLIHLDTQRLAKLBREF
361 CKTDPAQAPAGCEIIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTDLRQHIVT
                                       EEFWITPLDIQAKYYSNOGSIYGVVADREKONLGEKAPORSSELSNLYFVGGSVNPGGGWPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 QRVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPH
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                                                                                                                                                                                                                                      Sequence 14, Application US/10358917

Publication No. US20030182687A1

Publication No. US20030182687A1

GREREAL INFORMATION:

APPLICANT: Cheng, Qiong

APPLICANT: Cheng, Qiong

APPLICANT: Cheng, Qiong

TILLE OF INVENTION: FUNCTIONALIZATION OF CAROTENOID COMPOUNDS

FILE REFERENCE: CL1929 US NA

CURRENT PLIJNG DATE: 2003-02-05

PRIOR FILING DATE: 2003-02-05

PRIOR PLIJNG DATE: 2003-02-11

NUMBER OF SEQ ID NOS: 28

SOFTWARRE: Microsoft Office 97

TENTAL OF 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 51.9%; Pred. No. 6e-120;
Matches 254; Conservative 85; Mismatches 148;
                                                                                                                                             481 VELSGQLVRDKIVADLO 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Staphylococcus aureus
                                                                                                                   481 VFLSGOLVRDKIVADLO 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 ÇQVADKINA 490
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                            ELGVEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSPASELK 300
                                                                                360
                                                                                                    KOORFEPSCSGLVLHLGVDRLYPQLAHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAP 360
                                                                                                                                                        CKTDPAQAPAGCBIIKILPHIPHLDPDXLLTAEDYSALRERVIVKLERMGLTDLRQHIVT 420
                                                                                                                                                                              CKTDPAQAPAGCELIKILPHIPHIDPDKLITAEDYSALRERVIVKIERMGLTDLRQHIVT 420
                                                                                                                                                                                                                                    EEYWTPLDIOAKYYSNOGSIYGVVADRFKNLGFKAPORSSELSNLYFVGGSVNPGGGMPM 480
                                                                                                                                                                                                                                                               EEYWIPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPM 480
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      ELGVEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSPASELK 300
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                                                                                XWQRFEPSCSGLVLHLGVDRLYPQLAHINFFYSDHPREHFDAVFKSHRLSDEPTIYLVAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/10358917
Publication No. US20030182687A1
GENERAL INFORMATION:
APPLICANT: Cheng, Qiong
APPLICANT: Cheng, Qiong
APPLICANT: No. US20030182687A1ton, Kelley C.
APPLICANT: Tao, Luan
TILE REPERENCE: CL1929 US NA
CURRENT APPLICATION NUMBER: US/10/358,917
CURRENT PILLING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: 60/355,939
PRIOR FILING DATE: 2002-02-11
                                                                                                                                                                                                                                                                                                                VILSGOLVRDKIVADLO 497
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Methylomonas sp.16a
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SOFTWARE: Microsoft Office 97
SEQ ID NO 8
LENGTH: 497
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Matches 497, Conservative
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                                         241
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Best Local S
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126

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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: John S.
APPLICANT: John S.
APPLICANT: John S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: John S.
APPLICANT: Goldman, Barry S.
APPLICANT
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31.1%; Score 809; DB 15; Length 517;
Best Local Similarity 34.9%; Pred. No. 7.5e-72;
Matches 175; Conservative 100; Mismatches 204; Indels 2;
                                                                                                                                                                                                                                   Sequence 19519, Application US/10369493
Publication No. US26030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-941-947A-32; Sequence 32, Application US/09941947A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Myxococcus xanthus
US-10-369-493-19519
426 P 426
                                                               422 P 422
                                                                                                                                                                                                     US-10-369-493-19519
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APPLICANT: Oblish, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Tayskind, Judith W.
APPLICANT: Tranie, John D.
APPLICANT: Tranie, John D.
APPLICANT: Tranie, John D.
APPLICANT: Tranimoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 10011A
CURRENT PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-13
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Best Local Similarity 48.7%; Pred. No. 5.4e-95;
Matches 205; Conservative 80; Mismatches 134; Indels
                                                                                                    Sequence 5696, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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TENGTH: 439
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Rouviere, Pierre
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US-10-369-493-234
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APPLICANT:
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                                           APPLICANT: Brosewicz, Patricia C.
APPLICANT: Cheng, Qiong
APPLICANT: Cheng, Qiong
APPLICANT: Dicosimo, Deana J.
APPLICANT: Dicosimo, Deana J.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Odon, J. Martin
APPLICANT: Odon, J. Martin
APPLICANT: Picataggio, Steve
APPLICANT: Picataggio, Steve
TITLE OF INVENTION: CANOTENDID PRODUCTION FROM A SINGLE CARBON SOURCE
FILE REPERENCE: CL1903 US M.
CURRENT APPLICATION NUMBER: US/09/941,947A
CURRENT APPLICATION NUMBER: 06/229,907
PRIOR APPLICATION NUMBER: 66/229,907
PRIOR APPLICATION NUMBER: 66/229,907
PRIOR APPLICATION NUMBER: 66/229,858
PRIOR FILING DATE: 2000-09-01
SCOTWARER MICROSOFT Office 97
SEQ ID NO 32
LENGTH: 492
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     Publication No. US20030003528A1
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ORGANISM: Pantoea stewartii
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Matches 164; Conservative
                              SENERAL INFORMATION:
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IS-10-218-118-8
Sequence 8, Application US/10218118
Publication No. US20030148319A1
GENERAL INFORMATION:
APPLICANT: Bzzostowicz, Patricia

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Sequence 234, Application US/10369493

Sequence 234, Application US/10369493

Sublication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Coldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 30-10(52052)8

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.4%; Score 687; DB 14; Length 4
Best Local Similarity 33.3%; Pred. No. 1.2e-59;
Matches 164; Conservative 87; Mismatches 229; Indels
APPLICANT: Picataggio, Stephen
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Encoding Carotenoid Compounds
FILE REFERENCE: CL1976 US NA
CURRENT APPLICATION NUMBER: US/10/218,118
CURRENT FILING DATE: 2002-08-13
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEG. 10 NOS: 14
SOFTWARE: Microsoft Office 97
TEMPORAL: A00 8
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
, ORGANISM: Pantoea stewartii
US-10-218-118-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 VRRFISDPKLVBILNYFIKYVGSSPYDAPALANLLPYIQYHYGLWYVKGGMYGMAQAMBK 237
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                                                                                                                                                                                               68 FEALFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQFQ
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231 INKOLGVNIELNAEIEQIIIDPXFKRADAIKV-NGDIRKFDKILCTADFPSVABSLMPDF
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llarity 31.5%; Pred. No. 3.8e-58;
Conservative 120; Mismatches 191; Indels
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US-10-369-493-18644
          Local Similarity
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                                                            Matches 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 RFLDYSKNICTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFISDPKL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSVTDPTLAPPGCASYYVLAPVPHLGNAQINWLEESPRIRDRIFSYLEKYYIPGLRDQLV 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 FEALFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQFQ 127
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Sequence 12, Application US/10358917

Schemee 12, Application US-10358917

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
TILL OF INVENTION:
FILLE REFERENCE:
CLURAL US-10358,917

CURRENT APPLICATION NUMBER: US/10/358,917

CURRENT PILING DATE: 2002-02-05

PRIOR FILING DATE: 2002-02-1

SRIOR FILING DATE: 2002-02-1

SOFTWARE: Microsoft Office 97

SEQUENCE:
SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 491;
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                              60/360,039
                                                                                                                                                                                                                                                                                                         ORGANISM: Xenorhabdus nematophilus
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                    PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 234
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US-10-358-917-12
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INGTH: 502
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Glaman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
TITLE OF INVENTION: RAPRESSION OF MICROBIAL PROTBINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US 10/10/369,493
CURRENT PLILING DATE: 2003-02-28
PRIOR FILLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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25.5%; Score 662.5; DB 15;
Best Local Similarity 32.4%; Pred. No. 3.5e-57;
Matches 169; Conservative 81; Mismatches 217;
EALFTGAGKNMADYVOIQKVEPHWRNFFE---
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Length 502,

DB 14;

25.9%; Score 672;

Query Match

ORGANISM: Staphylococcus aureus

TYPE: PRT

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROFEITES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20438
                                                                                                                                                                                                     292 RGRYTDNKLGGMQPSCSTFMLYLGINRRYEDLPHHQIYLSDNIRRLERPWVDDSALDETD 351
                                                                       237 KLAVELGVEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSPA 296
                                                                                                                                                                             297 SEL---KKMQRFEPSCSGLVLHLGVDRLYPQLAHHNFFYSDEPREHFDAVFKSHRLSD-D 352
                                                                                                                                                                                                                                                                          PTIYLVAPCKTDPAQAPAGCBIIKILPHIPH----LDPDKLLTABDYSALRERVLVKLER 408
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                                                                                                                                                                                                                                                                                                                                                                          409 MGLTDLRQHIVTEBYWTPLDIQAKYYSNQGSIYGVVADRFKNLG-PKAPQRSSELSNLYF 467
                                                                                                                                                                                                                                                                                                                                                                                                          70 ALFTGAGKAMADYVQLQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQFQRF 129
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                                                                                                       10 IVIGACLGCLSAAISLATAGFSVQLIEKNDKVGCKLNIMIKDGFTFDLGPSILTMPHIFE
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al Similarity 30.8%; Score 645; DB 15; Length 4
al Similarity 30.8%; Pred. No. 1.9e-55;
153; Conservative 103; Mismatches 218; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 20438, Application US/10369493 ; Publication No. US20030233675A1
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; ORGANISM: Rhodopseudomonas palustris
US-10-369-493-20438
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466 IGGAVHPGSGL 476
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Sest Local :
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Gao, Yongwei
APPLICANT: Glater, Steven C.
APPLICANT: Glater, Steven C.
APPLICANT: Gladman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: CARRY S.
APPLICANT: ELANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER: OF SEQ ID NOS: 47374
SEQ ID NO 18983
LENGTH: 499
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  EEFFASFDSHPSDYYG:TRLDPHYRIFFKONEGRRPGRDAPGLNVDTDGDTDUTPDREQ 128
                                                                             111 QRRELDKLGPGTYAQPQRFLDYSKNLCTETEAGYFAKGLDGF------WDLLKFYG 160
                                                                                                                          129 VKQVPDAYEPGAGDVLDDYLAQAKE-----NYEVGMEHFVKTDRPRVRDWMDPKLAE 180
                                                                                                                                                                             161 PLRSLLSFDVFRSMDQGVRRFISDPKLVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYG 220
                                                                                                                                                                                                             LWYVKGGMYGMAQAMEKLAVELGVEIRLDAEVSEIQKQDGRACAVKLAN--GDVLPADIV 278
                                                                                                                                                                                                                                                                                                                                                                               279 VSNMEVIPAMEKLL----RSPASELKKMQRFEPSCSGLVLHLGVDRLYPQLAFHNFFYSD 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 SY---RDLVLDDIAENTGVDLRDRIVVEERFSVSEFADRYNSHQGTALGLAHTLRQTALF 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 HPREHFDAVFKSHRLSDDPTIYLVAPCKTDPAQAPAG-CEIIKILPHIPHLDPDKLLIAE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 HLYKELFEEAGLNFADYVQLKRLEPYTRLKFWDGTQLDITSDLQSFKTQLATLRSDLPLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORFLDYSKNLCTETEAGYF----AKGLDGFW---DLLKFYGPLRSLLSFDVFRSMDQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 FDRW--YSEHI-RKYELGYKPYLAGPARSIFGYLRPDELMKF-----LSFRPWENLYQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 NORVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMP
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Matches 158; Conservative 112; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Anabaena PCC7120
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5-10-369-493-18983
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306 IEKSRYSMSLFVWYPGTKRRYEDVKHHTILLGPRYKELISDIFSRKVVAEDFSLYLHRPT 365
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                                                                                                                                 362 KTDPAQAPAGCELIKILPHIPHL--DPDKLLTARDYSALRERVLVKLERMGLTDLRQHIV 419
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                                                                                                                                                                                                                                                                                                        TEEYWTPLDIOAKYYSNOGSIYGVVADRPKNIGPKAPQRSSELSNLYFVGGSVNPGGGMP
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Best Local Similarity 31.2%; Pred. No. 1.2e-54;
Matches 155; Conservative 90; Mismatches 233; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Van Locn, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
ADDRESSEE: HOffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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NAME: POKCAS, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEPHONE: (201) 235-5801
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09547267
Patent No. US20020014371A1
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Hoffmann-La Roche
340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVTLSGOLVRDKIVAD 495
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MOLECULE TYPE: protein
US-09-547-267-5
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MEDIUM TYPE: Floppy
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CITY: Nutley
STATE: NJ
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US-09-547-267-5
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70 ALFTGAGKNWADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQFQRF 129

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190 ILNYPIKYVGSSPYDAPALMNILLPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVEIRLD 249
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                                                                                                                                                    RFEPSCSGLVLHLGVDRLYPQLAHENFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKT 363
                                                                                                                                                                                                       364 DPAQAPAGCEIIKILPHIPHL---DPDKLLTAEDYSALRERVLVKLERMGLTDLRQHIVT 420
                    HDYAEEVYRE---GYLKIGTTPFLKIGOMINAAPALMRLQAYRSVHSWVARFIQDPHLRQ
                                                                  250 AEVSEIOKODGRACAVKLANGDVLPADIVVSNMEVIPAMEKLL-----RSPASELKKMQ
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Matches 497
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Sequence 10, Appl
Sequence 10, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 17, Appli
Sequence 16, Appli
                                                                             Pebruary 29, 2004, 14:35:44 ; Search time 15.1029 Seconds
(without alignments)
1698.885 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-547-65-4

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US-09-91-726-15

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US-08-105-6-94-4

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Maximum Match 100%
Listing first 45 summaries
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effect score:
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TELEPHONE: 3128567180
TELEFAX: 3128564972
INPORMATION FOR SEQ ID NO:
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US-08-096-043-10
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241 ELGVEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSPASELK 300
                                                                 KMORFEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAP 360
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APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus, Indrani
APPLICANT: Yarger, James G
APPLICANT: Yarger, James G
APPLICANT: Yarger, James G
APPLICANT: Yar, Huei-Che B
TITLE OF INVENTION: Beta-Carotene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
SITREET: 200 E Randolph St
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.1%; Score 703.5; DB 1; Best Local Similarity 32.9%; Pred. No. 1.5e-63; Matches 166; Conservative 96; Mismatches 212;
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ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-JUL-1993
CLASSIPICATION: 435
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-007-1994
ATTORNEY/AGENT INFORMATION:
NAME: GABLOWAY, NO. 5530188val B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
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TELEPAX: 3128564972
INFORMATION FOR SEQ ID NO: 10: SECURNCE CHARACTERISTICS: LENGTH: 489 amino acids
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                                                                                         ORFLDYSKNLCTETEAGYFAKG---LDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFIS 183
                                                                                                                                                                                                                                                                           244 VEIRLDABVSEIQKODGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRS-PASELK-- 300
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67 IFBALFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDABTQRRELDKLGPGTYAQF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Amoco Corp., Patents and Licensing Dept STREET: 200 E Randolph St CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L
APPLICANT: Ausich, Rodney L
APPLICANT: Prinkhaus, Priedhelm L
APPLICANT: Proffitt, John H
APPLICANT: Proffitt, John H
APPLICANT: Proffitt, John H
APPLICANT: Prink Huel-Che B
ITILE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRAR APPLICATION DATA:
APPLICATION NUMBER: US/08/096,043
FILING DATE: 22-UUL-1993
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08096043
Patent No. 5530189
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ZIP: 60680-0703
COMPUTER READABLE PORM:
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APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Winharii, Indrani
APPLICANT: Yarger, James G.
APPLICANT: Yarger, James G.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huei-Che B.
TITLE OF INVENTION: Blosynthesis of Zeaxanthin and
TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Karr r. r.
                                                                                                                                                                                                                                                                                                                   126
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                                                                                                                                                                                                31;
                                                                                                                                                     27.1%; Score 703.5; DB 1; Length 489; 32.9%; Pred. No. 1.5e-63; tive 96; Mismatches 212; Indels 31
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Parent No. 5684238
GENERAL INFORMATION
APPLICANT: AMSICH, Rodney L.
APPLICANT: Brinkhaue, Friedhelm L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TOPOLOGY: 1489 amino acids TOPOLOGY: 1400 acid
                                                                                                                                                                                              Conservative
                 SEQUENCE CHARACTERISTICS
                                                                                           MOLECULE TYPE: protein 3-08-096-043-10
                                                                                                                                                                        Best Local Similarity
Matches 166; Conserv
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301 KMORFEPSCSGLVIHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDSPTIYLVAP 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 ORPLDYSKOLCTETEAGYFAKG----LDGFWDLLKFYGPLRSILSFDVFRSMDQGVRRFIS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 VEIRLDAEVSEIQKODGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRS-PASELK-- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVTDPSLAPPPCASFYVLAPVPHIGNAPLDWAQBGPKLRDRIFDYLBERYMPGLRSQLVT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 EEYWTPLDIQAKYYSNOGSIY-----GVVADRFKNLGFKAPQRSSELSNLYFVGGSV 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ALEALPTLAGRRMEDYVRLLPVKPFYRLCWESGKTLDYANDSPELEAQITQFNPRDVEGY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPKLVEILNYFIKYVGSSPYDAPALMNILPYIQYHYGLWYVKGGMYGMAQAMEKLAVELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EXTVVIGAGFGGLALAIRLQAAGIPTVLLEQRDKPGGRAYVWHDQGFTFDAGPTVITDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ORVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 27.1%; Score 703.5; DB 1; Best Local Similarity 32.9%; Pred. No. 1.5e-63; Matches 166; Conservative 96; Mismatches 212;
                                                                                                   CLASSIFICATION 435
CLASSIFICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-MAX-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/52,551
FILING DATE: 02-MAX-1990
ATIONERY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 NPGGGMPMVTLSGQLVRDKIVADLQ 497
                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-UJL-1993
CLASSFFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMOTICATION INPORMATION
TELEPRA: (312) 655-1500
TELEPRA: (312) 655-1501
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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67 IFEALFTGAGKNWADYVQIQKVEPHWRNFFZDGSVIDLCEDAETQRRELDKLGPGTYAQF 126
                                             296 RIERKSMSNSLFVLYPGLNQPHSQLAHHTICFGPRYRELIDBIFTGSALADDPSLYLHSP 355
                                                                                                                                                                                                                                        421 BEYWTPLDIQAKYYSNOGSIY-----GVVADRFKNLGFKAPQRSSBLSNLYFVGGSV 472
               301 KMORFEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFXSHRLSDDPTIYLVAP 360
                                                                                                                        361 CKTDPAQAPAGCELIKILPHIPHLDPDKILTAEDYSALRERVLVKLERMGLTDLRQHIVT 420
                                                                                                                                                                                                                                                                                           416 ORIFTROTSRHAWIAILGSLFIEPPSLTOGLFA-----ANATRHSNLYLVAAGT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ORVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMIKDGFTFDLGPSILIMPH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 31; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharii, Indrani
APPLICANT: Mukharii, Indrani
APPLICANT: Yen, Huei Che B
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
27.0%; Score 702.5; DB 1;
Best Local Similarity 32.9%; Pred. No. 1.9e-63;
Matches 166; Conservative 96; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERALING SYSTEM: PC-DOS/Mo-DOS SOFTWARE: Batentin Release #1.24 CURRENT AFPLICATION DATA:
APPLICATION NUMBER: US/08/06,043 FILING DATE: 22-UIL-1993 CLASSIFFCATION DATA:
APPLICATION NUMBER: US 07/785,568 PRIOR APPLICATION NUMBER: US 07/785,568 PRIOR APPLICATION NUMBER: US 07/785,568 TRIBOTANEY GABNY INFORMATION:
NAME: Galloway, NO. 5530189val B TRIBOTANEY APPLICATION INFORMATION:
TRIBOTANEY ASSOCIATION:
                                                                                                                                                                                                                                                                                                                                                                                                        465 HPGAGIPGVVGLAESTASLMIEDLQ 489
                                                                                                                                                                                                                                                                                                                                                              473 NPGGGMPMVTLSGQLVRDKIVADLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 8, Application US/08096043; Patent No. 5530189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      489 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ALBALPTLAGRRMEDYVRLLPVKPFYRLCWESGKTLDYANDSFELEAQITQFNPRDVBGY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 VEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLIRS-PASELK-- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 QRFLDYSKNLCTETEAGYFAKG---LDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFIS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 DPKLVBILNYPIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGWYGMAQAMEKLAVELG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KKTVVIGAGFGGLALAIRLQAAGIPTVLLEQRDKPGGRAYVWHDQGFTFDAGFTVITDPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 QRVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 489;
                                                                                                                                                         Sequence 8, Application US/08095726
Patent No. 5530188
GRNEAL INFORMATION:
APPLICANT: Busich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Proffitt, John H
APPLICANT: Yeager, James G
APPLICANT: Yea, Huei-che B
TITLE OF INVENTION: Beta-Carotene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.0%; Score 702.5; DB 1; Best Local Similarity 32.9%; Pred. No. 1.9e-63; Matches 166; Conservative 96; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: ILC.
STATE: ILC.
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-UUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-07-1991
ATTORNEY/ACENT INFORMATION:
NAME: GALLOWAY, No. 5530188val B
TELECOMMUNICATION INFORMATION:
TELEPROKE: 3128567180
TELEPROKE: 3128564972
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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Ogyrd bomo sapien
Ogyrd bomo sapien
Ogyrd arabidopsis
Ogyrd arabidopsis
Ogyrd arabidopsis
Ogyrd arabidopsis
Ogyrd caulobacter
Ogyrd rhizobium 1
Ogyrd sulfolobus
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Q8yqs5 anabaena sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9ry57 deinococcus
                                                                                   February 29, 2004, 14:33:49; Search time 43.7446 Seconds (without alignments) 3837.172 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                              2768
1 MSAFLDAVVVGSGHNALVSA.....ALSDSRRGKASQWMRRSSRS 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                     1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                 tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                     1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                          st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         1 protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q55808
Q8YQ55
Q9BRQ1
Q8NZH3
Q8VYK3
Q9FGZ1
Q98FP6
Q9A3T1
Q98FP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0974W1
08PJ01
089FW3
098BS8
061196
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_bunda:*
sp_human:*
sp_human:*
sp_nretrebrate:*
sp_mammal:*
sp_mnc:*
sp_organelle:*
sp_phage:*
sp_plant:*
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sp_bacteriap:*
sp_archeap:*
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sp_vertebrate:*
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ximum DB seq length: 200000000
                                                                                                                                                 US-09-941-947A-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                     SPTREMBL 25:*
                                                                                                                                                              rfect score:
                                                                                                                                                                                                          oring table:
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Q93hp2 streptomyce	Q93HP2	16	513	9.4	261	45	
Q7v6u2 prochloroco	Q7V6U2	16	520		262.5	44	
-	Q9ZGE4	Ŋ	517	9.6	264.5	43	
Q55455 synechocyst	055455	16	501	•	270	42	
Q7txh1 mycobacteri	Q7TXH1	9	480		273	41	
	Q9EXL0	~1	507	9	274	40	
Q9rix9 streptomyce	Q9RIX9	16	523		275	39	
	Q83X01	N	588	10.0	276.5	38	
053244 mycobacteri	053244	91	480	10.2	283	37	
	Q70032	16	473	10.3	284	36	
	006826	16	473	10.3	284	35	
	Q82NF9	16	471	10.6	293.5	34	
Q8nt31 corynebacte	QBNT31	16	471	10.7	296.5	33	
В	Q9K566	N	499	10.9	302	35	
	Q82NN7	16	533	11.2	309	31	
	007794	16	536	11.4	314.5	30	
	Q7TVK4	16	536	11.5	318.5	53	
Q821s4 streptomyce	0825.84	16	472	12.1	335	28	
	Q8XYC4	16	535	12.2	336.5	27	
-	Q92BG4	16	472	12.3	340	26	
O9khel streptomyce	Q9KHE1	7	489	12.6	348	25	
	Q8FSA2	16	482	12.6	349.5	24	
Q9eyi5 streptomyce	Q9EYIS	N	472	13.0	359	23	
	098BS6	16	523	13.1	363.5	22	
Q9k4i4 streptomyce	Q9K414	16	540	13.9	385.5	21	
O9rvf5 deinococcus	Q9RYP5	16	489	15.1	418	20	
	ODDX60	17	538	15.9	439.5	19	
	Q9L187	16	539	16.0	441.5	18	
Q82pc2 streptomyce	Q82PC2	16	544	16.0	443	17	

ALIGNMENTS

```
[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=RI / ATCC 13339 / DSM 20539 / NCIB 9279; STRAIN=RI / ATCC 13339 / DSM 205366; Hickey B.K., Peterson J.D., White O., Eisen J.A., Heidelberg J.F., Hickey B.K., Fichardson D.L., Dodson R.J., Haft D.H., Grimm M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamethevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Mintcon K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 31.1%; Score 859.5; DB 16; Length 511; Best Local Similarity 39.7%; Pred. No. 1.9e-45; Matches 207; Conservative 80; Mismatches 208; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                               Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             511 AA; 56527 MW; 7DCC3FB1D79EE9CD CRC64;
                                                                                           Last sequence update)
Last annotation update)
                                         511 AA
                                                                    01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequel-JUN-2003 (TrEMBLrel. 24, Last annopytoene dehydrogenase, putative.
                                       PRT;
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ProDom; PD139017; Phytn dehydro; 1.
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Science 286:1571-1577(1999).
EMBL, AE001872; AAF09686.1; -.
PIR; B75561; B75561.
                                       PRELIMINARY;
                                                                                                                                                                  Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
SEQUENCE 511 AA;
                                                                                                                                                DR0093.
                                       Q9RY57
RESULT 1
Q9RY57
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InterPro; IPR000759; Adrndx_reductase.
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                                                                                                                                               DALLDEYFDSEALKAALAWFGAQSGPPMSEPGTAPMVGFAALMHVLPPGRAVGGSGALSA 238
                                                                                                                                                                                                            291 ---PAEYVPSAARNVRVGNGFGMILRLALSEKVKYR-HHTEPDSRIGLGLIKNERQIMO 346
                                                                                                                                                                                                                                                                                                                                                                                                      GYGEYLAGQPITDPPLVAMSFSAVDDSLAPPNGDVLWLWAQYYPFELA-TCSWETRTAEA 405
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                                                                                                                                                                                                                                                        ALASRMAVDGATVALGDGVTSIR-RNSNHWTVTTESGREVHARKVIAGCHILTTLDLLGN 297
                                                                                                                                                                                                                                                                                     233 ALRRATEABGGEVFTDAPVKBILVKDGKAQGIRLESGETYTARAVVSGVHILTTANAL-- 290
                                                                                                                                                                                                                                                                                                                    GGFDRITLDHWRRKIRVGPGIGAVLRLATSALPSYRGDATTRESTSGLQLLVSDRAHLRT 357
                                                                                                                                                                                                                                                                                                                                                                                   AHGAALAGELPPRPAVLGMSFSGIDPTIAPAGRHQVTI,WSQWQPYRLSGHRDWASVAEAE 417
                                                               HSGIIEELGLGAHGLRYIDCDPWAFAPPAPGTDGPGIVF-HRDLDATCQSI-ERACGTKD 123
                                                                                          W?PIVRELELTRHGLHYLEVDPMFHA----SDGBTPWFIHRDAGRTIRELDEKFPG--Q 117
 65
                                64
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Kaneko T., Sato S., Kotani H., Tanaka A., Asamoto S., Kimura T., Miyajima N., Hirosawa M., Sujura M., Sasamoto S., Kimura T., Myajima N., Hirosawa M., Muraki A., Nakazaki N., Naruo K., Okumura S., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Yamada M., Yasuda M., Tabata S.; Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; Takeuchi T., Perome of the unicellular cyanobacterium
6 DAVVVGSGHNALVSAAYLAREGWSVEVLEXDTVLGGAVSTVERFPGYKVDRGSSAHLMIR
                  124 ADAYRRFVAVWSERSRHVMKAFSTPPTGSNLIGAFGGLATARG-----NSELSRQFLAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADRIVGEMEARAPGFTDSVLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of the genome of the unicellular cyanobacterium Symechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
BME.; D64004; BAA105611; -.
PME.; O60004; S76417; S76417.

CO: GO: GO:0006118; P:electron transport; IEA.
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MEDLINE=96127529; PubMed=8590279;
MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
Sequence analysis of the genome of the unicellular ryanobacterium
Sequence postitoms postitoms 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHRVPGADGLYLTGASTHPGGGVSGASGRSAARIALSDSRR 519
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01-NOV-1996 (TrENBLrel. 01, Created)
01-NOV-1996 (TrENBLrel. 01, Last sequence update)
01-OCT-2003 (TrENBLrel. 25, Last annotation update)
Phytoene dehydrogenase.
CRTE OR SLR0088.
Synechocystis sp. (strain PCC 6803).
Synechocystis sp. (strain PCC 6803).
NCBL_TaxID=1148;
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GSGALSAALASRMAVDGATVALGDGVTSIR-RNSNHWTVTTESGREVHARKVIAGCHILT 290
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                                                                                                                                                                                                                                                                                                                                                                        62 LMIRHSGIIEELGLGAHGLRYIDCDPWAFAPPARGTDGPGIVFHRDLDATCQSIERACGT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROFLAPGDALLDEYFDSEALKAALAWFGAQSGPPMSEPGTAPMVGFAALMHVLPPGRAVG 231
                                                                                                                                                                                                                                                                                                                        64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GTGALITEALVKLVQAQGGKILTDQTVKRVLVENNQAIGVEVANGEQYRAKK----GVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 DAVVVGSGHNALVSAAYLAREGWSVEVLEXDTVLGGAVST----VERFPGYKVDRGSSAH
                                                                                                                                                                                                                                                                                                         122 KDADAYRRFVAVWSERSRHVMKAFSTPPTG-----SNLIGAFGGLATARGNSELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 TLD-----LLGNGGFDRTTLDHWRR-KIRVGPGIGAVLRL--ATSALPSYRGDATTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 NIDARRIFLQLVEPGALAKVNQNLGERLERRTVNNNEAILKIDCALSGLPHFTAMAGP-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STSGLOLLVSDRAHLRTAHGAALAGELPPRPAVLGMSF-SGIDPTIAPAGRHOVTLWSQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WQPYRLSG------HRDWA-SVAEAEADRIVGEMEAFAPGFTDSVLDRFIQTPRDIESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCMIGGNVMHVEMSLDQMMLWRPLPELSCHRVPGADGLYLTCASTHPGGGVSGASGRSAA
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                                                                                                                                                                                                                         48;
                                                                                                                                                                       24.9%; Score 688; DB 16; Length 5;
31.9%; Pred. No. 9.7e-35;
ive 97; Mismatches 229; Indels
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NCBL TaxID=103690;
                                                                                                                          542 AA; 59400 MW; CD673A75E5CE7928 CRC64;
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1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein All3744.
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InterPro; IPR000205; NAD BS.
InterPro; IPR008151; PbyTn debydro.
PRINTS; PR00419; ADXRDTASE.
ProDom; PD139017; Phytn_dehydro; 1.
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MEDLINB=21595285; PubMed=11759840;
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                                                                                                                                                                       Query Match
Best Local Similarity 31.95
Matches 175; Conservative
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                                                                                                  Complete proteome.
SEQUENCE 542 AA;
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01-MAR-2002 (
01-MAR-2002 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 ATTERSTSGLOLLVSDRAHLRTAHGAALAGELPR-PAVLGMSFSGIDPTIAPAGRHQVT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWSQ-WQPYRLSGHR-----DWASVABAE-ADRIVGEMBAFAPGFTDSVLDRFIQTPR 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 --ILTTLD-----LLGNGGFDRTTLDHWRR-KIRVGPGIGAVLR--LATSALPSYRGD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHKDEYLVGSILIADSVAHVEQAHSKCTLGEIPDSDPSMYVVMPSYLDPTLAPSGKH--T 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

23.9%; Score 660.5; DB 16; Length 565;
Best Local Similarity 31.7%; Pred. No. 5.3e-33;
Matches 174; Conservative 94; Mismatches 224; Indels 57;
"Complete genomic sequence of the filamentous nitrogen-fixing
           Cyanobacterium Anabaena sp. strain PCC 7120.",
DNA Res. 8:205-213(2001).

EMBL; AA12273.

BIR; AA12273.

GO; GO:0008237; F:metallopeptidase activity; IEA.

GO; GO:0008207; F:motiallopeptidase activity; IEA.

GO; GO:0008207; F:anc ion binding; IEA.

GO; GO:0006508; P:anc ion binding; IEA.

GO; GO:0006508; P:electron transport; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR000759; Pept M_Zn_BS.

InterPro; IPR0001509; Pept M_Zn_BS.

InterPro; IPR0001100; Pyr reductase.

InterPro; IPR001100; Pyr reductase.

PRINTS; PR00411; PWDRDTASE.

PRINTS; PR00411; PWDRDTASE.

PRODOM; PD139017; Phytn dehydro; I.

PRODOM; PD139017; Phytn dehydro; I.

PRODOM; PD139017; ENVERTASE.

PRODOM; PD139017; ENVERTASE.

PRODOM; PD139017; ENVERTASE; I.

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581 AA.

PRT;

PRELIMINARY;

Q9BRQ1

Q9BRQ1; 01-JUN-2001 (TrEMBLrel. 17, Created)

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435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMHVLPP-----GRAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWT--V 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 TTESGREVHARKVIAGCH-----ILTTLDILGNGGFDRTTLDHWRRKIRVGFGIGAVLR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 PQ-İYTDİBİKKHGLKLHLRNPYSFTPML--BEGAĞSKVFRCLLLGTDMAENQKQIAQ-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 GTKDADAYRRFVAVWSERSRHVMKAFSTPPTG-----SNLIGAFGGLATARG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 -NSELSROF---LAPGDALLDEYFDSEALKAALAW---FGAQSGPPMSEPGTAPMVGFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 LHHVMGGLEGMQGAMGYVQGGMGALSDALASSATTHGASIFTEKTVAKVQVNSEGCVQGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 LATSALPSY-----RGDATTRESTSGLQLLVSDRAHLRTAHGAALAGELPPRPAVLGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 SPSGIDPTIAPAGRHQVTLWSQWQPYRLSGHRDW-ASVABABADRIVGBMBAFAPGFTDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 581;
                                                                                                                                                                                                                                                Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (APR-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006431; PAH06431.1; -.
R GO; GO:0006418; P:electron transport; IEA.
R GO; GO:0066118; P:electron transport; IEA.
R InterPro; IPR001100; Pyr redox.
R InterPro; IPR001100; Pyr redox.
R PRINTS; PR00411; PNDRCTASEI.
R ProDom; PB139017; Phytn_dehydro; 1.
R Hypothetical portein.
Q SEQUENCE 581 AA; 63027 MW; 47B7F14CB0A20ED CRC64;
                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxiD=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 22.6%; Score 624.5; DB 4; Length Local Similarity 33.0%; Pred. No. 9.5e-31; Length les 185; Conservative 81; Mismatches 226; Indels
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
U-JUN-2003 (TIEMBLrel. 24, Last annotation update)
Hypothetical protein.
Homo sapiers (Human).
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   TISSUE=Uterus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMHVLPP------GRAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWT--V 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 TTESGREVHARKVIAGCH-----ILTTLDLLGNGGFDRTTLDHWRRKIRVGPGIGAVLR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 VLEDGTEVRSKOMVLSNTSPQITFLKLTPQSWLPBRFLERISQLDTRSPV-----TKIN 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | | | : | | | : | | | 379 VAVDRIPSFLAAPNAPRGQPLPHHQCS-IHLNCBDTLLLHQAFEDAMDGLPSHRPVIBLC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 IPSSLDPTLAPPGCHVVSLFTQYTEYTLAGGKAWDEQERDAYADRVFDCTEVYAPGFKDS 497
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                                                                                                                                                                                 | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 
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                                                                                               Euteleostomi;
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                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ll protein.
581 AA; 63067 MW; 7029E211983920EE CRC64;
      Last annotation update)
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Homo sapiens (Human).
      (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 HSGIIEELGLGAHGLRYIDCDPWAFAPPAFGTDGPGIVFHRDLDATCQSIERACGTKDAD 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LRIATSALPSYRGDATTRESTSGLQLLVSDRAHLRTAH-GAALAGB---- 366
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Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
Chen M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Linn J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Lee J.M., Linn J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Rang C.J., Torluni M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
Shinnozaki K., Davis R.W., Theologis A., Ecker J.R.;
Shinnozaki K., Davis R.W., Theologis A., Ecker J.R.;
EMBL, AV070478; AAL49944.1;
EMBL, AV070478; AAL49944.1;
EMBL, AV070478; AAL49944.1;
EMBL, BT068815; AAUG6750.1;
InterPro; IPR00815; Phytin dehydro.
R. ThrerPro; IPR00815; Phytin dehydro:
R. Probom; PD139017; Phytin dehydro; 1.
R. Probom; PD139017; Phytin dehydro; 1.
R. Probom; PD139017; Phytin dehydro; 1.
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                                                                                                               ATSG49550/K6M13-10.
Arabidopais thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                            Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Neuyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M. Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamanıra Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Arabidopsis cDNA clones.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
(TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Matches 181, Conservative
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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EMBL; AP003002; BAB50521.1; -
EMBL; AP003002; BAB50521.1; -
GO; OGO1016919; F: Oxidoreductase activity; IEA.
GO; GO:0006118; F: Oxidoreductase activity; IEA.
InterPro; IPR002937; Amino oxidase.
InterPro; IPR001815; Phytn dehydro.
InterPro; IPR001815; Phytn dehydro.
PR001993; Amino_oxidase.
InterPro; IPR003042; Rng mnoxygenase.
Pfam; PF01593; Amino_oxidase; 1.
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ProDom; PD139017; Phytn_dehydro; 1.
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MEDLINE=21082930; PubMed=11214968;
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01-OCT-2001 (TYEMBLrel.
01-OCT-2003 (TYEMBLrel.
Phytoene dehydrogenase.
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SEQUENCE 521 AA
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Matches 188;
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   417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FLAPGDALLDEYFDSEALKAALAWFGA-QSGPPMSEPG 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 S----GYVLLHHVMGETDGEKGIWSYVEGGMGSVSMALANAAKBAGAEIFTNAEVSEI-- 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 -----LRLATSALPSYRGDATTRESTSGLQLLVSDRAHLRTAH-GAALAGE---- 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 by covered by sixty P1 and TAC
                       CHDSENGLESRRPVIEMTIPSTLDNTISPPGKHVINLFIQYTPYKDSDGSWEDPTYERF
-----IPPRPAVLGMSF-SGIDPTIAPAGRHQVTLWSQWQPYRLS-GHRDWASVAEAE
                                                                       ADRIVGEMEAFAPGFTDSVLDRFIQTPRDIESELGMIGGNVMHVEMSLDOMMEMRPLPEL
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                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thallana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=COlumbia;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu B., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.3%; Score 562.5; DB 10; Length 647; 30.9%; Pred. No. 7.9e-27; Live 78; Mismatches 213; Indels 109;
                                                                                                                                          SCHRVPGADGLYLTGASTHPGGGVSGASGRSAARIALSDSRR 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; ABO23033; BAB10768.1; -.
InterPro; IPR00205; NAD BS.
InterPro; IPR008151; PhyEn dehydro.
ProDom; P0139017; PhyEn dehydro; 1.
SEQUENCE 647 AA; 70687 MW; 3DC4C5918A8D0PC6 CRC64;
                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT--2003 (TrEMBLrel. 25, Last annotation update)
Phytoene dehydrogenase-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 30.9
les 179, Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tabata S.;
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DNA Res. 7
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Matches
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ADRIVGEMEAFAPGFIDSVLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPEL 477
                                          119 CGTKDADAYRRFVAVWSE-----RSRHVMKAFST--PP--TGSNLI--GAFG--GLATA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 YGEVLIGASPSEQSAWKDLRAQLLRYAGILKPFLITRRPPDLAGMSLMETASLGQTALALK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLGKEDMRDFLRVILAMVAD-LLDEQLRDDRLKGLLAFDATLGSHLGPRSPTSLLGLYYR 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 TAPMYGFAALMHYLPPGRAVGGSGALSAALASRMAVDGATVALGDGYTSIRRNSNEWT-V 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto & Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic back
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Last annotation update)
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66 HSGIIBELGLGAHGLRYIDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSIERACGTKDAD 125
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                                                                                                                                                                                                                                                                                   | | : | | : | | | | 353 ASHHQSGIVIAPSLDYMDAAY-RDAKGQGIS----KAPIVEMLIPSSLDTSLAPPGGHVA 407
                                                                                                                                                                                                                                                                                                                                                               239 GHÄVGGMGAITQAMAKACBAAGVBILLDAPVBAVHIDGGKAAGVQLVDGRQIMAPIVSAN
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                                                                                                                                                                           286 CH-ILTTLDLIGNGGFD---RTTLDHWRRKIRVGPGIGAV-LRLATSALPSYR---GDAT
                                                                                                                                                                                                             299 VNPALLYKKLVPPSALTPDFRKAVDGYKN-----GSGTFRMNVALSELPSFTCLPGKET
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                 LAPGDALLDEYFDSBALKAALAWFGAQSGPPMSBPGTAPMVGFAALMHVLPP-
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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SEQUENCE 539 AA; 59427 MW; 9DD78A7115A50BED CRC64;
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Last annotation update)
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InterPro; IPR008151; Phytn dehydro
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MEDLINE=21082930; PubMed=11214968;
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DNA Res. 7:331-338(2000)
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-- Tocal Similarity
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01-JUN-2003
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                                                                                                                                                                                                                                                                                                                            181
                                                                                        279 TLGTGEELRARTVVSAINPATTFLDEVGPREIDTGFVRKV-----KNIRM-KGDAAKLHE 332
                                                                                                                                          ATSALPSYRG-DATTRESTSGLQLLVSDRAHLRTAHGAALAGELPPRPAVLGMSFSGI-D 382
                                                                                                                                                                                 33 ALDRSPOFTGADAAHK---GRLVIAPSPDHVERAFNPCKYGEFSPEP-VZEITLPSLAD 388
                                                                                                                                                                                                                          PTIAPAGRHOVTLWSOWOPYRLSGHRDWASVAEABADRIVGEMEAFAPGFTDSVLDRFIO 442
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                                                              TIESGREVHARKVIAGCHILIT-LDLLG----NGGFDRITLDHWRRKIRVGPGIGAVLRL 324
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X MEDLINE-21173699; PubMed=11259647;

X MEDLINE-21173699; PubMed=11259647;

A Distribution W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

A Zisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

A Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

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I Complete genome sequence of Caulobacter crescentus.";

I Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

R EMBL, AE005975; AAK25083.1; --.
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LAGEAGGAAGAQVLPQ----GGMGAVVAAIRABABEKAGVTIRTSVAAAKIIVEKGHAVGV
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Caulobacter crescentus.
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteracea; Caulobacter.
Caulobacteracea; Caulobacter.
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 AA
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01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequen
01-UUN-2003 (TrEMBLrel. 24, Last annota
Phytoene dehydrogenase-related protein.
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ProDom; PD139017; Phytn dehydro; 1.
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Matches 180; Conservative
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SEQUENCE 543 AA;
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518 AA; 57944 MW; B538CF7B74ACD72B CRC64;

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SEQUENCE FROM N.A.
STRAIN=ATCC 35092 / DSM 1617 / P2;
STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
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Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
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                                   AYDRYARDVIRQCRFIQPLIMRIAPDPISFKPRDIGBLLYLGKKFAGLSABEMALTLRFW 178
                                                                                                                                                                     279
AYRRFVAVWSERSRHVMK-AFSTPPTGSNL----IG-----AFGGLATARGNSELSRQ 173
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                                                                                                                                                                   ----GRAVGGSGALSAALASRMAVDGATVALG---DGVTSIRRNSNHWTVTTESGREVHA
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Sulfolobus.
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BMBL; AR06842; AAK42566.1;
PIR; 930413; G90413.
G0; G0:0015036; F:disulfide oxidoreductase activity; IRA.
G0; G0:0015036; F:disulfide oxidoreductase activity; IRA.
InterPro; IPR00132; Palectron transport; IRA.
InterPro; IPR001327; PAD pyr_redox.
InterPro; IPR00205; NAD BS.
InterPro; IPR003151; Phytn_dehydro.
InterPro; IPR003151; Phytn_dehydro.
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phytoene dehydrogenase related protein.
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ProDom; PD139017; Phytn_dehydro; 1.
Complete proteome.
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PRINTS; PR00368; FADPNR.
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Sulfolobus solfataricus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 IIVSNADPKTTFFKLLRNAELEEDFL----RRVRALKNVGVSFKIVGYLEELPDFGNGKS 338
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                                                                                                           61
                                                                                                                                              65 RHSGIIRBLGLGAHGLRYIDCDPWAFAPPAPGTDGPGIVFHRDLDATCOSIERACGTKDA
                                                                      5 LDAVVVGSGRNALVSAAYLAREGWSVEVLENDTVLGGAVSTVERFPGYKVDRGSSAHLMI
                                                                                           117 KNYKKWVKFWDLFAEMADFFM--INPPPHIDEASNLINIFRG----NVNEELALSFLRTF
                                                                                                                                                                                                                                                                                             175 LAPGDALLDEYFDSEALKAALA---WFGAOSGPPMSEPGTAPMVGFAALMHVLPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 TRESTSGLQLLVSDRAHLRTAHGAALAGELPPRPAVLGMSFSGIDPTIAPAGRHQVTLWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 VMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGASTHPGGGVSGASGRSAARIALSDS
                                                                                                                                                                                                                     125 DAYRRFVAVW---SERSRHVMKAFSTPP---TGSNLIGAFGGLATARGNSELS----RQF
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                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                       26;
Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                   ; Pred. No. 4e-25;
93; Mismatches 226;
DB 17;
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19.3%; Score 533; 30.9%; Pred. No. 46
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STRAIN=JCM 10545 / 7;
MEDLINE=21456156; PubMed=11572479;
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                                     Matches 168; Conservative
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                 Similarity
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513 RKG 515
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Query Match
                     Local
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Q974W1
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MEDLINE=22022145; PubMed=12024217;
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Matches 182;
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                                                                                                                                                                                                                                                                         61 FSLFRKK-IIDDLRLYDFGLKVYLKDPSLFVPFG---QNKSITIWTSTKKTVKBIEK-FS 115
                                                                                                                                                                                                                                                                                                  TYDADAYRRFV---AVWSERSRHVWKAFSTP---PTGSNLIGAFGGLATARGNS-ELSRQ 173
                                                                                                                                                                                                                                                                                                                        116 KKDAOSYEKFVKILEIFSEIADFLI--INKPINLSEABELIKLFKGLNVDENTALTIARM 173
                                                                                                                                                                                                                                                                                                                                                 FLAPGDALLDEYFDSBALKAAL---AWFGAQSGPPMSEPGTAPMVGPAALMHVLPP---- 226
                                                                                                                                                                                                                                                                                                                                                                         FFODGKSFLDEFFESEEVKSALIEDSVVGTYASP--STPGTA----YVLLHHNFGEVNGV 227
                                                                                                                                                                                                                                                                                                                                                                                                                 228 KGAWGYVEGGMGNVSNALRRVABYYGABIFLNSEVDBIIVRNGBAKGIKLKNGKIIESKI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIAGCHILTT-LDLLGNGGFDRTTLDHWRRKIRVGPGIGAVLRL--ATSALPSYRGDATT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 RESTSGLOLLVSDRAHLRTAHGAA------LAGELPPRPAVLGMSFSGIDPTIAPA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389 GRHQVTLWSQWQPYRLSGHRDWASVAEAEADRIVGEMEAFAPGFTDSVLDRFIQTPRDIE 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 SELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGASTHPGGGVSGASGRS 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GRAVGGSGALSAALASRMAVDGATVALGDGVTS-IRRNSNHWTVTTESGREVHARK 281
                                                                                                                                                                                                                          1 MYRIYDVVIIGGGHNGLVAASYLAKBGLKVAVFERRNVIGGATVTEBLWPGIKVSTASYV 60
                                                                                                                                                                                                  1 MSAFLDAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVBRFPGYKVDRGSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                     517;
R EMBL, AP000982; BAB65546.1; -. RGO: GO: 0006118; P:electron transport; IEA.

R GO: GO: 0006118; P:electron transport; IEA.

R InterPro; IPR000205; Ada BS.

R InterPro; IPR00815; Phytn dehydro.

R InterPro; IPR00815; Phytn dehydro.

R RINTS; PR00891; RABGDIRAP.

R RINTS; PR00891; RABGDIRAP.

R PRINTS; PR00891; RABGDIRAP.

R Probom; PD139017; Phytn dehydro; 1.

R Probom; Protecn; Complete protecome.

SEQUENCE 517 AA; 57965 MW; E129448C73AZ7AZ4 CRC64;
                                                                                                                                                                             Indels
                                                                                                                                                     Length
                                                                                                                                                   19.0%; Score 525; DB 17; 30.1%; Pred. No. 1.3e-24; iive 89; Mismatches 228;
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Last annotation
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STRAIN=306 / ATCC 13902 / XV 101;
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NCBI_TaxID=92829;
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                                                                                                                                                Query Match
Best Local Similarity 30.1%
Matches 165; Conservative
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XAC2744.
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A Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Audilinas-Zorzias).

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F. Ciapina L.P., Cararotte G., Cannavan F., Cardozo J., Chambergo F. Ciapina L.P., Reinia J.B., Ferreira L.L., Cursino-Santos J.R., El-Dorry H., Formighieri E.P., Franco M.C., Ferreira R.C.C., Ferro M.I.T., Roringineri E.P., Franco M.C., Greegio C.C., Gruber A. M. T., Martins E.C., Macidanis J., Marcher R.P., Lemos E.G., Moro D.H., Martins E.C., Macidanis J., Mandeira A.M. B.M., Miyaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Spinola L.A.F., Rossi A., Sana J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teiseira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Comparison of the genomes of two Xanthomonas pathogens with differing L. Host specificities. F. The Genomes of two Xanthomonas pathogens with differing R. Rubbi, Asoliyaly AAM37589 1.

R. Rubbi, Asoliyaly AAM37589 1.

R. Rubbi, Asoliyaly Phytn dehydro. The Reise M. R. Rubbi, Abully Phytn dehydro. The Proposity Phytn dehydro. The Complete protecome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456
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SEQUENCE 539 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 AV-LRLATSALPSYR-----GDATTRESTSGLOLLVS----DRAHL-RTAHGAALAGELP 368
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                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-22484999 PubMed=12597275;
Maneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Sohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada h
Tabata S.;
"Complete genomic sequence of nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.0%; Score 497; DB 16; Length 545; 30.5%; Pred. No. 7.4e-23; ive 77; Mismatches 217; Indels 102;
                                                                                                             Bactéria, Protechacteria, Alphaprotechacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
NCBI_TaxiD=375,
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                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                             Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
BMBL, AP005959; BAC51851.1; -
GO; GO:0016491; F:oxidoreductase activity;
GO; GO:0006118; P:electron transport; IEA.
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GO; GO:0006118; P:electron transport; IE
InterPro; IPR000205; NAD BS.
InterPro; IPR00103; Pyridine_redox_2.
PRINTS; PR00469; PNDRDTASEII.
Complete protecome.
SEQUENCE 545 AA; 58480 MM; 0B2DDC6F3
    Created)
  24,
24,
25,
              01-JUN-2003 (TEBMBLFE). 24,
01-OCT-2003 (TEBMBLFE). 25,
BLR6586 protein.
BLR6586.
Bradyrhizobium japonicum.
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Best Local Similarity 30.5%
(TrEMBLrel. 2 (TrEMBLrel. 2 (TrEMBLrel. 2
  01-JUN-2003
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60 AHLMIRHSGIIEELG--LGAHGLRY---IDCDPWAFAPPAPGTDGPGIVFHRDLDATCQS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAILWARF23099;
MEDLINE=21062930;
PubMed=11214966;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Natanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | ::||: BRENPNLVGGDQVCGSHHLAQNFLFRPARGYAGWNTP-VGNLHLTGAATWPGAGTGAASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSAFLDAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVE-RFPGYKVDRGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 IERACGTXDADAYRRFVAVWSERSRHVMKAFSTPPTGSNLIGAFGGLATARGNS---ELS
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                                                                                                                                                                                                                                 auizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
Phyllomarib=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.9%; Score 469; DB 16; Length 5 29.8%; Pred. No. 3.9e-21; ive 81; Mismatches 238; Indels
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24, Last annotation update)
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InterPro; IPR008151; Phytn dehydro.
ProDom; PD139017; Phytn dehydro; 1.
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Complete proteome.
SEQUENCE 524 AA;
                                                                                                                                01-0CT-2001
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Search completed: February 29, 2004, 14:51:13 Job time: :48.7446 secs

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using sw model 4 protein - protein search,

February 29, 2004, 14:27:18 ; Search time 8.96629 Seconds (without alignments) 3089.496 Million cell updates/sec

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US-09-941-947A-38 2768 1 MSAFLDAVVVGSGHNALVSA.....ALSDSRRGKASQWMRRSSRS 532 .tle: rfect score: quence:

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BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues sarched:

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stal number of hits satisfying chosen parameters:

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt 42:* tabase: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ption						cercospora										myxococcus	myxococcus			synechocyst	-			-						mus n	рошо	homor	homo
Descri	P06108	Q10555	P54971	P54981	001671	P48537	P21334	P54980	P21685	002861	P22871	P17059	P54982	P54978	P17054	P54979	P56601	09hv£1	024163	Q55629	053230	Q04829	Q05355	050311	P12255	094526	032434	P55349	P19471	09 2008	651960	P98161	014686
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178 GDALLDBYFDSEALKAALAWFGAQSGPPMSEPGTAPMVGFAALMHVLPPGRAVGGSGALS 237

124 ADAYR----RFVAVWSERSRHYWKAFSTPPTGSNLIGAFGGLATARGNSELSROFLA--P 177

64 IRHSGIIEELGLGAHGLRYIDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSIERACGTKD 123

2 LDAVVVGAGPNGLTAAVELARRGFPVAVFEAQGTVGGGARTEELTLAGFRHDPCSAAHFL

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5 LDAVVVGSGHNALVSAAYLARBGWSVEVLEKDTVLGGAVSTVE-RFPGYKVDRGSSAHLM

Query Match 11.8%; Score 327; DB 1; Length 469; Best Local Similarity 27.6%; Pred. No. 8.6e-15; Matches 147; Conservative 64; Mismatches 223; Indels 98; Gaps

QByv57 anabaena sp Q59160 agrobacteri P26661 h genome po Q03133 saccharopol P29905 paracoccus P13608 bos taurus QBkcw2 chlorobium Q94012 aeropyrum p Q04616 rhomo sapien Q9ubn7 homo sapien Q9566 homo sapien Q9566 homo sapien	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	3) 1te)	Etepcomyces livradas. Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. [1] TaxID=1916;	ng for XP55, a major 18.°;	produced through a collaborattics and the EMBL outstations on as its content is in no '. Usage by and for commerc. http://www.isb-sib.ch/announ	dro. ; 1. :2AE7533G7C701CB CRC64;
YL24 ANASP OOXA AGRT4 POLG HCVU8 ERY3 SACER NOXY PARDE PGCA BOVIN DLDH CHLTE DRHB AERYE HDAG HUYAN SHX1 HUYAN	ALIGNMENTS PRT: 469 P	ruence updat	ctinobacteridae etaceae; Strept	chardt T.; the gene codin comyces lividan 1926(1987).	pyright. It is prod e of Bioinformatics Institute. There utions as long as is not removed. U agreement (See htt) @isb-sib.ch).	reductase. lehydro. rdro; 1.
4.2 1683 1 4.2 3033 1 4.2 3033 1 4.2 3172 1 4.2 3466 1 3.9 2669 1 3.9 206 1 3.9 206 1 3.9 206 1 3.9 206 1 3.9 206 1 3.9 206 1 3.9 206 1 3.9 206 1 3.9 206 1	STANDARD:	Creat Last Last	ilvidans. :inobacteria; Actinobactae; sae; Streptomycetaceae;	SEQUENCE FROM N.A. STRAIN-66 / 1326; STRAIN-86 / 1326; BUEDINE=8721086; PubMed=3453116; Burnert W.V., Henner J., Eckhardt T.; "The nucleotide sequence of the gene coding for XP55, secreted protein from Streptomyces lividans."; Nucleic Acids Res. 15:3926-3926(1987).	IS-PROT entry is copyright. It is the Swiss Institute of Bioinform bean Bioinformatics Institute. The non-profit institutions as long and this statement is not remover requires a license agreement (See n email to license@isb-sib.ch).	CAA68336.1; - 509189. 000759; Adrndx 000205; NAD BS 0008151; Phytn 19; ADXRDTASE. 117; Phytn deh;
34 117.5 335 117 337 117 338 115 339 115 440 109 441 108 444 108 45 107.5	NT 1 STRL1 P49 STR11	P06108; 01-JAN-1988 01-JAN-1988 01-OCT-1996 P49 protein. P49.	Streptomyces ilvidans Bacteria; Actinobacte Streptomycineae; Stre NCBI_TaxID=1916;	SEQUENCE FROM N.A. STRAIN-66 / 1326; MEDLINE=87231086; Burnett W.V. Henn "The nucleotide se secreted protein f Nucleic Acids Res.	This SWISS-PR between the the European use by non- modified and entities requ or send an em	MBL; Y00 IR; Y00 iterPro; iterPro; iterPro; iterPro; RINTS; P roDom; P
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-ARWHEPSIMON 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 DLVEBAPAAVGEPMADRLELIRLDP---AYRARFADGSQLDVHTDGAAMBAAVEQFAGAR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 DADAYRRFVAVWSERSRHVMKAPSTPPTGSNLIGAFGGLATARGNSELSRQFLAPGDALL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 DEYFDSE-----ALKAALAWFG---AQSGPPMSEPGTAPWVGFAALMHVLPPGRAV- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 DANFDSPFQLVHPDLARLAALGGFGRLDARIGHFVSDERLRRVFSFQALYAGVPPARALA 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: This enzyme converts phytoene into zeta-carotene via the intermediary of phytofluene by the symmetrical introduction of two double bonds at the C-11 and C-11, positions of phytoene. COPACTOR: FAD (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 ------GGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWTVTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%; Score 285; DB 1; Length 508;
25.3%; Pred. No. 6.3e-12;
Live 64; Mismatches 208; Indels 150; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAD; Flavoprotein, NAD
                                                                                                                                                           Streptomyces setonii.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ISP 5395;
Hoshi K.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
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508 AA; 54610 MW; 486DEFC076D51CB5 CRC64;
                                                                                                                                                                                               Streptomycineae; Streptomycetaceae; Streptomyces.
                                     508 A.A.
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PROSITE; PS00982; PHYTOENE_DH; 1.
Carotenoid biosynthesis; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000759; Adridx reductase, InterPro; IPR002937; Amino_Oxidase. InterPro; IPR008150; Bac_phytoene_dh. InterPro; IPR008150; BAD_BS. InterPro; IPR008151; Phyth dehydro. Pfam; PF01593; Amino_Oxidase; IPRNINTS; PR00419; ADXRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Carotenoid biosynthesis.
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                                    STANDARD;
                                    STRSE
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273 SGREVHARKVIAGCHILTTLDILGNGGFDRTTLDHWRRKIRVGPGIGAVIRLATSALPSY 332
                                                                                   269 DOERIACDAVVLTPDLPVSYRLIGR------SPHRPLPLRHSPSAVILH 311
                                                                                                                                                                            333 RGDATTRESTSGLQLLVSDR----AHLRTAHGAA-----LAGELPPRPAVLGMSF 378
                                                                                                                                                                                                                                                                                                                                                                                                                                        357 TASDPSLAPPSKH-----LHYVLAPCPNTEVGPGVREWRELGPRYRDELLAELERRE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APGFTDSVLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGL 488
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Activation and analysis of cryptic crt genes for carotenoid
biosynthesis from Streptomyces griseus.";
Mol. Genet. 252:658-66(1996).
-!- FUNCTION: This enzyme converts phytoene into zeta-carotene via the
intermediary of phytofluene by the symmetrical introduction of two
double bonds at the C-11 and C-11' positions of phytoene.
                                                                                                                                                                                                                                                                -------TDRTWPNLAHHTISFGAAWKSTFHBLTRTGBLMSDPSLLITRP
                                                                                                                                                                                                                                                                                                                                                         379 SGIDPTIAPAGRHQVTLMSQWQPYRLS-----GHRDWASVARABADRIVGEMB-AF
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INTERPRO; IPR000759; Adradx reductase.
InterPro; IPR000357; Amino oxidase.
InterPro; IPR000315; Amino oxidase.
InterPro; IPR000315; Phytosene_dh.
InterPro; IPR000315; Phytosene_dh.
InterPro; IPR003151; Phytosene_dh.
InterPro; IPR003151; Phytoses; IPR01393; Amino oxidase; 1.
PR01393; Amino oxidase; 1.
PR031TE; PR00419; ADXETASE;
ProDom; PD139017; Phytosene_dhydro; 1.
PR031TE; PS00982; PHYTORNE DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
NP BIND
12 #RD (ADX PART) (POTENTIAL).
SEQUENCE 507 AA; 54509 MW; PBB977FTE5696B2AC CRC64;
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P54981; P72447;
D-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-PRB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (BC 1.14.99.-) (Phytoene desaturase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489 YLTGASTHPGGGVSGA--SGRSAAR 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463 VLAGCGTTPGVGVPTVLISGKLAAQ 487
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MEDLINE=97074881; PubMed=8917308;
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                                                                                                                              DLVED-AFAAVGERMADRLELIRLAPAYRARFADGSQLDVHTDGAAMEAAVEEFAGARQA 126
                                                                                                                                                                                                           YPDSE----ALKAALAWFG---AQSGPPMSEPGTAPMVGFAALMHVLPPGRAV--- 230
                                                                                                                                                                                                                                    151 NFDSPLQLAHPDLARLAALGGFGRLDARIGHFVSDERLRRVFSFQALYAGVPPARALAAY 210
                                                                                                                                                                                                                                                                             211 AVIAYMDTVAGVYFPRGGMHALPRAMADAASDAGAVLRYGQRVTRLERSGDRVTAVTDQ 270
                                                                                                                                                                                                                                                                                                                                 APAGRHQVTLWSQWQPYRLS-----GHRDWASVABAEADRIVGEME-AFAPGFTDS 435
                                                                                                    68 GIIEELGLGAHGLRYID-CDPWAFAPP--APGTDGPGIVFHRDLDATCQSIERACGTKDA 124
                                                                                                                                                       125 DAYRRFVAVWSERSRHVMKAFSTPPTGSNLIGAFGGLATARGNSELSRQFLAPGDALLDE 184
                                                                                                                                                                                ------MRRF-----1DT 150
                                                                                                                                                                                                                                                             ------GGSGALSALASRMAVDGATVALGDGVTSIRRNSNHWTVTTESG 274
                                                                                                                                                                                                                                                                                                                275 REVHARKVIAGCHILITLEDLLGNGGFDRTTLDHWRRKIRVGPGIGAVLRLATSALPSYRG 334
                                                                                                                                                                                                                                                                                                                                                                    335 DATTRESTSGLQLLVSDRAHLRTAHGAA------LAGELPPRPAVLGMSFSGIDPTI 385
                                                                                                                                                                                                                                                                                                                                                                                           314 TDRT------WPDLAHHTISPGAAWKKNTEHELTRTGRLMSDPSLLITRPTATDPSL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPGKH------LHYVLAPCPNTEVGPGVREWRELGPRYRDELLAELERREMPGLGAA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 VLDRFIQTPRDIESBLGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGAST 495
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                                                    67
                                                                           VVVGAGLAGLAAALHLIGAGRRVTVVVBREDVPGGRAGLLES-GGFRIDTGPTVJTM----P 67
                                                   VVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIRHS
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
NCBI_TaxID=1063;
                          Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE=22307398; PubMed=1612412;
Gari E., Toledo J.C., Gibert I., Barbe J.;
"Nucleotide sequence of the methoxyneurosporene dehydrogenase from Rhodobacter sphaeroides: comparison with other bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
BEDLINE-25218278; Pubmed=7721699;
Lang H.P., Cogdell R.J., Takaichi S., Hunter C.N.;
"Complete DNA sequence, specific TnS insertion map, and gene
  Length 507;
Query Match
9.7%; Score 268; DB 1; Le
Best Local Similarity 25.0%; Pred. No. 8.6e-11;
Matches 139; Conservative 65; Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Methoxyneurosporene dehydrogenase (EC 1.14.99.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 AA
                                                                                                                                                                                127 VGYRR-LRIWLERLYRVQ------
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                      This SWISS-FROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 PODIFEVOGORIDHHITLI ------POPLLARHWEDGSTIDLITDLEANVEAVAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 CGTKDADAYRRFVAVWSERSRHVMKAFSTPPTGSNLIGA----FGGLATARGNSELSRQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 ----GGSGALSAALASRMAVD-GATVALGDGVTSIRRNSNHWT-VTTESGREVHARKVI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 LIPGMTLDRLIREFRDRRLRQLFGRYATTVGGTPYGAPGVLALIWAA-----EARGV
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assignment of the carotenoid biosynthesis pathway of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Mismatches 233; Indels 124;
                                                                                                                                                      -!- PATHWAY: Carotenoid and chlorophyll biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ••
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CRC64;
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157 T -> P (IN REF. 2).
170 L -> M (IN REF. 2).
273 L -> I (IN REF. 2).
443 PHGA -> A'COP (IN REF. 2).
52900 MW; 62227931415B253E CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.2%; Score 226; DB 1; 26.2%; Pred. No. 5.5e-08;
                         sphaeroides.";
J. Bacteriol. 177:2064-2073(1995).
-!- FUNCTION: CONVERTS HYDROXYNEUROSPORENE
METHOXYNEURGSPORENE TO SPHEROIDENE.
-!- COFACTOR: FAD (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ010302; CAB38743.1; ALT SEQ.
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157
170
273
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170
170
273
440
495 AA;
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STANDARD;
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----FPASQGSIYGLSPHGALA----SLKRPLARTA-----LPGLWLAGGGAHPGAGV 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 DAL---LDEYFDSEALKAALAWFGAQSG-PPMSEPGTAPMVGFAALMHVLPPGRAVGGSG 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 AIVIGSGVGGVSTAARLARAGFHVTVLEKNNPTGGRCSLIHH-EGYRFDQGPSLLLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 SGIIE----ELG--LGAHGLRYIDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSIERACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 PGLFHRTFAELGTSLEQEGVKLLKCEPNYM---IHFSDGEKFTLSSDLSVMKTEVEKWEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 ---XEGYTRYLEFLKESHGHYELS----VREVLLRNFEGL-TAMLRPEFLRHLLQLHPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 224; DB 1; Length 621;
22.1%; Pred. No. 9.9e-08;
iive 73; Mismatches 245; Indels 138; Gaps
                                                                                                                                                                                                                                                                                                                                    InterPro; 1PR008150; Bac_phytoene_dh.
InterPro; 1PR008151; Phytn_dehydro.
Prodom, PD139017; Phytn_dehydro; 2.
PROSITE; PS00982; PHYTOENE_DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;
                                                                                                                                                                                                                                                             Eukaryota, Fungi, Ascomycota, Pezizomycotina,
Dothideomycetes et Chaetothyriomycetes incertae sedis,
Mycosphaerellaceae, mitosporic Mycosphaerellaceae, Cercospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- COFACTOR: FAD {Probable}.
-!- PATHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last annotation_update)
Phytoene dehydrogenase (BC 1.14.99.-) (Phytoene desaturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAD (ADP PART) (POTENTIAL).
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536 556 POTENTIAL.
621 AA, 69529 MW, 61B9EA7784963CA8 CRC64;
                                                                                                                                       621 AA
                                                                                                                                                                                      Last sequence update)
                               516
                                                                                                                                                                   (Rel. 33, Created)
(Rel. 33, Last seq
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                             --SGASGRSAARIALSD
                                                         473 РМАЛЬSGRHAAEAILAD
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Best Local Similarity 22.1%
Matches 129; Conservative
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                Cercospora nicotianae.
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                                                                                                                                                                                                                                                                                                             NCBI_TaxID=29003;
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01-FEB-1996 (
28-FEB-2003 (
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TRANSMEM
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P48537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426
235 ALSAALASRMAVDGATVALGDGVTSIRRNSNHWT---VTTESGREVHARKVIAGCHILLT 291
                                                                                                                                                                                                                                                                                                                                  ------IPIKİPYAESLKGRPGSCSSISFYWALDRQ 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 VPELE-AHNIFLADEYRESFDSIFKKHLIPDEPSFYVNVPSRVDSTAAPEGKDSVVVLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 RVVBALVKIGERBGVDFRMETAVKKILLSEDGGVAKGVELEDGRRLBADVVVNNSDLVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 VGHLLEEDRHASQAHQLSASRNGHISSASPPDQPGLTPTEKQDWPAMISLARKTILSTIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 AFA-PGFTDSVLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLMRPLPELSGHRVPGA
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Clohing, sequence, and photoregulation of al-1, a carotenoid
biosynthetic gene of Neurospora crassa.";
Mol. Cell. Biol. 10:5064-5070(1990).
-!- FUNCTION: This enzyme converts phytoene into zeta-carotene via
intermediary of phytofluene by the symmetrical introduction of
double bonds at the C-11 and C-11' positions of phytoene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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1-WAY-2091 (Rel. 18, Last sequence update)
15-WAR-2004 (Rel. 143, Last annotation update)
Phytoene dehydrogenase (BC 1.14.99.-) (Phytoene desaturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502 FDAQLLKFGVLGRAAEVIIDAFRGRGKDIKGLYMVGASAHPGTGV 546
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-!- PATHWAY: Carotenoid biosynthesis.
-!- INDUCTION: By photoinduction.
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InterPro; IPR000205; NAD_BS.
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InterPro, IPR008150; Bac_phytoene
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MEDLINE=90377195; PubMed=2144609;
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Pfam; PF01593; Amino oxidase; 1.
                                                                                                                                                                                                                                                                                                                                  292 YEKL------
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sphaeroides.
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Matches 135;
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                  67 SGI----IEELG--LGAHGLRYIDCDP----WARAPP---APGIDGPGIVFHRDLDAICQ 113
                                                                                                                                                                                                                                    114 -SIERACGTKDADAYRRFVAVWSERSRHVMKAFSTPPTGSNLIGAFGGLATARGNSELSR 172
                                                                                                                                                                                                                                                                                                  116 VEIEKWEG---PDGFRRYLSWLAEGHOHYETSL----------RHVLHR 151
                                                                                                                                                                                                                                                                                                                              152 NFKSILBLADPRLVVTLLMALHPFESIWHRAGRYFKTDRWQRVFTFATWYMGMSPFDAPA 211
                                                                                                                                                                                                                                                                                                                                                                                  TAPMVGFAALMHVL--PPGRAVGSSGALSA--ALASRMAV-----DGATVALGDGVTSIR 261
                                                                                                                                                                                                                                                                                                                                                                                                    TYSLLQYSELAEGIWYPRG---GFHKVLDALVKIGERMGVKYRLWTGVSQVLTDGGKN-G 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 KKPKATGVQLENGEVLNADLVVVNADLVYTTNNL--------LPKEIGGI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 KKYANKL------NNRKASCSSISFYWSLSGMAKELETHNIFLAEEYKESFDAIFERQA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 LPDDPSFYIHVPSRVDPSRAPPDRDAVIALVPVGHLLQNGQP-----ELDWPTLVSKARA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNSNHWTVTTESGREVHARKVIAGCHILTTLDLLGNGGFDRTTLDHWRRKIRVGPGIGAV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 RIVGEMEA-----FAPGFTDSVLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPL 474
                                                                                                                                                                              7 AVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIRH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRLATSALPSYRGDATTRESTSGLQLL--VSDRAHLRTAHGAALAGE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 LPPRPAVLGMSFSGIDPTIAPAGRHQVT-----LWSQWQPYRLSGHRDWASVAEAEAD
                                                                                                                                     Gaps
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STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE=94292403; PubMed=8021167;
Lang H.P., Cogdell R.J., Gardiner A.T., Hunter C.N.;
"Early steps in caroleneoid biosynthesis: sequences and transcriptional analysis of the crtl and crtB genes of Rhodobacter
              PROSITE; PS00982; PHYTOENE_DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRII.
Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
                                                                                                       Query Match 7.5%; Score 208.5; DB 1; Length 595; Best Local Similarity 21.7%; Pred. No. 1e-06; Matches 123; Conservative 79; Mismatches 212; Indels 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P54980, OSRPD0, 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 28-FBS-2003 (Rel. 41, Last annotation update) Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
                                                    FAD (ADP PART) (POTENTIAL)
                                                 11 44 FAD (ADP PART) (POTENTIAL 578 595 POTENTIAL. 595 AA; 66367 MW; 0FF3DF07328ED784 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475 PELSCHRVPGADGLYLTGASTHPGGGV 501
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PD139017; Phytn_dehydro; 1.
                                                                                                                                 Matches 123; Conservative
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                                     Transmembrane.
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TRANSMEM
SEQUENCE
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choudhary M., Kaplan S.;

Choudhary M., Kaplan S.;

"DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2.4.1.";

Nucleic Acids Res. 28:862-867(2000).

-!- FUNCTION: This enzyme converts phytoene into zeta-carotene via intermediary of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11' positions of phytoene.

-!- CORACTOR: FAD (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE=95238278; PubMed=7721699;
Lang H.P., Cogdell R.J., Takaichi S., Hunter C.N.;
"Complete DNA sequence, specific Th5 insertion map, and gene assignment of the carotenoid biosynthesis pathway of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.4%; Score 203.5; DB 1; Length 518; 22.2%; Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
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T -> S (IN REF. 3).
C -> F (IN REF. 3).
Q -> P (IN REF. 3).
423B3515639EF8F1 CRC64;
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reactivation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement ((or send an email to license@isb-sib.ch)
        Journal Coli and R. sphaeroides."; J. Bacteriol, 176:3859-3869(1994).
                                                                                                                                                                                                                                                                                                  [3]
SEQUENCE FROM N.A.
STRAIN=ATCC 17023 / 2.4.1 / NCIB 82
MEDLINE=20115911; PubMed=10648776;
                                                                                                                                                                                                                                                       iaeroides.";
Bacteriol. 177:2064-2073(1995)
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EMBL, AJ010302; CAB38739.1; -.
EMBL, AF195122; AAF24289.1; -.
PIR, S49620; S49620.
PIR, T50745; T50745.
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292 292 L
395 395 Q
518 AA; 57244 MW;
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395
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                                                                                                                                                                                                                                                                                                                                                  --IFLKGKLAKDMSLYIHRPSI-----TDPTVAPEGDDTFYALSPVP 389
                                                                                          | : | | | : : | | : | | 184 KDERLRMALSFHPLFIGGDPFNVTSMYILVSQLEXEFGVHYAIGGGVAAIAAAMAKVIEGQ 243
                                                                                                                                                  GATVALGDGVTSIRRNSNHWT-VTTESGREVHARKVIAGC---HILTTLDLLGNGGFDRT 303
                                                                                                                                                                                                                                   TLDHWR-RKIRVG-------PGIGAVLRLATSALPSYRGDATTRESTSGLQL 347
                                                                                                                                                                                                                                                                                                                       LVSDRAHLRTAHGAALAGELPP-----RPAVLGMSFSGIDPTIAPAG-----RHQVT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               444 WGAGFSIEPRILOSAWFRP-----HNISBEVANLFLYGAGTHPGAGVPGVIGSAEVMAK 497
---GRAVGGSGALSAALASRMAVD 247
                                                                                                                                                                                           GGSFRMNTEVDEILVEKGTATGVRLASGEVLRÄGLVVSNADAGH--TYMRLLRNHPRRRW 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           455 GGNVMHVEMSLDQMMLWRPLPELSGHRV-PGADGLYLTGASTHPGGGVSGASGRSAARIA
                                                                                                                                                                                                                                                                                                                                                                                                                                       390 HLKQAQPV-----DWQAVABPYRSSVLEVLEQSMPGIGERIGPSLVPTPETFRDRYLSP
                                                                                                                                                                                                                                                                                                                                                                                                          395 LWSQWQPYRLSGHRDWASVAEAEADRIVGEMEAFAPGFTDSVLDRFIQTPRDIESELGMI
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- FUNCTION: This enzyme convertes phytoene into lycopene via the intermediaries of phytofluene, zeta-carotene and neurosporene the introduction of four double bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pantoea ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
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STRAIM-20D3;
MEDLINE-91072214; PubMed=2254247;
Misawa n., Nakagawa M., Kobayashi K., Yamano S., Izawa Y.,
Nakamura K., Harashima K.;
"Blucidation of the Erwinia uredovora carotenoid biosynthetic pat
by functional analysis of gene products expressed in Escherichia
coli:"
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PATHWAY: Carotenoid biosynthesis.
SIMILARITY: Belongs to the phytoene dehydrogenase family.
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01-MAY-1991 (Rel. 18, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
CRII.
                                                                                                                                                                                                                                                                            TDAHVKSRRWSMGLFVWYFGTKGTKGMWPDVG---HHTIVNAPRYKG---
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PIR; D37802; D37802.
InterPro; IPR002937; Amino_oxidase.
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134 LKDSE-
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P21685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 PEGCCSYYVLAP-VPHLGTANLDWTVEGPKLRDRIFAYLEQHYMPGLRSQLVTHRMFTPF 422
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                                                                                                                                                                                                                                                                                         9 VVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIRHSG
                                                                                                                                                                                                                                                                                                                        69 IIEEL-GLGAHGLR-YIDCDP-----WAFAPPAPGIDGPGIVFHRDLDAT-CQSIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 QENPEDVEGYRQFL----DYSRAVFKEGYLKLGTVPFLSFRDMLRAAPQLAKIQAWRSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 SRQFLAPGDALLDEYFDSBALKAALAWFG-AQSGPPMSEPGTAPMVGFAALMFVLPPGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 V----GGSGALSAALASRMAVDGATVALGDGVTSIRRNSNH-WTVTTBSGREVHARKVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 NADVVHTYRDILSQHPAAVKQSNKLQTK------RMSNSLFVLYRG-----
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                                                                                                       FAD; Flavoprotein; NAD.
tt) (POTENTIAL).
                                                                                                                                                                                                6.9%; Score 191.5; DB 1; Length 492; 23.9%; Pred. No. 1.1e-05; Live 65; Mismatches 242; Indels 111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Myxococcus.
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01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
                                                                                                                                                       FA4CD4E34A9C6413 CRC64;
                                                                                                                                                                                                                ,le-05;
les 242;
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                   InterPro; IPR008151; Phytn dehydro.
Pfam, Pf61593; Amino_oxidase; 1.
ProDom; P0139017; Phytn dehydro; 1.
PROSITE; P50992; PHYTORNE DH; 1.
Carotenoid biosynthesis; Oxidoreductase; PAI
NP BIND.
InterPro, IPR008150; Bac_phytoene_dh
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                                                                                                                                                       SEQUENCE 492 AA; 55007 MW;
                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                   Best_Local Similarity
Matches 131; Conserv
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CRII MY
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PIR; A39273; A33120
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Brwinia herbicola
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                                                                                                                                                   CRII ERWHE P22871;
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                                                                                                              RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ---LDGFFHDDRVTYALAY------PSKYLGLHPTT-CSSVFSVIPFLELAFGVWHVEG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 HSGIIEEL-GLGAHGLR-YIDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSIERACGTKD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 LPGVLEQIFRRAARRLEDYVKLLPLDVNTRVHFWDGTHLDTTRHLDRMBAELAK-FGPRQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 ADAYRRFVAVWSERSRHVMKAFSTPPTGSNLIGAFGGLATA-----RGNSELSRQFLAPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 DALLDEYFDSEALKAALAWFGAQSGPPWSEPGTAPMVGFAALMHVLP-----PGRAVG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 GSGALSAALASRMAVD-GATVALGDGVTSIRRNSNHWTVTTESGRBVHARKVIAGCHILT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 GFRELSRGM-MRCARDLGATFRMGTPVEKVR------VDAGRAVGVK--LVGGEVLD 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 TLDLLGNGGFDRTTLDHWRRKIRVGPGIGAVLRLATSALPSYRGDATTRESTSGLQLLVS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 ADAVVVNADLAYAARSLIPABARBGS-----RLTDAALBRAKYSCSTFMAYYGLDTVYA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 DRAH-----LRTAHGAALAG----ELPP----RPAVLGMSFSGIDPTIAPAGRHQV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 DLPHHLIYLSESARRTDRDALEDRHVDLEDPFFYVCNPGV-----TDPSGAPAGHS-- 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 TLWSQWQPYRLSGHRDWASVAEAEADRIVGEMEAFA-PGFTDSVLDRFIQTPRDIESELG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 MIGGNVMHVEMSLDQWMLWRPLPELSGHRVPGAD--GLYLTGASTHPGGGVSG--ASGRS 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443 VFRGAVFNLSHTWLQLGPLRP-----KVKNRDIEGLYFVGGGTHPGSGLLTIMESANI 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 IVVGAGPGGLSAAINLAGQGFRVTVVZKDAVPGGRMKGLTLGASGEYAVDTGPS---1LQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 VVVGSGHNALVSAAYLAREGMSVEVLEXDTVLGGAVS--TVERFEGYKVDRGSSAHLMIR 65
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carotenoid synthesis by blue light.";
EXHO J. 122.1255.1275(1993).
-!-BENDO J. 122.1265.1275(1993).
-!-BENDO J. 122.1265.1275(1993).
-!-BENDO J. 122.1265.1275(1993).
-!-BENDO J. 122.1265.1275(1993).
-!-COPACTOR: FAD (Probable).
-!-PATHWAY: Carotenoid biosynthesis.
-!- PATHWAY: Carotenoid biosynthesis.
-!- INDUCTION: By blue light.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000759; Adrndx reductase.
InterPro; IPR000759; Adrndx reductase.
InterPro; IPR001815; Baino oxidase.
InterPro; IPR001815; Baino oxidase.
InterPro; IPR001815; Phytin dehydro.
InterPro; IPR001815; Phytin dehydro.
InterPro; IPR001815; Phytin dehydro.
ProDom; PD139017; Phytin dehydro; 1.
PROSITE; PS00982; PHYTORNE DH; 1.
Carotemoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
NP_BIND

12 45 FAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 529 AA; 58420 MW; 53536A8DFD0D24BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.8%; Score 189.5; DB 1;
Best Local Similarity 23.7%; Pred. No. 1.7e-05;
Matches 132; Conservative 74; Mismatches 256;
                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M94727; AAA25390.1; -. PIR; S35306; S35306.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TALEALPTIA-GRRMEDY--VRILLPVKP-----PYRICWESGKTIDYANDSAELEAQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ----GTKDADAYRRFVAVWSERSRHVMKAFSTPPTGSNLIGAFGGLATARGNSELSRQFL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 ITQFNPRDVEGYRRFLAY----SQAVFQ-----EGYLRLGSVPFLS------FRDML 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S VVIGAGEGGLALAIRLQAAGIPTVLLEQRDXPGGR-AYVWHDQGFTFDAGPT---VITDP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILINE-91088634; PubMed=2263648;
Armstrong G.A., Alberti M., Hearst J.E.;
Connerved enzymes mediate the early reactions of carotenoid
Connerved enzymes mediate the early reactions of carotenoid
biosynthesis in nonphotosynthetic and photosynthetic prokaryotes.";
Proc. Natl. Acad. Sci. U.S.A. 87:9975-9979(1990).
-!- FUNCTION: This enzyme converts phytoene into lycopene via the intermediaries of phytofluene, zeta-carotene and neurosporene by the introduction of four double bonds.
-!- CORACTOR: FAD [Probable].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Enterobacteriaceae; Pantoea.
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InterPro; IPR008150; Bac_Bhytoene dh.
InterPro; IPR008151; Phytn dehydro.
Pfam; PF01593; Amino_oxidase; 1.
Probom; PR13017; Phytn dehydro; 1.
PR051TE; PS01082; PHYTOENE DH; 1.
Carotenoid biosynthesis; Oxidoreductase; PAD; Flavoprotein; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.5%; Score 179.5; DB 1; Length 492; 22.8%; Pred. No. 7.2e-05; tive 62; Mismatches 239; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Created)
1-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogensse (EC 1.14.99.-) (Phytoene desaturase)
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                                                                                                                                                                                                                                                                      PRT;
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                                              496 AADYLTREAGKGPLPGW 512
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509 AARIALSDSRRGKASOW
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Matches 129; Conservative
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InterPro; IPR002937; Amino oxidase.
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                                                                                                                                                                                                 494 AA; 52312 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phycomyces blakesleeanus.
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NCBI_TaxID=4837;
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                                                                                                                                                                                               SEQUENCE
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                                                                                                   279 ARKVIAGCHILTILDILGNGGFDRTTLDHWRRKIRVGPGIGAVIRLATSALPSYRGDATT 338
                     ---GGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWT-VTTESGREVH 278
                                                           LEREWGVWFPEGGTGALVNGMVKLFTDLGGEIELMARVEELVVADNRVSQVRLADGRIFD 266
                                                                                                                                                    -----LGHHPVGQKRAAALE 298
                                                                                                                                                                                             RESTSGLOLLV---SDRAHLRTAH------GAALAGELP---PRPAVL 374
                                                                                                                                                                                                                           433
                                                                                                                                                                                                                                                                                                                            -----TDPSLAPPGCASFYVLAP-VPHLGNAPLDWAQEGPKLRDRIFDYLBERYMPGLR 410
                                                                                                                                                                                                                                                                                                                                                                              493
                                                                                                                                                                                                                                                                                                                                                                                                                    SQLVTQRIFTPADFHDTLDAHLGSAFSIEPLLIQSAWFRP-----HNRDSDIANLYLVGA 465
                                                                                                                                                                                                                                                                                    GMSFSGIDPTIAPAGRHQVTLWSCWOPYRLSGHRDWASVARAEADRIVGEM-EAFAPGFT
                                                                                                                                                                                                                                                                                                                                                                       434 DSVLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGA
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"Nucleotide sequence, organization, and nature of the protein
products of the carotenoid biosynthesis gene cluster of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90368827; PubMed=2144293;
Bartley G. E., Schmidhauser T.J., Yanofsky C., Scolnik P.A.;
"Carotenoid desaturases from Rhodobacter capsulatus and Neurospora
crassa are structurally and functionally conserved and contain
domains homologus to flavoprotein disuifide oxidoreductases.";
J. Biol. Chem. 265:16020-16024 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhodobacter capsulatus (Rhodopseudomonas capsulata),
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHOXYNEUROSPORENE TO SPHEROIDENE.
-- COFACTOR: RAD (Probable).
--- PATHWAY: Carotenoid and chlorophyll biosynthesis.
--- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Methoxymeurosporene dehydrogenase (BC 1.14.99.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 STHPGGGVSG--ASGRSAARIALSD 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466 GTHPGAGIPGVVASAKATASLMIED 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-SB1003 / St Louis, and BEC404;
MEDLINE-89313663; PubMed=2747617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY TO CAROTENOID DESATURASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gen. Genet. 216:254-268(1989).
                                                                                                                                                  TDAVASNADVVNTYKKL-----
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EMBL; Z11165; CAA77544.1; -.
PIR; S04406; S04406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRID RHOCA
P17059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 TCQSIERACGTKDADAYRRF----VAVWSERSRHVMKAFSTPPTGSNLIGAFGGLATARG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 -----IGVDLAHHNVFFTADPELEFGPIGAGEMPEEPTLY-----ICAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRSETDVVVIGARMGGLAAAIGAAAGLRVTVVBAGDAPGGKARAVPT-PGGPADTGPTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 NSELSROFLAPG-----DALLDEYFDSEALKAALAWFGAQSGPPMSEPGTAPMVGFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 -ATVTRPQLWPALRPGLTMRDLLAHHFXDPRLAQLFGRYATYVG---GRPGATP----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::::
208 VLSLIWQAEVQGVWAIREGMHGVAAALARVARAKGVRFHYGAKAKRIVRKEGRVTAVEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 SGREVHARKVIAGCHILFTLD-LLGNGGFDRTTLDHWRRKIRVGPGIGAVLRLATSALPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 TCVSIPCGACIFNGDPGALRDGLLGDAA--RASME---KSPRPAPSLSAWV-WAFGATP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 YRGDATTRESTSGLQLL---VSDRAHLRTAHGAALAGELPPRPAVLGMSFSGIDPTIAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 PALLSRRFPGSLGAIYGG-----SPEGTLATFRRPLARTGLKGLYLAGGGT
                                                                                                                                                                                                                                                                                                                                                                                             1 MSAFLDAVIVIGSGHMALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 GRHQVTLWSQWQPYRL----SGHRDWASVAEAEADRIVGEMEAFAPGFTDSVLDRFIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 DREMQAPVPEIERFEIIMNGPAGHQPPPQEEAQCRARTFPMLAAMGLTFSPDPETRALTT
                                                                                                                                                                                                                                                                                                                                           Gaps
InterPro; IPR008150; Bac_phytoene_dh.
InterPro; IPR008151; Phytha dehydro.
Pfam; PF01593; Amino oxidase; Prodom; PD139017; Phytha dehydro; 1.
ProDom; PD139017; Phytha dehydro; 1.
PR051TE; PS00982; PHYTOENE DH; 1.
Photosynthesis; Chlorophyll biosynthesis; Carotenoid biosynthesis; oxidoreductase; FAD; Flavoprotein; NAD.
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                                                                                                                                                                                                                                                                             Query Match 6.4%; Score 176; DB 1; Length 494; Best Local Similarity 23.4%; Pred. No. 0.00012; Matches 132; Conservative 55; Mismatches 254; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 NIBAIRAFAGDKEAAFRRFDHLTTGLWEAFHRSVIAA---PKPDLWRIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last unotation update)
Phytoene dehydrogenase (BC 1.14.99..) (Phytoene desaturase)
                                                                                                                                                                                             AD (ADP PART) (POTENTIAL)
D1180A023FFBB5A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 P----RDIESELCMIGGNVMHVEMSLDOMMLWRPLPELSGHRVP
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STRAIN-NRRL 1555;
Ruiz-Hidalgo M.J.;
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                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-cib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 -LPEEAFEALDEKIEDHVELLRCHNNYKVHFD------DGDKIQLSSDLSRMKPE 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 EFAEGIWYPKGGFNTVIQKL-----ENIATEKFGARFIYEAPVAKINTDDKGKKVTG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 IRRNSNHWTVTTESGREVHARKVIAGCHIL------TTLDLLGNGGFDRTTLD-H 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 ------VILQSGEVIEADAVVCNADLVYAYHNLLPPCRWTTNTLAEKKLTSSSISFY 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409 -----VLERRLGLTNFIDLVEHSEVNDPSIWQKKFNLWRGSILGLGHDVLQVLWFRF9TQ 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 VVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERPPGYKVDRGSSAHLMIRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIIGAGAGGTATAARLAREGIKVTVVEKANFGGGRCSLINH-NGHRFDQGPSLYLMPK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSRQFLAPGDALLD-----EYFDSEALKAALAWFGAQSG-PPMSEPGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                FUNCTION: This enzyme converts phytoene into zeta-carotene via intermediary of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11' positions of phytoene.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfan; PF01593; Amino oxidase; 1.
Probom; PD139017; Phytn dehydro; 1.
PROSITE; PS00982; PHYTOENE DH; 1.
Carotenoid blosynthesis; Oxidoreductase; PAD; Flavoprotein; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.4%; Score 176; DB 1; Length 583;
21.2%; Pred. No. 0.00015;
tive 68; Mismatches 219; Indels 158;
                                                                     COFACTOR: FAD (Probable).
PATHWAY: Carotenoid biosynthesis.
SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 WSLK-RVVPELDVHNIFLAEAFKESFDBIFFDHKMPSELSFYVN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAD (ADP PART) (POTENTIAL).
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOEBF682B12FB591 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR002937, Amino oxidase.
InterPro, IPR008150, Bac_Dhytoene_dh.
InterPro, IPR008151, NAD_BS.
InterPro, IPR008151, Phytn_dehydro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65983 MW;
                                                                                                                                                                                                                                                                                                                EMBL; X78434; CAA55197.1; -. PIR; S43139; S43139.
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531
583 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 SGIIBELGLGAHGLRYIDCDPWAFAPPAPGTD---GPGIVFHR------DLDATCQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 IERAC---GTKDADAYRRFVAVWSERSRHVMKAFSTPPTGSNLIGAFGGLATARGNSELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 LERQIAQFNPDDLEGYRRFRDYAEEVYQEGYVKLGTVP----FLKLGQMLKA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 RQFLAPGDALLDEYFDSEALKAALAWFGAQ------SGPPMSEPGTAPMVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurosporene by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96062243; PubMed=7592436;
Misawa N., Satomi Y., Kondo K., Yokoyama A., Kajiwara S., Saito T.,
Ohtani T., Miki W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 24.1%; Pred. No. 0.00016;
Score 174.5; DB 1; Length 501;
S5; Conservative 51; Mismatches 251; Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=44155;
                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 45 FAD (ADP PART) (POTENTIAL)
501 AA; 54806 MW; 5F251AF11D679358 CRC64;
464 DSTGRY---KNLFFVGASTHPGTGV 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR002937; Amino oxidase. InterPro, IPR008150; Bac_phytoene_dh. InterPro, IPR008151; Phytn dehydro. Pfam. PF01593; Amino_oxidase; 1. ProCom; PD139017; Phytn dehydro; 1. PROSITE; PS00982; PHYTOENE_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D58420; BAA09594.1; -.
                                                                                                                                                                                                                                                                                                                                          Agrobacterium aurantiacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Matches
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or send an email to license@isb-sib.ch).

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|| || || || 208 YALNHALERRGGVWFAKGGTNQLVAGMVALFERLGGQMLINAKVARIDTDGPRATGVTLA 267
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                                                                                                       SGREVHARKVEAGCHILTTL-DILGNGGFDRTTLDHWRRKIRVGPGIGAVLRLATSALPS 331
                                                                                                                                                                             ----SLNA 306
                                                                                                                                                                                                                                                332 YRGDATTRESTSGLQLLVSDRAHLRTAHG---AALAGELPPRPAVLGMSFS-----GI 381
                                                                                                                                                                                                                                                                                                                  KÄWSMSLFVLHFGLREAPKÖVÄHHTILFGPRYKELVNEIFKGPK-LAEDFSLYLHSPCTT 365
                                                                                                                                                                                                                                                                                                                                                                                        DPTIAPAG--RHQVTLWSQWQPYRLSGHRDWASVAEAEADRIVGEM-EAFAPGFTDSVLD 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 TRIPTPSDFASELNAHHGSAFSVEPILTQSAWFRP-----HNRDKTIRNFYLVGAGTHPG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPEMAPPGMSTHYVL---APVPHLGRADIDWAVEGPRYADRILASLEERLIPNLRANLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGASTHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE-89313663; PubMed-2747617.
Armstrong G.A., Alberti M., Leach F., Hearst J.E.;
Nucleotide sequence, organization, and nature of the protein
products of the carotenoid biosynthesis gene cluster of Rhodobacter
capsulatus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
1-AUG-1990 (Rel. 15, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
                                                                                                                                                           268 DGRALTADMVASNGDVMHNYRDLIGH-----TARGOSRAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  524 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=SB1003 / St Louis, and BEC404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: | | : | |: | | AGIPGVVGSAKATAQVMLSD 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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PRINTS; PR00419; ADXEDTASE.
ProDom; PD139017; Phytn dehydro; 1.
PROSITE; PS00902; PRYTOENE DH; 1.
PROSITE; PS00902; PRYTOENE DH; 1.
Photosynthesis; Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
12 45 PAD; PART) (POTENTIAL).

InterPro; IPR000759; Adrndx reductase.
InterPro; IPR002937; Amino_oxidase.
InterPro; IPR008150; Bac_phytoene_dh.
InterPro; IPR008151; Phyth dehydro.
InterPro; IPR008151; Phyth dehydro.
Pfam; PF01593; Amino_oxidase; 1.

EMBL; J04969; AAA50313.1; -. EMBL; X52291; CAA36533.1; -. EMBL; Z11165; CAA77540.1; -. PIR; A32617; A32617.

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67 SGIIBELGLGAHGLRYIDC-----DPWARAPPAP-----GIDGPGIVFHRDLDATCQSIE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 PDRLREL-----WADCGROFDKOVSLVPMEPFYTIDFPDGEKYTAYGD-DAKVKAEV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 HVLPPGRAVGGSGALSAALASRMAVDGATVALGDGVTSI--RRNSNHWTVTTESGREVHA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 RKVIAGC---HILTTLDLLGNGGFDRTTLDHWR-----RKIRVGPGIGAVLRLATSAL 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 QVVVSNADACH--TYKRILIRN-----RDRWRWTDEKEDKK-------RWSMGLF 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 AEKITEEVVPTPETPRDRYLSPLGAG-PSLEPRILQSAWFRP-----HNASEEVDGLYL 474
                                                                                                                                                                                                                                                                                                                                                                                                                 7 AVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIRH
                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AVVIGAGLGGLAAAMRLGAKGYKVTVVDRLDRPGGRGSSITK-GGHRFDLGPT---IVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 RACGIKDADAYRREVAVWSERSRHVM-----KAFSTPPTGSNLIGARGGLATAR---G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 HAK------KMVKDDHİRPALSFH------PLFIGGDPFHVTSMYILVSQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 PSYRGDATTRESTSGLQLLVSDRAHLRTAHGAA-----LAGELPP-----RPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 VWYPG-----TKGTAXMWKDVGHHTVVVGPRYKZHVQDIFIKGELAEDMSLYVHRPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 LGMSFSGIDPTIAPAGRHQVTLMSQWQPYRLSGHRDWASVABAEADRIVGEM-EAFAPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 TDSVLDRFIQTPRDIESE-LGMIGGNVMHVEMSLDQMMLWRPLPELSGHRV-PGADGLYL
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                        Query Match 6.3%; Score 174; DB 1; Length 524;
Best Local Similarity 21.7%; Pred. No. 0.00018;
Matches 128; Conservative 76; Mismatches 238; Indels 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6425A7E5A06AA6B9 CRC64;
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completed: February 29, 2004, 14:45:20 he : 11.9663 secs Search comp Job time :

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-!- COFACTOR: FAD (Probable).
-!- PATHWAY: Carotenoid and chlorophyll biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.

Bartley G.E., Scolnik P.A.; "Carocteria Genetic "Caroctenoid biosynthesis in photosynthetic bacteria. Genetic characterization of the Rhodobacter capsulatus Crtl protein."; J. Biol. Chem. 264:13109-13113(1989).

Gen. Genet. 216:254-268(1989)

MEDLINE=89327279; PubMed=2546948;

SEQUENCE FROM N.A.

Bartley G.E., Scolnik P.A.; J. Biol. Chem. 264:18260-18260{1939}.

ERRATUM

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February 29, 2004, 14:34:14 ; Search time 14.808 Seconds (without alignments) 3455.835 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                          ! protein - protein search, using sw model
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US-09-941-947A-38 2768 1 MSAFLDAVVVGSGHNALVSA.......ALSDSRRGKASQHMRRSSRS 532 tle: :rfect score: :danence:

tal number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

arched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

oring table:

nimum DB seq length: 0 ximum DB seq length: 200000000

st-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
i: pir4:* tabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		probable phytoene	hypothetical prote		phytoene dehydroge	phytoene dehydroge	hypothetical prote		P49 secreted prote	probable dehydroge	49K protein - Stre	oxido	probable oxidoredu	hypothetical prote	hypothetical prote	ı								phytoene dehydroge	methoxyneurosporen	hypothetical prote	probable carotenoi	phytoene dehydroge		Ď.
SUMMARIES	ID	E75561	(n)	AI2273	G87635	\circ	T32568	\sim	F75591	593	809189	A70523	F70782	C70915	H70854	T36968	875951	T31463	H84320	B84327	T51119	T46822	523633	T48646	S49624	B72567	T34971	027	AI2185	91
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	Score	859.5	688	6.099	538.5	533	466.5	439.5	418	340	327	314.5	303	284	283	275	270	264.5	249	247	229.5	225	224	224	222	214.5	212.5	212	211	208.5
	sult No.	H	7	٣	4	Ŋ	Q	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

phytoene dehydroge	phytoene denydrode	hydroxyneurosporen	phytoene dehydroge	phytoene dehydroge	phytoene dehydroge	methoxyneurosporen	phytoene dehydroge	hypothetical prote	hypothetical prote	phytoene dehydroge	hypothetical prote	phytoene dehydroge	hypothetical prote	methoxyneurosporen	phytoene dehydroge
TS0745	S49620	S32171	T50910	C75466	D37802	T50749	835306	AB2064	E84212	S52586	A86203	A33120	AC2446	S04406	.843139
OI (N	a	N	N	C)	C)	C4	N	N	7	Ŋ	7	C)	C)	C)
518	518	485	511	548	492	486	529	206	430	492	587	492	503	494	583
7.4	7.4	7.3	7.2	7.1	6.9	6.9	6.8	6.B	8.9	6.8	6.5	6.5	6.4	6.4	6.4
204.5	203.5	202	200	197.5	191,5	191	189.5	189	188	187.5	181	179.5	176.5	176	176
۰,	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Sull 1 Species: Delinococcus radiodurans (strain R1) Species: Delinococcus radiodurans Species: Delinococcus radiodurans Accession: E15561 Milto, O.; E1880, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; I.M.; Shen, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zal, Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zal, Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zal, Smith, H.O.; Vamathevan, J.J.; Jane, P.; McDonald, L.; Utterback, T.; Zal, Smith, H.O.; Vamathevan, J.J.; Jane, P.; McDonald, L.; Utterback, T.; Zal, Smith, H.O.; Vamathero, O. J.; Deser, C.M. Recession: E7556, Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036896; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A75250; MID:20036899; PMID:10567266 Reference number: A	OY 358 AHGAALAGELFPRPAVLGMSFSGIDPTIAPAGRHQVTLWSQWQPYRLSGHRDWASVAEAE 417
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hypothetical protein all3744 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Strain PCC 7120
C;Accession: A12273
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C;Accession: A12273
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An. A;Recession: A12273
A;Accession: A12273
A;Accession: A12273
A;Accession: A12273
A;Accession: A12273
A;Accession: DNA
A;Residues: 1-565 cKUR>
A;Cross-references: GB:BA000019; PIDN:BAB75443.1; PID:g17132878; GSPDB:GN00179
A;Accession: a113744
C;Superfamily: phytoene dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMIRHSGIIEELGLGAHGLRYIDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSIERACGT
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                                                                532 RVFLKQQRR 540
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                 511 RIALSDSRR
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.Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PIDN:BAA10561.1; PID:g100172
.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
'SUperfamily: phytoene dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Ya. O'kunura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, NA Res. 3, 109-136, 1996

'Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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ADRIVGEMEAFAPGFTDSVLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPEL 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              !ypothetical protein - Synechocystis sp. (strain PCC 6803)
.;Species: Synechocystis sp.
i;Variety: PCC 6803
.;Variety: PCC 6803
.;Late: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                            SGHRVPGADGLYLTGASTHPGGGVSGASGRSAARIALSDSRR 519
                                                                                                                                                                                                                                                                                       466 SQYRWPGVQGLYLTGASTHPGGGIMGASGRNAARVIVKDLTR 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .; Accession: 875617
.; Status: preliminary
.; Molecule type: DNA
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                                                                                                        418
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A;Residues: 1-544 <LAN>
A;Cross-references: EMBL:AF036705; PIDN:AAB95172.1; GSPDB:GN00022; CESP:F37C4.6
A;Experimental source: strain Bristol N2; clone F37C4
C;Genetics:
                                                                                                                                                                                                                                                     A;Residues: 1-518 <KUR>
A;Crosa-references: GB:AE006641; NID:g13815726; PIDN:AAK42566.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO2422
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 GAMGYVEGGMGEVTQALKRSAEHLGVBIYTNAEVDEV--LVKNGRVEGIKLKNGKTINAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.3%; Score 533; DB 2; Length 51 30.9%; Pred. No. 6.8e-29; ive 93; Mismatches 226; Indels
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Reference: G90413
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Rylangston, Y.; Sansone, J.; Wohldmann, P.
submitted to the EMBL Data Library, December 1997
A, Description: The sequence of C. elegans cosmid F37C4.
A, Reference number: Z21193
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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Best Local Similarity 30.9°
Matches 168; Conservative
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A;Molecule type: DNA
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Species: SH1folobus solfataricus
Accession: G90413
Accession: G90413
Shc, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chanong, I.; Jeffries, A.C.; Kozera, C.J.; Wedina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, rett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GB:AE005673; NID:g13424781; PIDN:AAK25083.1; GSPDB:GN00148
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                                     protein [imported] - Caulobacter crescentus
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                                Mytoene dehydrogenase-related
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Residues: 1-543 <STO>
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Cyacterion: F7551

K; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
K; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A7526; MUID:20036896; PMID:10567266
A; Arcession: F75591
A; Assesioner F75591
A; Residues: DNA
A; Residues: 1-489 cWHIS
A; Residues: 1-489 cWHIS
A; Residues: 1-489 cWHIS
A; Cross-references: GR:AB001863; GB:AB001825; NID:g6460670; PIDN:AAF12427.1; PID:g64607
A; Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 ARBPLKPAEBYRHGEDLYTSSV----ITMFCMEYAEKAYGEAVSRGVSREPHLSVNVLAN 377
                                                                                                                            RHSGIIEELGLGAHGLRYIDCDPWAFAPPAPGT-----DGPGIVFHRDLDATCQSIERAC 119
                                                                                                                                                                            -----ERSRHVMKAFSTPPTGSNLIGAFGGL 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 RVDPGLAPEGWILASIFLQYIWRPARSWGEEDKSEVAE----RGLGVLBSVFTLPREGVR 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 VGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSA-----HLMI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P49 secreted protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                       218 AALMHVL--PPGR-----AVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STHPGGGVSGASGRSAARIALSD----SRR---GXASQWMRRSSR
                                                                                                                                                                                                                                        120 GIKDADAYRRFVAVWS------
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C, Superfamily: phytoene dehydrogenase
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.YTile: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr ;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 TARGNSELSRQFLAPGDALLDEYPDSEALKAALAWFG--AQSGPPMSEPGTAPMVGFAAL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 SNGKELHSKIVMSNATPHVTFNKLVK---KESLPEFFRRNINQIDYTSPVTKINVAVKEL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : : : : | | : | | : DNFLAKPNGGSEPMPHHQTTIHM ---NCENMQVVHDAVMDYKNGRYSRRPVIEMTIPSSV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPTIA-PAGRHQVTLWSQWQPYRLSGHRDWASVABAE-ADRIVGEMBAFAPGFTDSVLDR 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGASTHPGG 499
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                                                                                                                                                                                                                                                                                                                       66 HSGIIEELGLGAHGLRYIDCDPWAFAPPAFGTDGPGIVFHRDLDATCQSIERACGTKDAD 125
                                                                                                                                                                                                                                                                                                                                                                    76 -PVVMQBLNLKKFGLRYHIRNPNSFTPIR--NTHESLLLGMDMAENQKEIAK-FSQRDAG 131
                                                                                                                                                                                                                                                                                                                                                                                                                             221 MHVLPP-----GRAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSN-HWTVTT 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSY-----RGDATTRESTSGLQLLVSDRAHLRTAHGAAL---AGELPPRPAVLGMSFSGI 381
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.;Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 NYPKYEHFISEIVHSFEQLMDYEPLDLQKPIHKLLPHLYLLFKTVQPLGLRNAVDFYELM 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 HHVIGGLDEHKGAWGYVYGGMGAVSNAIAECAKSEGAEIYTEQDVQEVLLDGNVAKGVRL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Aeropyrum pernix
Spate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
Accession: B72609
                                                                                                                                                                                                                                             16 DAIIIGGGHNGLTAAAYLTKAGKKVCVLERRHYVVGGAAVTEIVPGFRFSRASYLLSLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-----APISKIMNKWFESDVLKATLGTDGVIGLAASPM-DPGT----GYVLL
                                                                                                                                                                                                              6 DAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIR
                                                                                                                                                           75;
                                                                                                        Length 544;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ypothetical protein APE1336 - Aeropyrum pernix (strain K1)
                                                                                                     Query Match
16.9%; Score 466.5; DB 2;
Best Local Similarity 28.3%; Pred. No. 2.5e-24;
Matches 157; Conservative 92; Mismatches 231;
                         ", Map position: 4 "Introns: 29/3; 230/2; 397/2; 484/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVSGASGRSAARIAL 514
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GResidues: 1-538 < KAW>
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, Gene: CESP: F37C4.6
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9
                                                                              2 SAFLDAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVE-RFPGYKVDRGSSA
                               Gaps
                               92;
15.1%; Score 418; DB 2; Length 485
30.2%; Pred. No. 4.6e-21;
ive 68; Mismatches 215; Indels
   Query Match
Best Local Similarity 30.2%
Matches 162; Conservative
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25;

Gaps

Indels 117;

Length 538;

Ouery Match 15.9%; Score 439.5; DB 2; Best Local Similarity 29.4%; Pred. No. 1.8e-22; Matches 172; Conservative 70; Mismatches 227;

Superfamily: phytoene dehydrogenase

Db 204 FALAAHARGWPVARGGSQSISDALTAYLKDLGGAVHTDYEVKRLDDLPPAR 254 Qy 281 KVIAGCHILTILDLIGNGGFDRTTLDHWRRKIRVGPGIGAVIRIATSALPSYRGDATTRE 340 : : : : : :	unidans Levision 30-Sep-1991 #text_change 22-Oct-1999 Eckhardt, T. 1987 nce of the gene coding for XP55, a major secret UD:87231086; PMID:3453116 ce not shown; translation not shown 42; NID:44218; PIDN:CAA68336.1; PID:947219 mitted to the EMBL Data Library, May 1987 rogenase 8%; Score 327; DB 2; Length 469; 6%; Pred, No. 7.38-15;	TATIVE THALVEAN THALVEAN THALVEAN THERYCHIA TH
9 61 HIMIRHSGIIEELGLGARGLRYIDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSIE 116 77 HPLAASPAFREWPLEAFGLRWIHPPAPLGQTLAGGGSVTLRRDLSATA 125 9 117 RACGTKDADAYRRFVAVWSERSRHVMKAPSTPFTGSNLIGAFGCLATARGNSELSR 172 126 -AVIGADGPAWERLFAPLVQEWEELLDDILRPLPHVPRHPFTLARFGLRA	345 IQLLVSDRAHLRTAHGAALAGELPRRAVLGMSFSGIDPTIAPAGHQVTIMSQMQPYRL 404 ::: :	Reference number: 221551 Reference number: 221551 Rocession: 13991 Rocession: 13991 Rocession: 13991 Rocession: 13991 Rocession: 1472 «SEB. Cross-references: SRELAID35206, PIDN:CAA22758.1; GSPDB:GN00070; SCOEDB:SC9B5.16 Experimental source: strain A3(2) Experimental source: strain A3(2) Cuery Match 12.34; Score 340; DB 2; Length 472; Gane: SCOEDB:SC9B5.16 Superfamily: phytoene dehydrogenase Query Match 12.34; Score 340; DB 2; Length 472; Gane: SCOEDB:SC9B5.16 Superfamily: phytosne dehydrogenase Cuery Match 12.34; Score 340; DB 2; Length 472; Best Local Similarity 27.84; Pred. No. 9.6e-16; Matches 149; Conservative 63; Mismatches 226; Indels 98; Gaps 24; Matches 149; Conservative 63; Mismatches 226; Indels 98; Gaps MSPLDAVVVGSGNALARDGMSVENTARDGMSVENTEATLILEGERHDFCSA 60 MSPLDAVVVGSGNALARATARDGMSVENTARDGMSVENTEATLILEGERHDFCSA 60 MAHMIRHSGIIEELGLGAHGLRYIOCDPWARAPPAPAPGTOGGSGIVFREDLDATCQSIERAC 119

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probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: In-Jul-1998 #text_change 20-Jun-2000
C.Accession: F70782
R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, F.; Connor, R.; Davies, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998
A.Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Authors: Scapers, R.; Sulston, J.B.; Paylor, R.; Whitehead, S.; Barrell, B.G.
A.Authors: Seeders, R.; Sulston, J.B.; Paylor, R.; Whitehead, S.; Barrell, B.G.
A.Authors: Seeders, R.; Sulston, J.B.; Paylor, R.; Whitehead, S.; Barrell, B.G.
A.Authors: Seeders, R.; Sulston, J.B.; Paylor, R.; Whitehead, S.; Barrell, B.G.
A.Authors: Seeders, R.; Sulston, J.B.; Paylor, R.; Whitehead, S.; Barrell, B.G.
A.Authors: Seeders, R.; Sulston, J.B.; Seeders, R.; Massidues: 1-538 (COL)
A.Authors: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGIDPII-----APAGRHQVTLWSQWQPYRLSGHRDWASVAEAEADRIVGEMEAFAPGFT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 DSVLDRRIQ-----TPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPEL 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 VGFAALMHVLPPGRAV-----GGSGALSAALASRMAVDGATVALG------DGVTSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 AVLRLATSALPSYRGDATT-RESTSGLQLLVSDRAHLRTAHGAALAGELPPRPAVLGMSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 DAVVVGSGHNALVSAAYLAREGWSVEVLEXDTVLGGAVSTVERFPGYKVDRGSSAHLM-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 RHSGIIEELGLGAHGLRYIDCDPWAFAPPAPGTDG-PGIVFHRDLDATCQSIERACGTKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 ADAYRRF-----VAVW----SERSRH-----VMKAFSTPPTGSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 IGAFGGLATARGNSELSROFLAPGDALLDEYFDSBALKAALAWFGAQSGPPMSBPGTAPM
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10.9%; Score 303; DB 2; Length 535;
Best Local Similarity 24.4%; Pred. No. 3.8e-13;
Matches 147; Conservative 74; Mismatches 214; Indels 168;
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A;Gene: Rv0897c
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**Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
**Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
**Arterier Deciphering the biology of Mycobacterium tuberculosis from the complete genome **Reference number: A70500; MuID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wolecule type: DNA.
!,Fesidues: 1-536 <COL.
!,Cross-references: GB:297188; GB:AL123456; NID:G3261805; PIDN:CAB10023.1; PID:e1300070;
';Experimental source: strain H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 SSAVSSELGLDS--LPTVDLEVMSVALRGVGDD--PVVQFTDPTKMLTHLHRVHGA-DAV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 TGMAGLLAWSQAPTRALGRFEAGTLPKSFDEMYACATNEFERSAIDDMLFGSVTDVLDRH 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 IGALITHLSQLLERTGGEVRLRSKVTEIVVDNSRSSARVRGVRTAAGDTLTSPIVVSA-- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 ILTTLDLLGNGGFDRTTLDHWRRKIRVGPGIGAVLRLATSALPSYRGDATTRESTSGLQL 347
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                                                                                                                                                                                                                                           xrobable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)
;)Species: Mycobacterium tuberculosis
;)Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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                                      SGAVSGLQLEL-RPKISLFPYSTP-HPAVFICSSATPPGPGVHGMSGENAAAK 460
HVEMSLDQNMLWRPLPELSGHRVPGADGLYLTGASTHPGGGVSGASGRSAAR 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 24.3%; Pred. No. 6.2e-14;
Matches 138; Conservative 73; Mismatches 256; Indels 101;
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Athles: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: H70854

A;Accession: H70854

A;Accession: H70854

A;Accession: H70854

A;Accession: H70854

A;Accession: Geguence not shown; translation not shown

A;Accessidues: 1-480 <COL>
A;Cross-references: GB:AL021287; GB:AL123456; NID:G3261508; PIDN:CAA16082.1; PID:G279159
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C,Genetics:
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Matches 136, Conservative
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Best Local S
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                                                                                    Accession: C70915
COOL, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Coole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Iquaream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Author, S.; Sulston, J.E.; Taylor, K.; Mitchend, S.; Barrell, B.G.
Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome Reference number: A70500; MUID:98295987; PMID:9634230
Accession: C70915
Status: preliminary; nucleic acid sequence not shown; translation not shown. Residues: 1-73 ccol.
Cross-references: GB:295844; GB:AL123456; NID:93250713; PIDN:CAB09252.1; PID:92131064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWTVTTESGREVHARKVIAGCHILTT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 LDLSPAAVLGIYGDVMPTRINRSYRRYRAG-----SSARKVDFAIBGDVGWTNPD 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRGDATTRESTSGLOLLVSDRAHLRTAHGAALAGELPPRPAVL------GMSFSGID 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 PIIAPAGREOVILWSOWOPYRLSGHRDWASVAEAEADRIVGEMEAFAPGFIDSVLDRFIQ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 TPRDIESEL----GMIGGNVMHVEMSLDOM-MLWRPLPELSGHRVPGADGLYLTGASTH 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                     Species: Myccbacterium tuberculosis
|Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AVVVGSGENALVSAAYLAREGWSVEVLE-KDTVLGGAVSTVERFPGYKVDRGSSAHLMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 GSPFWAAIDLQRYGLTWKWPDVDC-----AHPLDDGTAGVLYRSIBATAAGLGPDGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 LAPGDALLDEYFDSEALKAALAWFGAQSGPPMSEPGTAP---MVGFAALMHVLPPGRAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSGIIEELGLGAHGLRY----IDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSI-----
                         /Pothetical protein Rv1432 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.3%; Score 284; DB 2; Length 473; Best Local Similarity 24.3%; Pred. No. 6.5e-12; Matches 139; Conservative 77; Mismatches 202; Indels 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDL----LG-NGGFDRTTLDHWRRKIRVGPGIGAVLRLATSAL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: phytoene dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rv1432
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9

Gaps

88;

10.2%; Score 283; DB 2; Length 48 25.7%; Pred. No. 7.7e-12; tive 65; Mismatches 241; Indels

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A,Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable phytoene dehydrogenase (phytoene desaturase) - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 0.200-0.1999 #sequence_revision 03-Dec-:999 #text_change 21-Jan-2000 C;Accession: T36968
R;Seeger, K.J.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandre submitted to the EMBL Data Library, September 1999
A;Reference number: Z21607
                                           : | | | : | | | : TYPDIAYANPLPGR--PAAIAYHDLAHTCAKLD----- 111
63 MIRHSGIIEELGLGAHGLRYIDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSIERACGFK 122
                                                                                                                                                                            237
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                                                                                                                                                                                                                                                                                                                                                                                                        238 AALASRMAVDGATVALGDGVTSIRRNSNHWTVTTESGREVHARKVIAGCHILTTLDLIGN 297
                                                                                                                                                                                                                                                                                                              --ALLDEYFDSEALKAALAWFGAQSGPPMSEPGTAPMVGFAALMHVLPPGRAVGGSGALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 GGFDRTTLDH----WRRXIRVGPGIGAVLRLATSAL----PSYRGDATTRESTSGLQLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 ----RDKLPHRYAKALRRYRPRAGIAKVDFVLSDEIPWSDPRLRRAATLH-----LG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 SDRAHLRTAHGAALAGELPPRPAVLGMSFSGIDPTIAPAGRHQVTLWSQWQPYRLSGHRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 GTRDOMARAEADVAAGRHADWPMVLAAC----PHVADPGRIDET---GRRPFWTYAHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 WASVAEABADRIVGEMBAFAPGFTDSVL-DRFIQTPRDIBSELGMIGGNVWHVEMSLDQM
                                                                                                                                     DADAYRRFVAVWSERSRHVMKAFSTPPTGSNLIGAFGGLATARGN-SELSRQPLAPGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 MLWR----PLPELSGHRVPGADGLYLTGASTHPGGGVSGASGRSAARIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 STWRAIAGPIPRINPWRTP-IPKVYLCSAATPPGAGVHGMCGWYAARTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-523 <SEE>
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0854
pothetical protein Rv2997 - Mycobacterium tuberculosis (strain H37RV)
Species: Mycobacterium tuberculosis
Date: 17.Jul-1998 #sequence_revision 17.Jul-1998 #text_change 20-Jun-2000
Accession: H70854

SULT 14

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26;
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                                                                                                                                                                                                                                                                                                                                                                       227 ---GGMHALPRAMADAAATAGADLRWSAEVKALERSAGRVRAVHLASGERIACDAVVLTC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 GIIEELGLGAEGLRYIDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSIERACGTKDADAY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 RRFVAVWSER-----SRHVMKAPSTP----PTGSNL--IGAFGGLATARGNSELSRQF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 RAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNH-WTVTTBSGRBVHARKVIAGC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 HILTTLDLLGNGGFDRTTLDHWRRKIRVGPGIGAVLRLATSALPSYRGDATTRESTSGLQ 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 LLVSDR----AHLRTAHGAA----LAGELPPRPAVIGMSFSGIDPTIAPAGRH- 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 ---TDRIWPHLAHHTLSFGAAWERTFEELTRIGELMSDPSLLITRPITHDPALAPPGRHL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 ------QVTLWSQWQP-YRLSGHRDWASVAEAEADRIVGEMEAFA-PGFTDS 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 VLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGAST 495
                                                                                                                                                                                                                                             12 VVVGAGLSGLACALHILGAGRRVTVVERDAGPGGRSGRV-RLGGYELDTGPTV-LIMPHL 69
                                                                                                                                                                                                         8 VVVGSGHNALVSAAYLAREGWSVEVLEXDTVLGGAVSTVERFPGYKVDRGSSAHLMIRHS 67
                                                                                Query Match
9.9%; Score 275; DB 2; Length 523;
Best Local Similarity 25.9%; Pred. No. 3e-11;
Matches 150; Conservative 65; Mismatches 223; Indels 142; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496 HPGGGVSG--ASGR-SAARIALSDSRRGKASQWMRRSSRS 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471 TPGVGVPTVLVSGKLAAARVT-----GGAGSRPARTRRS 504
*;Gene: crtE; SCOEDB:SCJ1.35
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earch completed: February 29, 2004, 14:53:00 ob time : 17.808 secs

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February 29, 2004, 14:51:24; Search time 35.3218 Seconds (without alignments) 3180.293 Million cell updates/sec
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1 MSAFLDAVVVGSGHNALVSA.....ALSDSRRGKASÇMMRRSSRS 532
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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rfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence
	QI		US-09-941-947A-38	US-10-209-372-2	US-10-209-372-4	US-10-369-493-23397	US-10-209-372-6	US-10-369-493-2831	US-10-369-493-18878	US-10-369-493-19986	US-10-369-493-12005	US-10-369-493-10809	US-10-369-493-20413	US-10-369-493-4938	US-10-369-493-7696	US-10-369-493-12144	US-10-369-493-5969
		- !	10	14	14	15	14	15	15			15		15	15	15	15
	Query Match Length DB	, ,	532	532	511	511	542	542	539	537	539	521	518	517	517	524	544
d۴۰	Query Match		100.0	99.9	31,1	31,1	24.9	24.9	23.9	23.5	19.4	17.5	17.2	17.0	17.0	16.9	16.9
	Score		2768	2764	859.5	859.5	689	689	6.099	651.5	537.5	484	477	471.5	471.5	469	466.5
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4801,	7560	8540	1049	1214	9474	8803	4041,	8883	2850	8562	1864	8142	2044	1864	2004	2090	7895	1362	1194,	5, Ap	4 A	234,	1924	2043	1783	7750	1951	540,	18,
Seguence	Seguence	Sequence	Seguence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 7750, Ap	Sequence	Sequence	Sequence
US-10-369-493-4801	15-10-369-493-7560	JS-10-156-761-8540	JS-10-369-493-10498	IS-10-369-493-12145	JS-10-156-761-9474	JS-10-156-761-8803	3-09-738-626-4041	JS-10-156-761-8883	JS-10-369-493-2850	13-10-156-761-8562	IS-10-369-493-18644	15-10-369-493-8142	18-10-369-493-20440	18-10-369-493-18646	JS-10-369-493-20048	IS-10-369-493-20907	18-10-369-493-7895	18-10-156-761-13629	1-09-738-626-4194	1-09-547-267-5	IS-09-920-923-4	IS-10-369-493-234	IS-10-369-493-19248	IS-10-369-493-20438	18-10-369-493-17830	S US-10-369-493-7750	IS-10-369-493-19518	IS-10-369-493-540	IS-10-128-713A-18
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16.4	16.4	16.0	15.3	13.1	12.0	11.2	10.7	10.6	9,6	9.4	9.0	9.0	8,0	8.9	8.3	8.2	8.1	8.1	7.9	7.9	7.9	7.7	7.7	7.6	7.5	7.4	7.2	7.1	7.0
453.5	453.5	443	424	363.5	331	309	296.5	293.5	270	261	249	248	247	247	229.5	226	225	225	219.5	217.5	217.5	213.5	212.5	209	208.5	203.5	200	197.5	192.5
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	. 41	42	43	44	45

ALIGNMENTS

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APPLICANT: BISOSCOMOZO, PARTICIA C.
APPLICANT: Cheng, Qiong
APPLICANT: Cheng, Obena J.
APPLICANT: Koffas, Mattheos
APPLICANT: Koffas, Mattheos
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Picateggio, Steve
APPLICANT: Picateggio, Steve
APPLICANT: Picateggio, Steve
APPLICANT: Rouviere, Pierre B.
TITLE OP INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
TILLE REPRENCE: CL1903 US NA
CURRENT APPLICATION NUMBER: 60/229,907
PRIOR PLING DATE: 2000-09-01
PRIOR PLING DATE: 2000-09-01
PRIOR PLING DATE: 2000-09-01
PRIOR FLING DATE: 2000-09-01
PRIOR FLING DATE: 2000-09-01
PRIOR FLING DATE: 2000-09-01
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PRIOR FLING DATE: 2000-09-01
PRIOR FLING DATE: 2000-09-01
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Best Local Similarity 100.0%; Pred. No. 3.6e-238;
Matches 532; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Rhodococcus erythropolis AN12
Sequence 38, Application US/09941947A Publication No. US20030003528A1 GENERAL INFORMATION:
                                                                                              APPLICANT: Brzostowicz, Patricia C. APPLICANT: Cheng, Qiong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-941-947A-38
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61 HIMIRHSGIIEELGLGAAHGLRYIDCDPWAFAPPARGTDGPGIVFHRDLDATCQSIERACG 120

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Cy 241 ASRWAVDGATVALCDGVTSIRRNSNHWTVTTESGREVHARKVIAGCHILTTLDLLGNGGF 300 241 ASRWAVDGATVALCDGVTSIRRNSNHWTVTTESGREVHARKVIAGCHILTTLDLLGNGGF 300 241 DSTTLDHWRRKIRVGPGIGAVLRIATSALPSTGBATTRESTSGLCLLVSDRAHLATAHG 360 301 DRTTLDHWRRKIRVGPGIGAVLRIATSALPSTRGDATTRESTSGLCLLVSDRAHLATAHG 360 Qy 361 AALAGELPPRPAVLGMSFSGIDPTIAPAGRHQVTLWSQWQPYRLSGHRDWASVAERADR 420 Db 361 AALAGELPPRPAVLGMSFSGIDPTIAPAGRHQVTLWSQWQPYRLSGHRDWASVAERADR 420 Qy 421 IVGEMEAPAPGFTDSVLDRFIQTPRDIESELGMIGGNVWHYEMSLDQWMLWRPLPELSGH 480 Qy 421 IVGEMEAPAPGFTDSVLDRFIQTPRDIESELGMIGGNVWHYEMSLDQWMLWRPLPELSGH 480 Qy 421 IVGEMEAPAPGFTDSVLDRFIQTPRDIESELGMIGGNVWHYEMSLDQWMLWRPLPELSGH 480 Db 361 ALAGELPREAPARGTTSSVLDRFIQTPRDIESELGMIGGNVWHYEMSLDQWMLWRPLPELSGH 480 Qy 421 IVGEMEAPAPGFTDSVLDRFIQTPRDIESELGMIGGNVWHYEMSLDQWMLWRPLPELSGH 480 HILLININININININININININININININININININ	US-10-209-372-4 ; Sequence 4, Application US/10209372 ; Publication No. US2030100045A1 ; GENERAL INFORMATION: ; APPLICANT: E. I. du Pont de Nemours, Inc. ; APPLICANT: Tao, Luan ; TITLE OF INVENTION: CARCTENOID KETOLASE GENE ; FILE REPRENCE: CL-1849 US NA ; CURRENT PILING DATE: 2002-07-30 ; PRIOR PELICATION NUMBER: US/10/209,372 ; CURRENT FILING DATE: 2002-07-30 ; PRIOR PELICATION NUMBER: ; NUMBER OF SEQ ID NOS: 47 ; SOFTWARE: Microsoft Office 97 ; SEQ ID NO 4 ; LENGTH: 511 ; TYPE: PRT ; ORGANISM: Deinococcus radiodurans R1 US-10-209-372-4	Query Match 31.1%; Score 859.5; DB 14; Length 511; Best Local Similarity 39.7%; Pred. No. 6.8e-68; Matches 207; Conservative 80; Mismatches 208; Indels 27; Gaps 11; Qy 6 DAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIR 65 DLIVMGAGHNALVTAAYAARAGLKVGVFBRHLVGGAVSTVEFPGYKVDRGSSAHLMIR 64 Qy 66 HSGIIEBLGLGAHGLRYIDCDPWAFAPPAPGTDGPGIVF-HKDLDATCQSI-ERACGTKD 123	118 GPAYGRPLDDWTPPARAVADLFNBAPGPLDLGKMYMRSGOGKD 179 DALLDEYFDSEALKAALAWFGAGSPPMSEPGTAPMVGFAALHVLP 173 GDVARFYFSEERVRAPLTWMAAGSGPPPSDPLSAPFLLWHPLYHEGG 173 GDVARFYFSEERVRAPLTWMAAGSGPPPSDPLSAPFLLWHPLYHEGG 173 ALASRMAVDGATVALGDGVTSIR-RNSNHWTVTTSGREVHARKVJF 1
	y 421 IVGEMEAPAPGFTDSVLDRFIGTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGH 480 421 IVGEMEAPAPGFTDSVLDRFIGTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGH 480 481 IVGEMEAPAPGFTDSVLDRFIGTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGH 480 481 RVGGADGLYLTGASTHPGGGVSGASGRSAARIALSDSRRGKASGWWRRSSRS 532 1	CURRENT FILING DATE: 2002-07-30 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: NUMBER OF SEQ ID NOS: 47 SQCTWARE: Microsoft Office 97 SEQ ID NO 2 IRNGTH: 532 TYPE: PRT ORGANISM: Rhodococcus erythropolis AN12 SS-10-209-372-2 Guery Match Best Local Similarity 99.8%; Score 2764; DB 14; Length 532; Matches 531; Conservative I Mismatches 0; Gaps 0;	MSAFLDAVWOSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSA 60

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466 SQYRWPGVQGLYLTGASTHPGGGIMGASGRNAARVIVKDLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 542
TYPES: PRT
TYRES: PRT
ORGANISM: Synechocystis sp. PCC6803
US-10-209-372-6
                                                                                                                                     Sequence 6, Application US/10209372; Publication No. US20030100045A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 47
SOFTWARE: Microsoft Office
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US-10-369-493-2831
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE COF INVENTION: ELANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT PLLING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-22
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23397
LENGTH: 511
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347 GYGEYLAGQPTTDPPLVAMSFSAVDDSLAPPNGDVLMIMAQYYPFELA-TGSWETRTAEA 405
                                                                                              418 ADRIVGEMBAFAPGFTDSVLDRFIQTPRDIBSELGMIGGRVWHVEMSLDQWMLWRPLPEL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 ADAYRRFVAVWSERSKHVMKAFSTPPTGSNLIGAFGGLATARG----NSELSRQFLAPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 DALLIDBYPDSEALKAALAWFGAQSGPPMSEPGTAPMVGFAALMHVLPPGRAVGGSGALSA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 ALASRMAVDGATVALGDGVTSIR-RNSNHWTVTTESGREVHARKVIAGCHILITTLDLLGN 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 GGFDRITILDHWRRKIRVGPGIGAVIRLATSALPSYRGDATTRESTSGLQLIVSDRAHLRT 357
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                                                                                                                                                             478 SGHRVPGADGLYLTGASTHPGGGVSGASGRSAARIALSDSRR 519
                                                                                                                                                                                     466 SQYRWPGVQGLYLTGASTHPGGGIMGASGRNAARVIVKDLTR 507
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Publication No. US20030233675A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.9%; Score 688; DB 14; 31.9%; Pred. No. 1.5e-52;
APPLICANT: E. I . du Pont de Nemours, Inc.
APPLICANT: Cheng, Qiong
APPLICANT: Teo, Juan
TITLE OF INVENTION: CAROTENOID KETOLASE GENE
FILE REFERENCE: CL-1849 US NA
CURRENT APPLICATION NUMBER: US/10/209,372
CURRENT APPLICATION NUMBER: US/10/209,372
PRIOR PELING DATE: 2002-07-30
PRIOR FILING DATE:
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RESULT 8
US-10-369-493-19986
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Sequence 2831, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Gas, Yongwei
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, WARFRER: US/10/369, 493
CURRENT APPLICATION UNMERR: US/10/369, 493
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH. 5431
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1S-10-369-493-18878
Sequence 18878, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Synechocystis sp.
S-10-369-493-2831
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
ILENGTH: 539
LENGTH: 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 RDAKKYABETEYMORAIGAMIPMENAPPKSIIDIVGNYDITKFXDLFSVIGSPNKTLDFI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 BFIHLGPVVBELELGKYGLEYLECDPVVF---CPHPDGKYFLAHKSLEKTCAEIAR-YSE 120
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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; ORGANISM: Anabaena PCC7120
US-10-369-493-18878
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528 GRNCARVFL 536
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REPERBNCE: 38-10 (52052)8
FILE REPERBNCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2003-02-28
PRIOR PILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AYRRFVAVWSERSRHVMK-AFSTPPTGSNL----IG------AFGGLATARGNSELSRQ 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385 IAPAGRHOVTLWSOWOPYRLSCHRDWASV-AEAEADRIVGEMEAFAPGFTDSVLDRFIQT
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                                                                                                                                                                                                                                                        19.4%; Score 537.5; DB 15; Length 539; 30.4%; Pred. No. 4e-39;
                                                                                                                                                                                                                                                                                                               92; Mismatches
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Publication No US20030233675A1
GENERAL INFORMATION:
APPLICANT: Gao, Yongwei
APPLICANT: Binkle, Gregory J.
APPLICANT: Blater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
CURRENT FILING DATE: 2003-02-28
PRIOR PEPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12005
LENGTH: 539
TYPE: PRT
                                                                                                                                                                                   ORGANISM: Mesorhizobium loti
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Best Local Similarity 30.4
Matches 168; Conservative
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  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILL REFERENCE: 38-10 (5.205.2)
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILLING DATE: 2002-02-11
SEQ ID NO: 47374
SEQ ID NO: 47374
SEQ ID NO: 47374
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Greven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (5205.) B
CURRENT APPLICATION NUMBER: US/10/369, 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 BFIHLGPVVSELELBKYGLHYLBCDPVVF---CPHPDGKYFLGHKSLBKTCAEIAR-YNE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 GSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWTVTTBSGREVHARKVIAG----- 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 -CHILITILD-----LIGNGGFDRTTLDHWRR-KIRVGPGIGAVLR-LATSALPSYRG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 KYGVISNIDAKRLFLOMTDKSDVDCADPDLWERLERRIVNNNETILKIDLALDBPLHFPH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 HAHKDEYLVGSILIADSVAHVEQAHSKCTLGEIPDADPSMYVVMPSYLDPTLAPPGKH-- 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 TLWSQW-QPYRLSGHR-----DWA-SVAEAEADRIVGEMEAFAPGFTDSVLDRFIQTP 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 RDIBSELGMISGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGASTHPGGGVSGA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 LMIRHSGIIEELGLGAHGLRYIDCDPWAPAPPAPGTDGPGIVFHRDLDATCQSIERACGT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 KDADAYRRFVAVWSBRSRHVMKAPSTPP-----TGSNLIGAFGGLATARGNS----BLS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATTRESTSGLQLLVSDRAHLRTAHGAALAGELPPR-PAVLGMSFSGIDPTIAPAGRHQV 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| :: ||:: | ::: | ::: | 408 TVWIEYFAPYQIAGAEGTGLKGTGWTDELKNKVADRVVDKLADYAPNVKNATIARRVESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 DAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVE----RFPGYKVDRGSSAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 RIMLISAEDLLNEWFDEEFLKAPLARLASELGAPPSOKTLAIGAIMMAMRHNPGMARPRG
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                                                                                                                                                                                                                                                                                                                                                                                                                           59
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                                                                                                                                                                                                                                                                                                                                                                   ; Score 651.5; DB 15; Length 537; Pred. No. 2.7e-49; 90; Mismatches 225; Indele 59;
                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: No. US20030233675Altoc punctiforme-10-369-493-19986
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Sequence 12005, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         23.5%;
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 32.0%
Matches 176; Conservative
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279

331 343 384 393 443 452

231

125

64

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APPLICANT: Cac, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVARION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVARION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4938
LENGTH: 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 SRLPSFTALPGDGDHLTAGIIIAPSLGYMDRAYQDARAHGWS-----REPVVEMLIPST 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 VLPP-----GRAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNEWT-VTTES 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 AFGEVNGKKGVWGRAIGGMGAITSAMAAARAAGABIETSAGVREVLVEKDRVVGVILDD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 GRNVRARFVASNVNPKLLYTRLLPQDALPDD--VRRRMQNWK-----TGSGTPRMNVAL 334
                                                                                                                                                                                                                                                    60 NPKVIADLKIHEHGIRIVERKAQNPL-PAP--DGGYLL--TGSNTTAASIAR-LSAHDAA 113
                                                                                                                                                                                                                                                                                                                126 AYRREVA----VMSERSRH-VMKAFSTPPTGSNLIGAFG-------GLATARGNSELSR 172
                                                                                                                                                                                                                                                                                                                                           168 EQORILIEDIFTCSAGEMIDARFEHDIUV.-ALFGFDAIUGNYASPYAAGSA----YUMLHH 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 IDPTIAPAGRHQVTLWSQWQPYRLSGHRDWASVAEAEADRIVGEMEAFAPGFTDSVLDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 IQTPRDIESELGMIGGNVMHVEMSLDOMMLWRPLPELSGHRVPGA-DGLYLTGASTHPGG
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                                                                                                                                                        173 Q-----FLAPGDALLDEYFDSEALKAALAWFGAQSGPPMS--EPGTAPMVGFAALMH
                                                                                                                                                                                                                         66 HSGIIEELGLGAHGIRYIDCDPWAFAPPAPGTDGPGIVPHRDLDATCQSIRRACGTXDAD
                                                                                    Gaps
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                                                                                  80;
                                     ; Score 477; DB 15; Length 51; Pred. No. 9.5e-34; 85; Mismatches 216; Indels
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Pred. No. 2.9e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4938, Application US/10369493 publication No. US20030233675A1
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CRGANISM: Burkholderia fungorum
US-10-369-493-4938
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29.6%;
                                          17.2%;
                                          Query Match 17.2%
Best Local Similarity 30.9%
Matches 170; Conservative
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Best Local Similarity
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JS-10-369-493-20413
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APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry J.
APPLICANT: Gldman, Barry C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFRENCE: 38-10(52052)B
TITLE OF INVENTION NUMBER: US010/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
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PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 ASLFCQQFAPQLPDGRSWDDCREEVADLIIDTVNDHAPNFKASVIARQIHSPLDLERKFG 459
                                                                                                                                                                                                                                                                                                                            66 HSGIIBELGLGAHGLRYIDCDPWARAPPAPGT----DGPGIVFHRDLDATCQSIERACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 -----GRAVGGSGALSAALASRMAVDGAFVALGDGVTSIRRNSNHWT-VTTESGREVH 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 ARKVIAGCHILTTLDLLGNGGFDRTTLDH-WRRKIR-VGPGIGAV-LRLATSALPSYR-- 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 -GDATTRESTSGLØLLVSDRAHLRTAHGAALAGELPPRPAVLGMSFSGIDPTIAPAGRHQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 NGKLGAWGHSVGGMGAITQAMAKACVDAGVEISLEAPVSRVLVNNGKAAGVKLEGGEELY 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGASTHPGGGVSGASGRSAA 510
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                                                                                                                                                                                                                                     6 DAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFFGYKVDRGSSAHLMIR
                                                                                                                                                                                        Gaps
                                                                                                                                                                                        26;
                                                                                                                                      Query Match
17.5%; Score 484; DB 15; Length 521;
Best Local Similarity 30.5%; Pred. No. 2.3e-34;
Matches 164; Conservative 84; Mismatches 234; Indels 5
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LOCATION: (1). (218)
CHORER INFORMATION: unsure at all Xaa locations
                                                    TYPE: PRT
ORGANISM: Sphingomonas aromaticivorans
S-10-369-493-10809
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Publication No. US20030233675A1
GENERAL INFORMATION:
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         SEQ ID NO 10809
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US-10-369-493-12144

Sequence 12144, Application US/10369493

Sequence 12144, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwel

APPLICANT: Garegory J.

APPLICANT: Galdman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL-----LDBYPDSEALKAALAWFGAQSGPPMS--EPGTAPMV--GFAA--LMHVLPP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRHQVTLWSQWQPYRLSGHRD--WASVAEAEADRI----VGEMBAFAPGFTDSVLDRFIQ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 SPADLERIFALPGGHVHHGELSADQIPPRRPVQGAADYCTP-VKGLYQCGASVHPGGGVT 509
                                                                                                                  62 -PRIIDBLBLAKYGYBIV-----VPPPMLHLYGDGRSLFRPEGERLSADIAR-FSEA 112
                                                                                                                                                                                                                                            227 GRAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWT-VTTTESGREVHARKVIAG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 CHILITL---DLLGNGGF-----DRTTLDHWRRKIRVGPGIGAVLRLATSALP 330
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DAVIIGAGHNGLVCGAYLARKGFKVCLLERRELAGGAAVSEAVWPGYRVSTASYTWALLQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DADAYRREVAVWSERSRHVM-KAFSTP--PTGSNLIGAFGGLATARGNSELSRQFLAPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 TPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGASTHPGGGVS
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16.9%; Score 469; DB 15; Length 524;
Best Local Similarity 29.8%; Pred. No. 5e-33;
Matches 161; Conservative 81; Mismatches 238; Indels 60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSAFLDAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVE-RFPGYKVDRGSS
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Sequence 7696, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Ainkle, Gregory J.
APPLICANT: Alater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, BAPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052)B
TUTLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052)B
FRICK APPLICATION NUMBER: US/0360,039
PRIOR PILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7696
LENGTH: 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 CHILITL---DILGNGGF------DRITLDHWRRKIRVGPGIGAVLRLATSALP 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 GRHQVTLWSQWQPYRLSGHRD--WASVARARADRI----VGEMEAFAPGFTDSVLDRFIQ 442
                                                                                                                                                                                                       66 HSGIIBELGLGAHGLRYIDCDPWAFAPPAP---GTDGPGIVFHRDLDATCQSIERACGTK 122
                                                                                                                                                                                                                                                                62 -PRIIDELELAKYGYEIV-----VPPPMLHLYGDGRSLLFRPEGERLSADIAR-FSEA 112
                                                                                                                                                                                                                                                                                                                             DADAYRREVAVWSERSRHVM-KAPSTP--PTGSNLIGAPGGLATARGNSELSRQFLAPGD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 AL-----LDEYFDSEALKAALAWFGAQSGPPMS--EPGTAPMV--GFAA--LMHVLPP 226
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                                                                             DAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIR
                                                                                                               2 DAVIIGAGHNGLVCGAYLARKGFKVCLLERRELAGGAAVSBAVWPGYRVSTASYTWALLQ
                75;
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17.0%; Score 471.5; DB 15; Length 517;
Best Local Similarity 29.6%; Pred. No. 2.9e-33;
Matches 162; Conservative 91; Mismatches 220; Indels 75;
                    Indels
                220;
                91; Mismatches
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ORGANISM: Burkholderia cepacia
                    162, Conservative
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Glaten, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xiaifen
TITLE OF INVENTION: REPRESSION OF MICROBIAL PROFIEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: 2003-02-28
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                VIAGCHILTTLDLL-----GNGGFDRTTLDHWRRKIRVGPGIGAVERLATSALPSYRGDA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 ITRESTSGLOLLVSDRAHLRTAHGAALAGELPPRPAVLGMSFSGIDPTIAPAGRHQVTLW 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 VQVRMLPAEITGDAGGKIAPAHWDQVKDAYABRVLDIIETYAPGLRSKILGRSVFSPIDL 455
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                                                                                                   114 M-AAFSAADAATWRKLVAAFPGEAEHLFRLLGSPMSARALAGTAWNLWRKKGVAGALDTG 172
                                                                                                                                                                                                                                                                                                                                                                                                              286 VIAGVAPKALIGILILPGGSGNAGFDTA----MKKFRYAPGT-MMIHLALDELPGWRAGS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 SOWQ--PYRLSGH-----RDWASVARAEADRIVGEMEAFAPGFTDSVLDRFIQTPRDI 447
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60 NLSLFAGSAFHRKYANELKTQGLEFAPVADC----FASAFP--DGRWFGVSNDLEKTASR 113
                                                    IERACGTKDADAYRRPVAVWSERSRHVMKAPSTPPTGSNLIGAFGGLATARGNS---3LS 171
                                                                                                                                                                                                                                                             -GRAVGGSGA--LSAALASRMAVDGATVALGDGVTSIRRNSNHWTVTTESGREVH--ARK 281
                                                                                                                                                                                        FGMVLGKGGADTIIRALAGMVTSAGGKIVTGAEVSEITVSNGKATGVRLTSGETHTATKA
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; Pred. No. 8.8e-33;
92; Mismatches 231; Indels
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PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-1
NUMBER OF SEQ ID NOS: 47374
LENGTH: 544
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Publication No. US20030233675A1
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S-10-369-493-5969
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Matches 157; Conservative
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295 SNGKELHSKIVMSNATPHVTFNHLVK---KESLPEEFKRNINQIDYTSPVTKINVAVKEL 351
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-----APISKIMNKWFESDVLKATLGTDGVIGLAASPM-DPGT----GYVLL 234
                                                          221 MHVLPP-----GRAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSN-HWTVTT 271
                                                                                                                                                                                                                                                                                       PSY-----RGDATTRESTSGLOLLVSDRAHLRTAHGAAL---AGELPPRPAVLGMSFSGI 381
                                                                                                                                                                                                                                                                                                                                              352 PNFLAKPNQGSEPMPHHOTTIHM -- - NCENMQVVHDAVMDYKNGRYSRRPVIEMTIPSSV 408
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                                                                                                                 235 HHVIGGLDEHKGAMGYVYGGMGAVSNALAECAKSHGAEIYTEQDVQEVLLDGNVAKGVRL
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Sequence 8, Sequence 8,

Sequence 6, A Sequence 6, A Sequence 14, Sequence 10, Sequence 10, Sequence 10, Sequence 10,

Sequence 8, Al Sequence 10, 1 Sequence 8, Al Sequence 10, 2 Sequence 8, Al

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66 HSGIIEELGLGAHG-LRYIDCDP---WAFAPPAPGTDGPGIVFHRDLDATCQSIBRACGT 121
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Local Similarity 24.6%; Pred. No. 2e-11;
Les 137; Conservative 65; Mismatches 228; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Improved methods for transforming Phaffia
and recombinant DNA for use therein
51
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Sequence 17, Application US/09091725

Patent No. 6329141

GENERAL INFORMATION:

MAPLICANT.

ITILE OF INVENTION: Improved methods for transforming Pha TITLE OF INVENTION: and recombinant DNA for use therein NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster 11p

STREET: 2000 Pennsylvania Avenue, N.W.

CITY: Washington

STREET: 20006-1888

CONDUTER: United States of America

ZIP: 20006-1888

CONDUTER: IDM PC COMPATIBLE

COMPUTER: IDM PC COMPATIBLE

COMPUTER: IDM PC COMPATIBLE

COMPUTER: BALDABLE FORM:

MEDIUM TYPE: 310PPy disk

COMPUTER: BALDABLE FORM:

MEDIUM TYPE: 310PPy disk

COMPUTER: BALDABLE FORM:

MEDIUM TYPE: 310PPy disk

COMPUTER: BALDABLE FORM:

MEDIUM TYPE: 310PPy disk

COMPUTER: BP PC COMPATIBLE

PRILING DATE: 23-DEC-1996

APPLICATION NUMBER: BP 95203620.0

FILING DATE: 11-RPR-1996

ATTORNEY/AGENT INFORMATION:

NAMME: B. VICCOR DOMABLE

REGISTRATION NUMBER: 35-492

INPORMATION POR SFO IT NO. 1.
US-09-071-296-6
US-09-192-268-6
US-08-09-171-998-6
US-08-095-726-10
US-08-095-726-10
US-08-095-726-10
US-08-096-623A-10
US-08-096-623A-10
US-08-096-623A-10
US-09-052-469-8
US-09-052-262-8
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amino acid
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Sequence 18, Appl
Sequence 5, Appl
Sequence 19574, A
Sequence 30706, A
Sequence 5, Appli
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Sequence 5, Appli
Sequence 17737, A
Sequence 28032, A
Sequence 22259, A
Sequence 6, Appli
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1 MSAFLDAVVVGSGHNALVSA.....ALSDSRRGKASGWMRRSSRS 532
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(GGDZ 6/ptodata/2/iaa/5B_COMB.pep:*
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(GGDZ 6/ptodata/2/iaa/6A_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/6B_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/PCTUS COMB.pep:*
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                           GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-298-718-5
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US-09-546-969-5
US-09-547-903-14
US-09-934-903-16
US-09-934-903-18
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US-09-252-991A-1773-18
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US-09-125-991A-1773-18
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    protein - protein search, using sw model
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seg length: 200000000
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Gaps

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496 HPGGGVSG--ASGRSAARIALSD 516
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Nutley
                                            : 494 amino acids
amino acid
  INFORMATION FOR SEQ ID NO:
                    SEQUENCE CHARACTERISTICS
LENGTH: 494 amino acid
                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                        single
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                                                                                      STRANDEDNESS:
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COUNTRY: U
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122 KDADAYRRFVAVWSERSRHVMKAPSTPPTGSNLIGAFGGLATARGNSELSRQF----L 175
                                                                                                           124 --KDGFDRFLSFIQEAHRHYELA-----VVHVLOKNFPGFA----AFLRLQFIGQILAL 171
                                                                                                                                                     176 APGDAL---LDEYFDSEALKAALAWFGAQSG-PPMSEPGT------APMVGF 217
                                                                                                                                                                                                                                           218 AALMHVL-----PPGRAVGGSGALSAALAŞRMAVDGATVALGDGVTSIRRNSNHWTVT 270
                                                                                                                                                                                                                                                                                     -----GVR 273
                                                                                                                                                                                                                                                                                                                            271 TESGREVHARKVIAGCHILITILDILGNGGFDRTTLDHWRRKIRVGPGIGAVLRLATSALP 330
                                                                                                                                                                                                                                                                                                                                                                      274 LESGBEHHADVVIVNADLVYASEHL-----IPDDARNK-----IGOLGEVKRSWWA 319
                                                                                                                                                                                                                                                                                                                                                                                                                  331 SYRGDATTRESTSGLQLLVS-DR-AHLRTAHGAALAGE------LPPRPAVLG 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 MSFSGIDPTIAPAGRHQVTLWSQWQPYRLSGHRDWASVAEAEADRIVGEMEAFA----- 429
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APPLICANT: Holmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: PERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADBRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                  232 WOVPNTILIQIVKRNNPSAKFNFNAPVSQVILIS-PAKDRAT
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Batenin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,645A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 435
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REGISTATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAM 6002/170
FELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2861
TELEFAK: (201) 235-2363
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APPLICATION NUMBER: E2 95108688.9
FILING DATE: 09-JUN-1995
ATTORNEY/AGENT INFORMATION:
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Patent No. 6087152
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CITY: Nutley
STATE: NJ
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487 DKL.FFVGASTHPGTGV 502
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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S-08-660-645A-5
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165 SVHSMVARFIQ--DPHLRQAFSFHTLLV------GGNPFSTS-----SIYALIHALE 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 TOSSIERACGTKDADAYRRFVAVWSERSRH-VMKAFSTP--PTGS--NLIGAFGGLATAR 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 --IDPTIAPAG--RHQVTLMSQWQPYRLSGHRDWASVAEAEADRIVGEMEAFA-PGFTDS 435
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                                                                                                                                                                       7 AVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIRH 66
                                                                                                                                                                                                                 4 AIVIGAGFGGLALAIRLQSAGIATTIVEARDKPGGR-AYVWNDQGHVFDAGPT---VVTD 59
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                                                                                         Gaps
Query Match 7.9%; Score 217.5; DB 3; Length 494; Best Local Similarity 23.6%; Pred. No. 7.3e-11; Matches 133; Conservative 61; Mismatches 240; Indels 129;
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APPLICANT: Holmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: van Loon, Adolphus
APPLICANT: van Loon, Adolphus
APPLICANT: van ENEMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
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US-09-546-969-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.9%; Score 217.5; DB 3; Length 494; 23.6%; Pred. No. 7.3e-11; tive 61; Mismatches 240; Indels 129;
                                                                         Patentin Release #1.0, Version #1.30
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E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
                                                                                                                                                                                                                                                                                                     NAME: POKTAS, Bruce A.
REGISTRATION NUMBER: 32,746
REFERENCE/DOCKET NUMBER: RAN (
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEPAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
                                                                                                                                                                                                                                                       FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 23.69
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
     MEDIUM TYPE:
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SSULT 4

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67 SGIIEBLGLGAHGLRYIDCDPWAFA------PPAP-----GTDGPGIVFHRDLDA 110
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                                            Patent No. 6207409
GRNERAL INFORMATION:
APPLICANT: Holmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES:
ADDRESSES: Hoffmann-la Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,969
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERRENCE DOCKET NUMBER: 82,748
REFERRENCE DOCKET NUMBER: 82,748
REFERRENCE JOUNGER: RAN 6002/170
TELEPHONE: (201) 235-5801
TELEPHONE: (201) 235-2363
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Hoffmann-La Roche Inc. STREET: 340 Kingsland Street CITY: Nutley STATE.
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APPLICATION NUMBER: 08/660,645
Sequence 5, Application US/09546969 Patent No. 6207409
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TOPOLOGY: lin
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Matches 133;
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106 LIROV-ASFNPADVDGYRRFHDYAEEVYREGYLKIGTTPFLKLGOMLMAAPALMRLQAYR 164
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Similarity 23.6%; Pred. No. 7.3e-11;
33; Conservative 61; Mismatches 240; Indels 129;
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pasamontes, Luis
APPLICANT: Testier, Michel
APPLICANT: Testier, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: FERMENPATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS: ADDRESSE: HOffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER READBALE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
NAME: POKISH, BRUCE A.
REGISTRATION NUMBER: 32,748
REPERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                             496 HPGGGVSG--ASGRSAARIALSD 516
                                                                                                           468 HPGAGIPGVVGSAKATAQVMLSD 490
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amino acid
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APPLICATION NUMBER: US
FILING DATE:
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Best Local Similarity 23.6°
Matches 133; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MOLECULE TYPE: protein
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STATE: N.
COUNTRY:
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                                                                                                   381 --IDPTIAPAG--RHQVTLWSQWQPYRLSGHRDWASVAEAEADRIVGEMEAPA-PGFTDS 435
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4 AIVIGAGEGGLALAIRLQSAGIATTIVEARDKEGGR-AYVWNDQGHVEDAGET---VVTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yurri
TITLS OF INVENTION: Improved Fermentive Carotenoid
FILS REFERENCE: Improved Fermentive Carotenoid
CURRENT APPLICATION NUMBER: US/08/980,832B
CURRENT FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
335 DATTRESTSGLOLLVSDRAHLRTAHGAALAGELPPRPAVLGMSFSG-
                                                                                                                                                                                                                                                                                                                                           HPGGGVSG--ASGRSAARIALSD 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08980832B
Patent No. 6291204
GENERAL INPORMATION:
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SEQ ID NO 4
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S-08-980-832-4
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TOPOLOGY: linear
MOLECULE TYPE: protein
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CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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226 PGRAV----GGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWT-VTTESGREVHAR 280
                                           RRGGVWFAKGGTNQLVAGMVALFERLGGTLLLNARVTRIDTEGDRATGVTLLDGRQLRAD 268
                                                                                       KVIAGCHILTTL-DILGNGGFDRT----TLDHWRRKIRVGPGIGAVLRLATSALPSYRG 334
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                                                                                                                                                                                                                                                                                                                                                                    495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 GNSELSRQFLAPGDALLDEYFDSEALKAALAWFGAQSGPPMSEPGTAPMVGFAALMHVLP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 SVHSMVARFIQ--DPHLRQAFSFHTLLV------GGNPFSTS-----SIYALIHALE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 PGRAV----GGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWT-VTTESGREVHAR 280
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                                                                                                                                     269 TVASNGDVMHSYRDILGHTRRGRIKAAILNRQRWSMSL-----FVLHFGLSKRPE---
                                                                                                                                                                                                                                                                        381 --IDPTIAPAG--RHQVTLWSQWQPYRLSGHRDWASVAEAEADRIVGEMEAFA-PGFTDS
                                                                                                                                                                                                                                                                                                                                                                  436 VLDRFIQTPRDIESELGMIGGNVMHVEMSLDOMMLWRPLPELSGHRVPGADGLYLTGAST
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                                                                                                                                                                                 335 DATTRESTSGLOLLVSDRAHLRTAHGAALAGELPPRPAVLGMSFSG-
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APPLICANT: Tsygankov, Yuri
TITLE OF INVENITON: Fermentative Carotenoid Production
FILE REFERENCE: 15464 US (C38435/125944)
CURRENY APPLICATION NUMBER: US/09/920,923B
CURRENT FILING DATE: 2001-08-02
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PRIOR FILING DATE: 199-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
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ORGANISM: Flavobacterium sp. R1534
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Best Local Similarity 23.6%;
Matches 133; Conservative 6
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--IDPTIAPAG--RHQVTLWSQWQPYRLSGHRDWASVARAEADRIVGEMEAFA-PGFTDS 435
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269 TVASNGDVMHSYRDLLGHTRRGRTKAAILNRQRWSMSL-----FVLHFGLSKRPE--- 318
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                                                                                                       ----NEAHHSVIFG--PRYKGLVNEIFNGPRLPDDFSMYLHSP
                                                                                                                                                                                                                                                                           436 VLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLMRPLPELSCHRVPGADGLYLTGAST
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APPLICANT: Nathan, Carl F.
APPLICANT: BLAC, Sabine
TITLE OF INVENTION: DNA MOLECULE CONFERING ON MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS RESISTANCE AGAINST ANTIMICER
TITLE OF INVENTION: COXYGEN AND NITROGEN INTERMEDIATES
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.2%; Score 200; DB J. Best Local Similarity 24.5%; Pred. No. 2e-09; Anaervative 57; Mismatches 205; Indels
                                                       335 DATTRESTSGLQLLVSDRAHLRTAHGAALAGELPPRPAVLGMSFSG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Nixon, Hargrave, Devans & Doyle LLP Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                        496 HPGGGVSG--ASGRSAARIALSD 516
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APPLICATION NUMBER: US 60/045,688
FILING DATE: 06-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6177086
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                                                                                 DSEALKAALAWFGAQSGPPMSEPGTAPMVGFAALMHVLPPGRAVGGSGALSAALASRMAV 246
                                                                                                                        101 DARALFTGVAAHAISPLPSLVSAGAGLML--ATLAHSVGWPIPVGGTQAIADALIADLRA 158
                                                                                                                                                                 247 DGATVALGDGVTSIRRNSNHWTVTTBSGRZVHARKVIAGCHILTTLDLLGNGGFDRTTLD 306
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132 AVWSERSRHYMKAFSTPPTGSNLIGAFGGLAFARGN-SELSRQPLAPGD----ALLDEYF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 TPRLNPWRTP-IPKVYLCSAATPPGAGVHGMCGWYAARTLL 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Misawa, No. 5429919ihiko
APPLICANT: Robayashi, Kazuo
APPLICANT: Robayashi, Kazuo
APPLICANT: Nakamura, Katsumi
APPLICANT: Yamano, Shigeyuki
TITLE OF INVENTION: DNA SEQUENCES USFUL FOR THE
TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
OWRESPONDENCE ADDRESS:
                                                                                                                                                                                                      159 HGGRLAAGVEITEPQRSVVVFDTAPTALLRVY--
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APPLICATION NUMBER: US/07/783,705A
FILING DATE: 19911023
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FILING DATE: 05-MAR-1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 19-ARR-1990
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: JP 1-103078
FILING DATE: 21-ARR-1989
APPLICATION NUMBER: JP 2-53225
FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/07783705A
Patent No. 5429939
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REGISTRATION NUMBER: 33,778
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TELEPHONE: 212-708-1935
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26 West 61 Street
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CITY: No
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213 VWFPRGGTGALVQGMIKLFQDLGGEVVLNARVSHMETTGNKIEAVHLEDGRRFLTQAVAS 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 ACGIKDADAYRRFVAVWSERSRHVWK----APSTPPTGS--NLIGAFGGLATARG-NSEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 SRQFLAPGDALLDEYFDSEALKAALAWFG-AQSGPPMSEPGTAPMVGFAALMHVLPPGRA 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 -----INHHHDQLAHHTVCFG---PRYRBLIDBIFNHDGLAEDFSLYLHAPCVTDSSLA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387 PAGRHQVTLWSQWQPYRLSGHRDWASVAEAEADRIVGEMEA-PAPGFTDSVLDRFIQTPR 445
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                                                                                                                                                                                                                                                                                                                                                      6 VIGAGFGGLALAIRLQAAGIPVLILEQRDKPGGRAYVYED-QGFTFDAGPT---VITDPS
                                                                                                                                                                                                                                                                                                                9 VVGSGHNALVSAAYLAREGMSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIRHSG
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TILLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
FILE REFERENCE: CLid46 US NA
CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT PILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: September 1, 2001
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                            Indels 111;
                                                                                                                                                                                                           Length 492
                                                                                                                                                                                                        Query Match 6.9%; Score 191.5; DB 1;
Best Local Similarity 23.9%; Pred. No. 1.5e-08;
Matches 131; Conservative 65; Mismatches 242;
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No. 6660507ton, Kelley C.
Tomb, Jean-Francois
Rouviere, Pierre
Picataggio, Stephen
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Patent No. 6660507
TVPE: AMINO ACID
TVPE: AMINO ACID
TOPOLOGY: lina
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APPLICANT: Koffas, Mattheos
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                                                                                                                    , MOLECULE TYPE: protein US-07-783-705A-4
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US-09-934-903-16
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 CGTXDADAYRRFVAVWSERSR------HVWKAFSTPPTGSNLIGAFGLATARG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 --NSELSROFLAPGDALLDEYFDSEALKAALAWFGAQSG-PPMSEPGTAPMVGFAALMHV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 YGIXHVKGGLNRIAAAMAQVIAENGGEIHLASEIESLIIENGAAKGVKLQHGAELRGDEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 IAG---CHILITIDILGNGGFDRITIDHWRRKIRVGPGIGAVLRLATSALPSYRGD-AIT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 IINADFAHAMTHL-------VKPGV-----LKKYTPENLKQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 -----SGIDPTIAPAGRHQVTLWSQWQPYRLSGHRDWASVAEAEADRIVGEMEAFAPGF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 VVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIRHS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 FYVQNASASDDSLAPAGKSALYVLVP-MPNNDSG-LDWQAHCQNVREQVLDTLGA-RLGL
                                                                                                                                                                                                                                                                                                                                                              68 GIIBELGLGAHGLRYIDC----DPWAFAPPAPG----TDGPGIVFHRDLDATCQSIERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 VFNN-----LGQYFNQEXMRLAFCPQSKYLGMSPWECPALFTMLPY--LEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 LPPGRAVGGSGALSAALASRMAVDGATVALGDGVTS-IRRNSNHWTVTTESGREVHARKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 RE-STSGLOLLVS-DRAHLRTAHGAALAGELPPRPAVLGMSF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 REYSCSTEMLYLGLDKIY------DLPHHTIVFAKDYTNIRNIPDNKTLTDDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TD---SVLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLY
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TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
FILE REPERENCE: CLICKE US NA
CURRENT APPLICATION NOBRE: US/09/934,903
CURRENT FILING DATE: 2001.08-22
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: September 1, 2001
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
                                                                                                                                                                 Query Match 6.7%; Score 185; DB 4; Length 511; Best Local Similarity 21.1%; Pred. No. 5.8e-08; Matches 124; Conservative 87; Mismatches 226; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490 LTGASTHPGGGVSG--ASGRSAARIALSDSRRGK----ASQWWRRS 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 LVGGGTHPGSGLPTIYESARISAKL-ISQXHRVRFKDIAHSAWLKKA 509
                                                                                            OTHER INFORMATION: Amino acid sequences encoded by ORF8 09-934-903-16
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Schenzle, Andreas J.
No. 6660507ton, Kelley C.
Tomb, Jean-Francois
Rouviere, Pierre
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Patent No. 6660507
GENERAL INFORMATION:
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                       TYPE: PRT
ORGANISM: Methylomonas 16a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Koffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: Schenzle, Andrea
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-09-934-903-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 FHRDLDAT---CQSIERACGTKDADAYRRFVAVWSERSRHVMKAPSTPPTGSNLIGAFGG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 MHVLPPGR------AVGGSGALSAALASRMAVD-GATVALGDGVTSIRRNSNHWTVTTE 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 DGR-----ACAV----KLANG--DVLPADIVVSNMEVIPAMEKLLRSPASELKKW 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSGIDPTIAPAGRHOVTLW---SQWQPYRLSGHRDWASVARAEADRIVGEMEAFAPGFTD 434
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                                                                                                                                                                                                                                                                                                                                          10 IVIGAGLGGLSAAISLATAGPSVQLIEKNDKVGGKLNIMTK-DGFTFDLGPSI-LTMPH-
                                                                                                                                                                                                                                                                                                                                                                                                                68 GIIEEL--GLGAHGLRYID---CDP-WA-FAPPAPGTD--------GPGIV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 RGDATTRESTSGLOL-LVSDRAHLRTAHGAALAGELPPR------PAVLGMS
                                                                                                                                                                                                                                                                                                   8 VVVGSGHNALVSAAYLAREGWSVEVLENDTVLGGAVSTVERFPGYKVDRGSSAHLMIRHS
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                                                                                                                                                                                                                                           Indels 137;
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APPLICANT: Zweiger, Gary
APPLICANT: Xweiger, Gary
APPLICANT: Sweiger, Gary
APPLICANT: Sweiger, Matthew R.
APPLICANT: Seilhammer, Jeffrey J.
APPLICANT: Williamer, Jeffrey J.
APPLICANT: Seilhammer, Jeffrey J.
APPLICANT: Azimzai, Yalda
APPLICANT: Baughn, Mariah
APPLICANT: Lal, Preeti
TILE OF INVENTION: MARMALIAN TOXICOLOGICAL RESPONSE MARKERS
FILE REFERENCE: PC-0007 US
CURRENT FILING DATE: 1999-11-19
CURRENT FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                      1 Similarity 23.3%; Score 165.5; DB 4; Length 497; Similarity 23.3%; Pred. No. 3e-06; 28; Conservative 75; Mismatches 210; Indels 137
                                                                                                       ; OTHER INFORMATION: Amino acid sequences encoded by ORF9
US-09-934-903-18
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US-09-443-184-55
Sequence 55, Application US/09443184A,
Patent No. 6372431,
GENERAL INFORMATION:
                       TYPE: PRT
ORGANISM: Methylomonas 16a
                                                                                                                                                                                                                       Best Local Similarity 23.3
Matches 128; Conservative
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LENGTH: 497
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                                                                                                                                                                                         Query Match
Best Local
                                                                               FEATURE:
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity
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             US-09-252-991A-19574
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                                                          Query Match
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Sequence 19574, Application US/09252991A
Patent NO. 6551795
GENERAL INPORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR INJENTICS
TITLE OF INVENTION: AERUGINOSA FOR INJENTICS
FILE REFREENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19574
                                                                                                                                                                                                                                29;
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                                                                                                                                                                                                                                                                                                                                                            65 RHSGIIEELGLGAHGLRYIDCDPWAFAPPAPGTD-----GPG----IVFHRDLDATCQSI 115
                                                                                                                                                                                                                                                                                                                                                                                                  121 HYIGRMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                           ERACGTKDA--DAYRRFVAVWSERSRHVMKAFSTPPTGSNLIGAFGGLATARGNSELSRQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 FLAPGDALLDEYFDSEALKAALAWFGAQSG--PPMS-------EPGTAPMVGFA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 SLA---EVLQQLGASSELQAVLSYIFPTYGVTPNHSAFSWHALLVNHYMKGGFYPRGGSS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 --VHARKVIAGCHILITLDLLGNGGFDRITLDHWRRKI-RVGPGIGAVLRLATSALPSYR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 VNIYCPIVVSNAGLFNTYEHLLPG--NARCLPGVKQQLGTVRPGLG----MTSVFICLR 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 GDATTRE----STSGLQLLVSDRAHLRTAHGAALAGELPPRPAVLGMSF-SGIDPTIAP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 G---TKEDLHLPSTNYYVYYDTDMDQAMERYVSMPRERAAEHIPLFFRFPSAKDPTWED 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 --AGRHQVTL------RSQWQPYRLSGHR--DWA----SVARARAD------RIVGE 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453 RFPGKSTMIMLIPTAYSWPEEWQA-ELKGKRGSDYBTFKNSFVERSMSVVLKLFPQLEGK 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 MEAFFAPGFTDSVLDR---FIQTPR----DIESELGMIGGNVMHVEMSLDQMMLWRPLPELS 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             512 VESVTAG---SPLTNOFYLAAPRGACYGADHDLGRLHPCVM----ASLRAQSPIP--- 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 AL-MHVLPPGRAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWTVTTESGRE-
                                                                                                                                                                                                                                                                         5 LDAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMI
                                                                                                                                                                                                                                                                                                  68 LDVVVIGSGFGGLAAAALLAKAGKRVLVLBQHTKAGGCCHTPGK-NGLEFDTG-----1
                                                                                                                                                                                   5.3%; Score 146; DB 4; Length 610;
23.6%; Pred. No. 0.00021;
tive 73; Mismatches 239; Indels 122;
                                                                                                NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6372431 1867333CD1
IS-09-443-184-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 BIAPHTIPVIQRAGGA-VLTKATVQSVLLDSAGKACG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 GHRVPGADGLYLTGASTHPGGGVSGASG 506
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                                                                                                                                                                                      Query Match
Best Local Similarity 23.64
Matches 134; Conservative
                                                                 ORGANISM: Homo sapiens
SEQ ID NO 55
LENGTH: 610
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                   PEATURE
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Sequence 30706, Application US/09252991A
Facent No. 6551795
GENERAL INFORMATION:
TYPILG DEPTATION:
TYPILG OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                           141 VMKAFSTPPTGSNLIGAFG-GLATARGNSELSROFLAPGDALLDEYFDSEALKAAL---A 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 -----RPVVRRTPGAGPRIRRPAGGVPRLRVGA-------CAARRAVRPGPGLP 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 WFGAQSGPPMSEPGTAPMVGFAALMHVLPPGRAVGGSGALSAALASRMAVDGATVALGDG 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 RTAVRPTLRR---CRTSVRPVHLPWLSGRADPPYRPGHRORGACPAPTGRP--GQGRGER
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                      36 PRRESPECTSAWEDGEGWPVSNTPSPISPPSAGPIRRGSSTSTS----ALLATWT---
5.0%; Score 139; DB 4; Length 863;
22.4%; Pred. No. 0.0015;
ive 51; Mismatches 187; Indels 156;
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20.9%; Pred. No. 0.002;
tive 73; Mismatches 187; Indels 206;
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40 VDMLLVGAG---IMSATL-
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                                                                   Best Local Similarity 22.4
Matches 114; Conservative
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114 VGINTMFEVSKQFWSHLVAKGTFGSPKTFINPVPHLSFVRGSBGIAYLKKRFES-----L 168
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RHSGIIEELGLGAHGLRYIDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSIERACGTKDA 124
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                                                                                                                                                                                                                                                                    -GALSAALASRMAVD-GATVALGDGVTSIRRNSNHWTVT---TESG--REVHARKVIAGC 286
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                                                                                                                                                                                                                                                                                            ------GALPLIQLSGIPEGKG-------
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                       Laitz, Richard H.

APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Medduri, Krishnamurthy
APPLICANT: Melo, Donald J.
APPLICANT: Treadway, Parti J.
APPLICANT: Treadway, Parti J.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow Arror
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442 LOFGTELVAAHDGSIAALLGASPGASVTVSIMLGLIERCPPEQARSPEW 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dow AgroSciences LLC Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/036,987A
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NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                      -----FLGAGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 09-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Indianapo
STATE: Indiana
COUNTRY: USA
                                             OESGAIE
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967 S.-H-------PWLSDHRYLGEIVVPGTAIVELVHHVGERLGCGRVEELALEA 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LGAHGLRYIDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSIBRACGTKDADAYRRFVA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 VWSERSRHVWKAPSTPPTGSNLIGAPGGLATARGNSELSROFLAPGDALLDEYPDSEALK 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 LGDGVTSIRR----NSNHWTVTTES-----GREVHARKVIAGCHILTTLDLLGNGGFD 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               871 MRKDRDEARTVL-AALAQIHTRGGEVDWRSFFAGTGAKQVDLPTYA-------FQRQ 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 PYRLSG---HRDWASVARARADR-IVGEMEAFAPGFTDSVLDRFIQTPRDIESELGMIGG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                        591 GLYSVPPVFADAFDEACAELDAHLGQELRVRDVVFGSQAKLLDRTVWAQSGLFALQIGLL 650
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                                                                                                                                                                                                                                                                                                                  3 AFLD--AVVVGSGHNALVSAAYLAREGWSV-EVLEKDTVLGGAVSTV----ERFPG---
                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                              238;
                                                                                                                                                                                                                                   4.8%; Score 133; DB 3; Length 4928; 23.4%; Pred. No. 0.062; ive 61; Mismatches 196; Indels 23
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he : 19.1665 Becs
                                                                                                                                                                                                                                                                                                                                                                                                      --YKV-----DR-----
            TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEPAX: (317)337-4846
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                   4928 amino acids
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                          Best Local Similarity 23.4 Matches 151; Conservative
                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                    amino acid
                                                                                                                                                                                              US-09-036-987A-5
                                                                                                                   LENGTH:
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Job time
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The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway, under the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q, Dicosimo DJ,
C, Rouviere PB;
                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Encoded by GTG"
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                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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01-SEP-2000; 2000US-0229907P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brzostowicz PC, Cheng Q, Odom JM, Picataggio SK,
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N-PSDB; AAD35515.
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Abp71894 Synechpcy
Adm33657 Human oxi
Adc3152 Human nov
Adg3152 Human nov
Adg3152 Human nov
Adg3152 Human nov
Adg3287 C glutami
Aav22815 Synechocy
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Aab76641 Corynebac
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DE	Rho	Rhodococcus	erythropolis AN12	polis	Ä	12 beta-carotene ketolase	(Crto)	enzyme.
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Ž	ant	anti-oxidant; steroid;	; stero		lav	flavour; fragrance; electro-optic application;	ptic appli	cation;
₹	agu	aquaculture;	елгуте		Ü	enzyme; beta-carotene ketolase; CrtO.		
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01-AUG-2002; 2002WO-US024317.

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control of regulatory sequences, and contacting the host cell with carbon substrate to produce a caroteenoid compound. The method is useful for producing caroteenoid compounds such as antheraxanthin and astaxanthin, by using microorganism having a nucleic acid molecule encoding enzymes in the caroteenoid biosynthetic pathway and which metabolise single carbon substrates. The caroteenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The caroteenoids are also useful as compounds for potential electro-optic applications. The present sequence is Rhodococcus erythropolis ANI2 beta-caroteene ketolase (CrtO) enzyme
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Sequence 532 AA;

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100.0%; Score 2768; DB 5; Length 532; 100.0%; Pred. No. 5.7e-223; ive 0; Mismatches 0; Indels 0.
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Carotenoid ketolase; enzyme; cyclic ketocarotenoid biosynthesis; crtO. R. erythropolis carotenoid ketolase crtO. ABP71892 standard; protein; 532 (first entry) Rhodococcus erythropolis. WO2003012056-A2. 10-MAY-2003 ABP71892; BSULT 2
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The invention relates to a novel isolated nucleic acid encoding a carotemoid ketolase enzyme which: (i) encodes an amino acid sequence containing all six conserved motifies of CTrO enzymes of Rhodococcus containing all six conserved motifies of CTrO enzymes of Rhodococcus errbiropolis ANIZ strain, Deinococcus radiodurans R1 strain, and acide, given in specification, or (iii) hybridises to (ii) or (ii). A nucleic acid of the invention is useful for obtaining a mucleic acid also useful for producing cyclic ketocarotenoid compounds. A chimeric gene is useful for regulating cyclic ketocarotenoid biosynthesis in an organism by introducing cyclic ketocarotenoid biosynthesis in an organism by introducing the gene into a host cell and growing the host cell under conditions whereby the carotemoid ketolase gene is expressed and the cyclic ketocarotenoid biosynthesis, where the carotenoid ketolase gene is expressed on a multicopy plasmid or is operably linked to a inducible or regulated promoter. Optionally the cyclic ketocarotenoid biosynthesis may be down regulated, where the cyclic ketolase gene is expressed in anishense orientation or is operably linked to a inducible or regulated promoter. Optionally the cyclic ketocarotemoid ketolase gene is expressed in anishense orientation or is disrupted by insertion of foreign DNA into the coding region. The present sequence represents the R. erythropolis strain ANIZ crtO polypeptide
                                                                                                                                                                                                                                                      New isolated nucleic acid encoding carotenoid ketolase enzyme, useful for producing cyclic ketocarotenoid compounds such as adonirubin, echinenone, and as probes or primers to identify nucleic acids encoding the enzyme.
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99.8%; Pred. No. 1.2e-222;
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                                               02-AUG-2001; 2001US-0309653P.
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Matches 531; Conservative
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ABP71893 standard; protein; 511 AA SULT 3 P71893

ABP71893;

radiodurans carotenoid ketolase crt0. Ö.

(first entry)

10-MAY-2003

Carotenoid ketolase; enzyme; cyclic ketocarotenoid biosynthesis; crtO

Deinococcus radiodurans.

WO2003012056-A2.

13-FEB-2003.

01-AUG-2002; 2002WO-US024317.

02-AUG-2001; 2001US-0309653P.

M (DUPO) DU PONT DE NEMOURS & CO

Cheng Q, Tao L;

2003-300493/29. WPI; 2003-300493 N-PSDB; ABZ75461 New isolated nucleic acid encoding carotenoid ketolase enzyme, useful for producing cyclic ketocarotenoid compounds such as adonirubin, echinenone, and as probes or primers to identify nucleic acids encoding the enzyme.

Claim 15; Page 69-71; 90pp; English.

The invention relates to a movel isolated nucleic acid encoding a carotenoid ketolase enzyme which: (1) encodes an amino acid sequence containing all six conserved motifs of Crto enzymes of Rhodococcus erythropolis AN12 strain, Deinococcus radiodurans R1 strain, and scids, given in specification; or (iii) encodes a sequence of 532 amino acids, given in specification; or (iii) hybridises to (1) or (ii). A nucleic acid of the invention is useful for obtaining a nucleic acid of the invention is useful for obtaining a nucleic acid of the invention square enzyme. A nucleic acid of the invention square enzyme. A nucleic acid of the invention gene is useful for regulating cyclic ketocarotenoid biosynthesis in an organism by introducing the gene into a host cell and growing the host cell under conditions whereby the carotenoid ketolase gene is expressed and the cyclic ketocarotenoid biosynthesis; where the carotenoid ketolase gene is expressed and the cyclic ketocarotenoid biosynthesis; where the carotenoid ketolase gene is overexpressed on a multicopy plasmid or is operably linked to a inducible or regulated promoter. Optionally the cyclic ketocarotenoid biosynthesis may be down regulated, where the carotenoid ketolase gene is expressed in antisense orientation or is disrupteed by insertion of foreign DNA into the coding region. The present sequence represents the D. radiodurans strain R1 crtO polypeptide

Sequence 511 AA;

11; 6 DAVAVGSCHNALVSAAYLAREGWSVEVLEXDTVLGGAVSTVERPPGYKVDRGSSAHLMIR 65 31.1%; Score 859.5; DB 6; Length 511; 39.7%; Pred. No. 3.6e-63; iive 80; Mismatches 208; Indels 27; Gaps Query Match
Best Local Similarity 39.7
Matches 207; Conservative

64

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118 GDAYGRFLDDWTPFARAVADLFNSAPGPLDL----GKMVMRSGQGKDWNEQLPR-ILRPY 172
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66 HSGIIEELGLGAHGLRYIDCDPWAFAPPAPGTDGPGIVF-HRDLDATCOSI-BRACGTKD 123
                          65 NTPIVRELELTRHGLHYLBVDPMFHA----SDGBTPWFIHRDAGRTIRELDEKFPG--Q
                                                                                                                                     24 ADAYRRFVAVWSBRSRHVMKAFSTPPTGSNLIGAFGGLATARG-----NSELSRQFLAPG
                                                                                                                   179 DALLDBYFDSEALKAALAWFGAQSGPPMSEPGTAPMVGFAALMHVLPPGRAVGGSGALSA
                                                                                                                                                                               239 ALASRMAVDGATVALGDGVTSIR-RNSNHWTVTTESGREVHARKVIAGCHILTTLDLLGN
                                                                                                                                                                                                                                          298 GGFDRTTLDHWRRKIRVGPGIGAVIRLATSALPSYRGDATTRESTSGLQLLVSDRAHLRT
                                                                                                                                                                                                                                                                                                    358 AHGAALAGELPPRPAVLGMSFSGIDPTIAPAGRHQVTLWSQWQPYRLSGHRDWASVARAE
                                                                                                                                                                                                                                                                                                                                                                  418 ADRIVGEMEAFAPGFIDSVLDRFIQIPRDIESBIGMIGGNVMHVEMSLDOMMLWRPLPBL
                                                                                                                                                                                                                                                                                                                                                                                                                            478 SCHRVPGADGLYLTGASTHPGGGVSGASGRSAARIALSDSRR 519
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ABP71894 standard; protein; 542 10-MAY-2003 ABP71894; RESULT

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Synechpcystis carotenoid ketolase crtO.

Carotenoid ketolase; enzyme; cyclic ketocarotenoid biosynthesis; crtO. 01-AUG-2002; 2002WO-US024317. Synechocystis sp. WO2003012056-A2. 13-FEB-2003.

(DUPO) DU PONT DE NEMOURS & CO E WPI; 2003-300493/29. Cheng Q, Tao L; N-PSDB; ABZ75462

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02-AUG-2001; 2001US-0309653P.

New isolated nucleic acid encoding carotenoid ketolase enzyme, useful for producing cyclic ketocarotenoid compounds such as adonirubin, echinenone, and as probes or primers to identify nucleic acids encoding the enzyme.

Disclosure, Page 72-74, 90pp, English.

The invention relates to a novel isolated nucleic acid encoding a carotenoid ketolase enzyme which: (i) encodes an amino acid sequence containing all six conserved motifs of CrtO enzymes of Rhodococcus erythropolis AN12 strain, Deinococcus radiodurans R1 strain, and

Symechocystis sp. PCC6803 strain, (ii) encodes a sequence of 532 amino acid, given in specification; or (iii) hybridises to (i) or (ii). A nucleic acid of the invention is useful for obtaining a nucleic acid encoding a carotenoid ketolase enzyme. A nucleic acid of the invention is encoding a carotenoid ketolase enzyme. A nucleic acid of the invention is also useful for producing cyclic ketocarotenoid compounds. A chimeric gene is useful for regularing cyclic ketocarotenoid biosynthesis in an organism by introducing the gene into a host cell and growing the host cell under conditions whereby the carotenoid ketolase gene is expressed and the cyclic ketocarotenoid biosynthesis; where the carotenoid ketolase gene is expressed on a unliciopy plasmaid or is carotenoid ketolase gene is overspressed on a multicopy plasmaid or is carotenoid ketolase gene is overspressed on a multicopy plasmaid or is carotenoid ketolase gene is overspressed on a regulated, where the carotenoid ketolase gene is expressed in antisense orientation or is operably linked to a inducible or regulated promoter. Optionally the cyclic ketocarotenoid biosynthesis may be down regulated, where the carotenoid ketolase gene is expressed in antisense orientation or is disrupted by insertion of foreign DNA into the coding region. The present sequence represents the Synechocystis sp. strain PCC6803 crto polypeptide Sequence 542 AA; ត្តម្ភិទីទីពិពីពិព័ព្ធពេលបាន

48; Query Match 24.9%; Score 688; DB 6; Length 542; Best Local Similarity 31.9%; Pred. No. 9.1e-49; Matches 175; Conservative 97; Mismatches 229; Indels

121 KDADAYRRFVAVWSERSRHVMKAFSTPPTG-----SNLIGAFGGLATARGNSELS 171 64 :||:||:|| |:: RDAEKYRQFVNYWTDLLNAVQPAFNAPPQAŁLDLALNYGWENLKSVLAIAGSKTKALDFI LMIRHSGIIEELGLGAHGLRYIDCDPWAFAPPAPGTDGPGIVFHRDLDATCQSIERACGT EPIFIGEVILORINIAQYGLEYLFCDESVF---CPGLDGQAFMSYRSLEKTCAHI-ATYSP ROFLAPGDALLDEYFDSBALKAALAWFGAQSGPPMSEPGTAPMVGFAALMHVLPPGRAVG 6 DAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVST----VERPPGYKVDRGSSAH 62 65 122 121 172

181

341 STSGLQLLVSDRAHLRTAHGAALAGELPPRPAVLGMSF-SGIDPTIAPAGRHQVTLWSQ- 398 :| |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: WQPYRLSG-----HRDWA-SVARARADRIVGEMEAFAPGFTDSVLDRFIQTPRDIESE 450 296 NIDARRIFIQLVEPGALAKVNONIGERLERRIVNNNEAILKIDCALSGLPHFTAMAGP-E 354

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LCMIGGNVWHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGASTHPGGGVSGASGRSAA 510 451

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06-NOV-2001 AAM93657; RESULT 5 ESULT e a

511 RIALSDSRR 519 |: | | || RVFLKQQRR 473 Ď,

581 AA Human polypeptide, SEQ ID NO: 3528 AAM93657 standard; protein; (first entry) 일정보정말

Human; full length cDNA; cDNA synthesis; oligo-capping.

Homo sapiens.

EP1130094-A2

05-SEP-2001

07-JUL-2000; 2000EP-00114089

08-JUL-1999; 99JP-00194486. 11-JAN-2000; 2000JP-00118774. 02-MAY-2000; 2000JP-00183765. 08-JUL-1999;

(HELI-) HELIX RES INST.

ai Y; Koga ai I, Hayashi K, Ishii S, Kawai Nagai K, Kojima S, Oteuki T, Ko Nishikawa T, Isogai Wakamatsu A, Sugiyama T,

WPI; 2001-524255/58. N-PSDB; AAK94592.

830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.

Claim 8; SEQ ID NO 3528; 1380pp + Sequence Listing; English.

The invention relates to primers for synthesising full length cDNA clones. 330 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length not form part of the printed specification, but was obtained in CD-ROM format directly from EPO

Sequence 581 AA;

69 Query Match 22.6%; Score 624.5; DB 4; Length 581; Best Local Similarity 33.0%; Pred. No. 2.1e-43; Matches 185; Conservative 81; Mismatches 226; Indels 69.

326 VLEDGTEVRSKAVLSNTSPQITFLKLTPQEWLPEEFLERISQLDTRSPV-----TKIN 378

LATSALPSY-----RGDATTRESTSGLOLLVSDRAHLRTAHGAALAGELPPRPAVLGM 376

324

270 TIESGREVHARKVIAGCH-----ILTTLDLLGNGGFDRTTLDHWRRKIRVGPGIGAVLR 323

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185; Conservative
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                                                                                      497
                                                                                                                     436 VLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLJGAST 495
                                                                                                                                                     The sequence represents a novel human oxidoreductase polypeptide of the invention, designated OXIRED-8. The proteins of the invention have cytostatic, neuroprotective, cardiant, immunosuppressive, antiinflammatory, neuroleptic, and endocrine activity. The polypeptide is used in the diagnosis and treatment of disorders associated with disorders include cancer, cell proliferative disorders, neurological, cardiovascular, autoimmune/inflammatory and metabolic disorders. Note: The sequence data for this patent did not form part of the printed security in the sequence data for this patent did not form part of the printed security contraction, but was obtained in electronic format directly from WIPO
                                          377 SFSGIDPTIAPAGRHQVTLWSQWQPYRLSGHRDW-ASVAEABADRIVGEMEAFAPGFTDS 435
379 VAVDRLPSFLAAPNAPRGQPLPHHQCS-IHLNCEDTLLLHQAPEDAMDGLPSHRPVIELC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           man oxidoreductase polypeptide, useful in the diagnosis and treatment disorders associated with its activity, e.g., cancer and autoimmune
                                                                  Human, oxidoreductase, OXIRED, cytostatic; neuroprotective, cardiant, immunosuppressive; antiinflammatory; neuroleptic; endocrine; cancer; neurological disorder; cardiovascular disorder; autoimmune disorder; inflammatory disorder; metabolic disorder;
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Elliott VS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human oxidoreductase protein OXIRED-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 8; 117pp; English.
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Sanjanwala MS, Yao MG, Ding L,
                                                                                                                                                                                                                                                                                                                                                         ABB77177 standard; protein; 581
                                                                                                                                                                                                            HPGGGVSGASGRSAARIALSD
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06-0CT-2000; 2000US-0238482P.
27-0CT-2000; 2000US-0244024P.
01-DEC-2000; 2000US-025805P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Score 624.5; DB 5; Length 581; Pred. No. 2.1e-43;

22.6%; 33.0%;

Query Match Best Local Similarity

Sequence 581 AA;

ftp.wipo.int/pub/published_pct_sequences

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18;
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                                                                                                                                                                                                                                                                                                                              212 LGAQLPRYYEVLTAPITKVLDQMFESEPLKATLATDAVIGAMTSP--HTPGS----GYVL 265
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379 VAVDRLPSFLAAPNAPRGQPLPHHQCS-IHLNCRDTLLLHQAPEDAMDGLPSHRPVIELC 437
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                                     6 DAVVVGSGENALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIR
                                                                             36 DAVVICAGHNGLVAAAYLORLGVNTAVFERRHVIGGAAVTEEIIPGFKFSRASYLLSLLR
                                                                                                                   66 HSGIIEELGLGAHGLRYIDCDPWAFAPPAPGTDGPG-----IVFHRDLDATCQSIERAC
                                                                                                                                                                                                                                               152 SOKDAQVFPKYEEFMHRLALAIDPLLDAAPVDMAAFQHGSLLQRMRSLSTLKPLLKAGRI
                                                                                                                                                                                                                                                                                         -NSELSRQF---LAPGDALLDRYRDSEALKAALAW---PGAOSGPPMSEPGTAPMVGFAA
                                                                                                                                                                                                                                                                                                                                                                           LMHVLPP-----GRAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWT--V
                                                                                                                                                                                                                                                                                                                                                                                                 326 VLEDGTEVRSKMYLSNTSPOITFLKLTPOEWLPBEFFLERISQLDTRSPV-----TKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377 SPSGIDPTIAPAGRHQVTLWSQWQPYRLSGHRDW-ASVAKAEADRIVGEMEAFAPGFTDS
69
                                                                                                                                                                                                       GTKDADAYRRFVAVWSERSRHVMKAFSTPPTG-----SNLIGAFGGLATARG-
81; Mismatches 226; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human novel polypeptide sequence, SEQ ID NO:1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPGGGVSGASGRSAARIALSD 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC31532 standard; protein; 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-2002; 2002WO-US030474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-SEP-2001; 2001US-0324631P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; chromosome 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402003029271-A2
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Wehrman T; Weng G;

Wang J, Wang Z, ≀

The invention relates to 971 novel human CDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99\$ identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a mucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of invention discloses methods of polympeptide of the invention; and methods of invention further discloses methods of polypeptide of the invention. The invention further discloses methods of perventing, treating or invention further discloses methods of polypeptide of the invention. The invention methods for the invention; and/or monoclonal antibodies for carrying out the methods of the invention or and/or methods for the invention of compounds that modulate the invention are invention; methods for the polypeptides and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention are inventily sequences corresponding to the cDNA sequences of the invention are useful in diagnostics, drug screening, for essenting (ADC32627) and the polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmume diseases or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as molecular weight markers, and in the recombinant production of a procein. The programmers, and in the recombinant production of apprehences the present sequence represents a specifically business. New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Haley-Vicente D, Drmanac RT; Claim 20; SEQ ID NO 1614; 1185pp; English 2003-371981/35. WPI; 2003-371981 N-PSDB; ADC30561

Seguence 504 AA;

ftp.wipo.int/pub/published_pct_sequences

and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

17; 166 66 HSGIIBELGLGAHGLRYIDCDPWAFAPPAPGTDGPG-----IVFHRDLDATCQSIBRAC 119 96 PQ-IYTDLEL/KKHGLRLHIRNPYSFTPML--EBGAGSKVPRCLLLGTDWAENQKQIAQ-7 151 167 -NSELSROF---LAPGDALLDEYFDSEALKAALAW---FGAQSGPPMSEPGTAPMVGFAA 219 325 95 65 GINDADAYRRFVAVWSERSRHVWKAFSTPPTG-----SNLIGAFGGLATARG-----152 SOKOAQVEPKYEEFWHRLALAIDPILDAAPVDMAAFQHGSILLQRMRSLSTLKPLLKAGRI LMHVLPP-----GRAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWT--V 6 DAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHLMIR 14.6%; Score 403; DB 7; Length 504; 29.2%; Pred. No. 6.1e-25; tive 71; Mismatches 200; Indels Conservative Query Match Best Local Similarity Matches 140; ጽ 쉱 ਨੇ 용 ጵ 9 ጽ မ္ပ \gtrsim

324 LATSALPSY-----RGDATTRESTSGLOLLVSDRAHLRTAHGAALAGELPPRPAVIGM 376 326 VLEDGTEVRSKMVLSNTSPQITFLKLTPQEWLPEEFLERISQLDTRSPV-----TKIN 378 270 TIESGREVHARKVIAGCH-----ILTILDILGNGGFDRTTLDHWRRKIRVGPGIGAVLR 323 377 SFSGIDPTIAPAGRHQVTLWSQWQPYRLSGHRDW-ASVABABADRIVGEMBAFAPGFTD 434 379 VAVDRLPSFLAAPNAPRGQPLPHHQCS-IHLNCRDTLLLHQAFEDAMDGLPSHRPVIELC ģ 셤 d ð ò

RESULT 8 ADC33152

Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; namenta platelet disorder; wound; burns; neurodegenerative disease; anseriment alsease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; meturoprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antialcer; osteopathic; immosuppressive; antilflammatory; cytostatic; gene therapy; chromosome 10. Human novel contig-encoded polypeptide sequence, SEQ ID NO:3234 Ę ADC33152 standard; protein; 322 (first entry) 18-DEC-2003 ADC33152;

Homo sapiens.

WO2003029271-A2

10-APR-2003

24-SEP-2002; 2002WO-US030474.

24-SEP-2001; 2001US-0324631P.

(HYSE-) HYSEQ INC

Wehrman T; Wang J, Wang Z, Ren F, Xue AJ, Zhao QA, Wang D, Ma Y, Asundi V, Drmanac RT; Tang TY, Zhang J, Zhou P, Ghosh M, Haley-Vicente D,

WPI; 2003-371981/35. N-PSDB; ADC32385 New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer.

Example 2; SEQ ID NO 3234; 1185pp; English

The invention relates to 971 novel human cDNA sequences (ADC29919-ADC3089) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to mucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or invention and methods of peventing, treating or invention and antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the invention, methods for the identification of compounds that modulate the invention, methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767

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contig sequences corresponding to the cDNA sequences of the invention (ADC31961-ADC32627) and the polypeptides encoded by the contigs (ADC32628 ADC3394). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmume diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a human contigenced polypeptide sequence used in an example of the invention. Note: The bequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipc.int/pub/published_pct_sequences
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Sequence 322 AA;

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284
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                                                                                                                                                                                                                                                                              -- LPREFLERISQLDTRS 117
                                                                                                                                                                                                                                                                                                                                      344 GLOLLVSDRAHLRTAHGAALA----GELPPRPAVLGMSFSGIDPTIAP-----AGR 390
                                                                                                                                                                                                                                                                                                                                                                                        173
                                                                                                                                                                                                                                                                                                                                                                                                                                                HRDWASVARAEADRIVGEM 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZAFAPGFTDSVLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVYAPGEKDSVVGRDILTPPDLERIFGLPGGNIFHCAMSLDQLYFARPVPLHSGYRCP-L 287
                                                                                                                                                                    85
                                                                                                               227 GRAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWT--VTTESGREVHARKVIA
                                                                                                                                                                    26 GYVQGGMGALSDALASSATTHGASIFTEKTVAKVQVNSEGCVQGVVLEDGTEVRSKMVLS
                                                                                                                                                                                                                         285 GCHILITLDLLGNGGFDRTTLDHWRRKIRVGPGIGAVLRLATSALP-SYRGDATTRESTS
                                                                                                                                                                                                                                                                                                                                                                         174 ROAAOPS-WRPPMLPGASRCPITNAPSTXTVKT2SSFIRPLKMPWMACLPTVFDCI----
                                                       19;
11.0%; Score 305.5; DB 7; Length 322; 30.5%; Pred. No. 4.9e-17; Indels 79; ive 34; Mismatches 117; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 DGLYLTGASTHPGGGVSGASGRSAARIALSD 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OGLYLCGSGAHPGGGVMGAAGRNAAHVAFRD 318
                                                                                                                                                                                                                                                                                 86 NTSPQIT-----FLKLTPQEW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 HOVTLWSOWOPYRLSG-
  Query Match
Best Local Similarity 30.5:
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229
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AAG90287 standard; protein; 471 AAG90287;

(first entry) 26-SEP-2001

amino acid synthesis; vitamin; saccharide; C glutamicum protein fragment SEQ ID NO: bacterium; Coryneform

368

320 H-----VGGSSEELAFAEAEVAAGRMPERPFIILCOOOVADPSRAREGRHVV--WA--

340 BSTSGLQLLVSDRAHLRTAHGAALAGBLPPRPAVLGMSFSGIDPTIAPAGRHQVTLWSQW

ð 셤 ò 셤 Ò g

453

399

:||:: 419 VGGDI-----TAGSALLRRMPTKIGEKT-----YMASASNAPGGGVHGMPGWWAAQAV 466

514 LSDSR 518 |:| |

454 IGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGASTHPGGGVSGASGRSAARIA 513

369

100 QPYRLSGHRDWASVARARADR----IVGEMBAFAPGFTDSVLDRFIQTPRDIBS-BLGM

Corynebacterium glutamicum.

organic acid synthesis.

EP1108790-A2

20-JUN-2001

18-DEC-2000; 2000EP-00127688

16-DEC-1999; 99JP-00377484. 07-APR-2000; 2000JP-00159162.

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly 1-1ysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 WPVAVGGSGRIVDALVNVINHHGGTIHCDSQIDSL-----SQFRDTDA--IILN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 HSGIIBELGIGAHGLRYIDCDPWARAPA---PGTDGPGIVFHRDLDATCQSIERACGTK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---AVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWTVTTESGREVHARKVIAG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 CHILTIDLLG---NGGFDRTTLDHWRRKIRVGPGIGAVLRLATSALP---SYRGDATTR 339
                                                                                                                                                                                                                        mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                  polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LLPAKRLASAAPETERARSLFIGSAMHSVTPPHKPMTASL---GLLFGALGMSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 QTPSQVLKLKGTDLNAGLPQ-RMSTWKH----GPSSYKVDYLLDGPIPWSNPQVGQATTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 AVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERF-PGYKVDRGSSAHLMIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 ASPAFHYLGLEDHGLE-----WAYSPFAMAHPLDYGRAGLLETSLPETAKKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------AFGGLATARGNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 LSRQFLAPGDALLDEYFDSEALKAALAWFGAOSGPPMSEPGTAPMVGFAALMHVLPPGR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AVVVGSGPNGLTTAAVLAKAGWQVDVYEAAPTPGGAARSESVLGEGTISDLGAAGHPFGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GPDA-RRWKNIHQGLTKNIDKHL----ANLIGPVLKWPAHPIRMAKFGPFA-----
                                                                              Yokoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 119;
                                                                                                                                                                                                                                                                                      Claim 17; SEQ ID NO 4041; 246pp + Sequence Listing; English.
                                                                              Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 296.5; DB 4;
Pred. No. 4.6e-16;
61; Mismatches 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 DADAYRRFVAVWSERSRHVMKAFSTPPTGSNLIG----
                                                                            S, Hayashi M,
Ozaki A;
                                                                              H, Ando S
Ikeda M,
03-AUG-2000; 2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%;
                                         (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141; Conservative
                                                                              Mizoguchi
Senoh A,
                                                                                                                                         MPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                             N-PSDB; AAH65506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 471 AA;
                                                                                 κ̈́z
                                                                              Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166
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  쉱
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(OOLJ/) OOLJEN A J J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT72943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-1996;
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10-MAR-1998
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                                                                                                                                                                                                                                  383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel isolated polypeptide having carotenoids isomerase catalytic activity, comprising a sequence at least 75 % similar to a 615 residue CRTISO amino acid sequence, given in the specification, as determined using the Standard protein protein BLAST (blastp) software of the NCBI. The novel polypeptide is useful for producing the all-trans geometric isomers of cis-carotenoids, including phytocene, phytofluene, zeta-carotene, neurosporene and lycopene. The polypeptide enables carotenoid biosynthesis in plants in the dark and in non-photosynthetic tissues. This sequence represents a synechocystis protein relating to the carotenoid isomerase catalytic polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIMIRHSGIIEELGLGAHGLRYIDC------DPWAFAPPAGTDGPGIVFHR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLIGAFGGLA--TARGNSELSRQFLAPGDALLDEYFDSEALKAALAWFGAQSGPPMSEPG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --MI------FGFGDRGTTNLLTRALAAVGQALETLPDPVQIHYHLPGGLDPKV--HR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLDATCQSIERACGTKDADAYRRFV-AVWS------ERSRHVMKAFSTPPTGS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 ---GACLGLVKYLPQNVGDIARRHIQDPDLL--KFIDME----CYCW-----SVVPAD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSAFLDAVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERPPGYKVDRGSSA 60
                                                                                                                                                                                                                                Carotenoid isomerase catalytic activity, CRTISO; cis-carotenoid; all-trans geometric isomer; phytoene; phytofluene; zeta-carotene; neurosporene; lycopene; plant; dark; non-photosynthetic tissue; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated polypeptide having carotenoids isomerase catalytic activity, useful for producing all-trans geometric isomers of ciscarotenoids, such as phytoene, phytofluene, zeta-carotene, neurosporene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPSYDAIVIGSGIGGLVTATQLVSKGLKVLVLERYLIPGGSAGYFER-EGYRFDVGAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.8%; Score 270; DB 6; Length 501;
24.3%; Pred. No. 8.3e-14;
tive 78; Mismatches 224; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 134-135; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zamir D, Isaacson T;
                                                                                                                                                                                              Synechocystis protein, SEQ ID No 20.
                                                                                        AA022615 standard; protein; 501 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-2002; 2002WO-IL000600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001; 2001US-0306144P
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 24.3
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-229567/22.
4
                                                                                                                                                                                                                                                                                                                             Synechocystis sp
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                                                                                                                                                                                                                                                                                                                                                             WO2003008534-A2.
467 LADHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirschberg J,
                                                                                                                                                                                                                                                                                          symechocystis.
                                                                                                                                                             15-MAY-2003
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                                                                                                                           AA022615;
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The present sequence represents a Phaffia derived carotenoid biosynthesis pathway enzyme. The nucleic acid encoding this protein can be used in the novel recombinant DNA of the present invention. The recombinant DNA comprises a transcription promoter operably linked to a downstream sequence to be expressed, where the transcription promoter comprises a region found upstream of the open reading frame (ORP) of a highly expressed Phaffia gene (preferably GAPDH, a ribosomal protein gene, an
TAPMVGFAALM---HVLPPGRAVGGSGALSAALASRMAVDGATVALGDGVTS-IRRNSNH 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTIAPAGRHOV-TLWSQW-QPYRLSGHRDWASVAEAEADRIVGEWEAFAPGFTDSVLDRF 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 PSLAPDGYHIIHTFTPSWLESWONLSPOBYEAKKEADSGKLIDRLEAIFPGL-DRALDYM 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phaffia derived GAPDH and carotenoid synthesis genes and promoter fragment - used in the recombinant production of therapeutically useful proteins e.g. carotenoids for use in food colouring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carotenoid; synthesis;
                                                                              209 LIPMINAGMVFSDRHYGGINYPKGGVGQIAESLVAGLEKFGGKIRYGARVIKIIQENNQA
                                                                                                                                                             267 WIVITESGREVHARKVIAGCHILITLDLLGNGGFDRT----TLDHWRRKIRVGPG-IGAVL
                                                                                                                                                                                                                          269 IGVELANGEKIYGRRIVSNA---TRWDTFGALTGDQPLPGKEKRWRRNYQQSPSFLSLHL
                                                                                                                                                                                                                                                                                                                              323 RIATSALPSYRGDATTRESTSGLQLLVSDRAHLRTAHGAALAGELPPRPAVLGMSFSGID
                                                                                                                                                                                                                                                                                                                                                                                                         326 GVEADLLP-----EGTECHHILLEDWDDLEKEQGTIFVS----IPTLL-----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441 -IQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPG------ADGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phaffia derived carotenoid biosynthesis pathway enzyme PRcrtI.
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promoter; recombinant DNA; astaxanthin; ribosomal protein;
food colouring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 CVGDSTFPGQGLNAVAFSGFACAHRLAV 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               490 LTGASTHPGGGVSGA--SGRSAA-RIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW22499 standard; protein; 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kanthophyllomyces dendrorhous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-EP005887.
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(first entry)
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enzyme involved in the biosynthesis pathway). The recombinant DNA can be used to transform hosts, preferably Phaffia. These transformed hosts are then used in the recombinant production of GAPDH or an enzyme involved in carotenoid synthesis, preferably astaxanthin. They may also be used to produce a pharmacoutical product. Purified carotenoids can be used as colourants in food and/or feed, and also in cosmetics. (Updated on 17-OCT-2003 to standardise OS field)
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Sequence 582 AA;

24; 123 217 270 273 429 121 231 TESGREVHARKVIAGCHILTTLDLLGNGGFDRTTLDHWRRKIRVGPGIGAVLRLATSALP 330 274 LESGERHHADVVIVNADLVYASEHL -----IPDDARNK-----IGOLGEVKRSWWA 319 485 486 ---KDGFDRFLSFIQEAHRHYELA-----VVHVLQKNFPGFA-----AFLRLQFIGQILAL 171 320 DIVGGKKLKGSCSSLSFYWSMDRIVDGLGGHNIFLAEDFKGSFDTIFEELGLPADPSFYV 379 70 71 FKQTFEDLGEKMEDWVDLIKCEPNYVCHF-----HDEETFTFSTDMALLKREVEREG-7 AVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVERFPGYKVDRGSSAHIM-IR 12 AIIVGCGIGGIATAARLAKEGFQVTVPEKNDYSGGRCSLIER-DGYRFDQGPSLLLLPDL 66 HSGIIBELGLGAHG-LRYIDCDP---WAFAPPAPGTDGPGIVFHRDLDATCQSIERACGT KDADAYRRFVAVWSERSRHVMKAFSTPPTGSNLIGAFGGLATARGNSELSRQF----L APGDAL---LDEYFDSEALKAALAWFGAQSG-PPMSEPGT-----APMVGF | ::: | :: | :: | HPPESIWTRUCRYFKTDRLRRVFSFAVMYMGOSPYSAPGTYSLLQYTELITEGIWYPRGGF 218 AALMHVL-----PPGRAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWTVT 331 SYRGDATTRESTSGLQ1LVS-DR-AHLRTAHGAALAGE------LPPRPAVLG ----PGFTDSVLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGA 376 MSFSGIDPTIAPAGRHQVTLWSQWQPYRLSGHRDWASVAEAEADRIVGEMEAFA-----380 NVPSRIDPSAAPEGKDAIVILVP----CGHIDASN--PODYNKLVARARKFVIQTLSA Gaps 8.1%; Score 225; DB 2; Length 582; 24.6%; Pred. No. 5.9e-10; iive 65; Mismatches 228; Indels 1: 232 WOVPNTLLOIVERNNPSAKFNFNAPVSOVLLS-PAKDRAT DGLYLTGASTHPGGGV DKLFFVGASTHPGTGV Query Match
Best Local Similarity 24.6
Matches 137; Conservative 122 172 486 487

615 AAO22614 standard; protein;

á

(first entry) 15-MAY-2003

Carotenoid isomerase catalytic activity, CRTISO; cis-carotenoid; all-trans geometric isomer; phytoene; phytofluene; zeta-carotene; neurosporene; lycopene; plant; dark; non-photosynthetic tissue; enzyme; Tomato plant protein, SEQ ID No 15.

Lycopersicon esculentum.

VO2003008534-A2

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The invention relates to a novel isolated polypeptide having carotenoids isomerase catalytic activity, comprising a sequence at least 75 % similar to a 615 residue CRIISO amino acid sequence, given in the specification, as determined using the Standard protein-protein BLAST (blastp) software of the NOTBI. The novel polypeptide is useful for producing the all-trans geometric isomers of cis-carotenoids, including phytochee, phytofluene, zeta-carotene, neurosporene and lycopene. The polypeptide enables carotene, neurosporene and lycopene. The polypeptide enables tissues. This sequence represents a tomato protein relating to the carotenoid isomerase catalytic polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHWTVTTESGREVHARKVIAGCHILTTLDLLGNGGFDRTTLDHWRRKIRVGPGIGAVLRL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 ATSALPSY-----RGDATTRESTSGLOLLVSDRAHLRTAHGAALAGELPPRPAVLGMS 377
                                                                                                                                                                                                                                                                              Novel isolated polypeptide having carotenoids isomerase catalytic activity, useful for producing all-trans geometric isomers of ciscarotenoids, such as phytoene, phytofluene, zeta-carotene, neurosporene and lycopene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 SGSYDAIVIGSGIGGLVAATHLAVKGAKVLVLEKYVIPGGSSGFYER-DGYKFDVGSSVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAFLDAVVVGSGHNALVSAAYLAREGWSVEVLEKDTYLGGAVSTVERFPGYKVDRGSSAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMIRHSG----IIEBIAGAHGLRYIDCDPWAFAPPAPGT-----DGPGIVFHRDLDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --------SECWKIFNSLVSKPPHEKEGIIKFY-----SECWKIFNSL-----NSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 LKSLEEPIYLFGQFFKKPLECLTLAYYLPQNAGSIARKYIRDPGLLSFIDAECFIVSTVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --TAPMVGFAALM---HVLPPGRAVGGSGALSAALASRMAVDGATVALGDGVTS-IRRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 ALQTPMINASMVICDRHFGGINYPVGGVGBIAKSLAKGLDXHGSQILYRANVTSIILDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 KAVGVKLSDGRKFYAKTIVSNA---TRWDTFGK------LLKAENLPKEEENFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSGIDPTIAPAGRH-----QVTTWSQWQPYRLSGHRDWASVAEAEADRIVGEME-AF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.1%; Score 225; DB 6; Length 615;
Best Local Similarity 22.3%; Pred. No. 6.4e-10;
Matches 132; Conservative 71; Mismatches 249; Indels 140; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 ROFLAPGDALLDEYFDSRALKAALAWFGAQSGPPMS----EPG-----
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                                                              18-JUL-2002; 2002WO-IL000600
                                                                                                     19-JUL-2001; 2001US-0306144P
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14-JUL-1999;
14-JUL-1999;
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31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHSGIIEELGLGAHGLRYIDCDPWAFAPPAPGTDGPGIVF---HRDLD------ATC 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 ARGNSELSRQFLAPGDALLDEYFDSEALKAALAWPGAQSGPPM---SEPGTAPWVGFAAL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 EAFDHFFAL-FGARTSDYLD-----LVELTPGYR----VFSGTHDAVDVPTGREKAIALF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHV-LPPG--RAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWTVTTESGREV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HARKVIAGCHILTTLD---LLGNGGFDRTTLDHWRRKIRV------GPGIGAVLRL- 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding enzyme of new carotenoid biosynthetic path, useful for
preparation of carotenoid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVE--RFPGYKVDRGSSAHLMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 AVVIGAGVAGLATSALLARDGWQVTVLEKNTDVGGRAGSLRISDFPGFRWDTGPSWYLMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Carotenoid; enzyme; catalyst; geranylgeranylpyrophosphate; phytoene;
489 YLIGASTHPGGGV----SG--ASGRSAARIALS-----DSRRGKASOWMR 527
                                             561 YCVGDSCFFGGGVIAVAFSGVMCAHRVAADLGFEKKSDVLDSALLRLIGWLR 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.0%; Score 221.5; DB 4; Length 548; 25.8%; Pred. No. 1.1e-09; arive 66; Mismatches 236; Indels 103;
                                                                                                                                                                                                                                                                                                                                             Enzyme involved in carotenoid biosynthetic pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 23-25; 33pp; Japanese
                                                                                                                                                                                       Ź
                                                                                                                                                                                       548
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                                                                                                                                                                                  AAB85728 standard; protein;
                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                               farnesylpyrophosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brevibacterium flavum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-499379/55
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                                                                                                                                                                                                                                                                                             29-0CT-2001
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                                                                                                                                                                                                                                        AAB85728;
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495
282 HNRKV-----QNLDADLVVSAGDLHHTENNLLPRELRTYPERYMSNRNPGIGAVLILL 334
                                                                          325 -ATSALPSY-RGDATTRESTSGLQLLVSDRAHLRTAHGAALAGELPPRPAVLGMSFSGID 382
                                                                                                                       335 GVKGELPQLDHHNLFFSKDWTDDFAVVPDGPQLTRPHNAS-----NSIYVSKPSTSE 386
                                                                                                                                                                                                                         387 DGVAPAGYENLFVI.IPAKASSSIGHGDAYMOSASASVETIASHAINQIATQAGIPDLTDR 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation;
                                                                                                                                                                                                                                                                                                      ... : | | : : | | : : | | 447 IVVKRTIGPADFEHRYHSWVGSALGPAHTLRQSAPLR--GRNSSRKV---DNLFYSGATT
                                                                                                                                                                         PTIAPAGRHOVTLWSQWQPYRLSGHRD-WASVAEAEADRIVGE------MEAFAPGFTDS
                                                                                                                                                                                                                                                                        VLDRFIQTPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum; brevibacterium lactofermentum; MCT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum MCT protein SEQ ID NO:262.
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99DE-01032124.
99DE-01032125.
99DE-01032180.
99DE-01032180.
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9908-01032191
9908-010322191
9908-01032212
9908-01032228
9908-01032229
9908-01032230
9908-01032230
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99DE-01040764.
99DE-01040765.
99DE-0104086.
99DE-01040830.
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99DE-01031454.
99DE-01031478.
99DE-01031563.
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99DE-01040833.
99DE-01041378.
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RESULT 15

AAB76641

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                                         99DE-01041395.
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99DE-01042078.
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membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation;
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                                                                                 Corynebacterium glutamicum; brevibacterium lactofermentum; MCT;
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                                                            Corynebacterium glutamicum MCT protein SEQ ID NO:264.
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                                                                                                                            genome mapping; genetic engineering.
AAB76641 standard, protein, 548 AA.
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                                                                                                                                               Corynebacterium glutamicum
                                        (first entry)
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N-PSDB; AAF67874.
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                    AAB76641;
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construction and membrane transport (WCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.

AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention
                                                                                                        AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane
Claim 20; Page 538-540; 1119pp; English
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Sequence 548 AA;

180 TRSL----QKYVNSQFSSPVLRQILTY-----PAVFLSSRPTTTPSM-YHLMSHTDLVQ 228 65 RHSGIIEELGLGAHGLRYID----CDPW--AFAPPAPGTDGPGIVFHRDLDATCQSIERAC 119 74 BAFDHFFAL-FGACTSDYLDLVBLTPGYRVFSGTHDAVDVP--TGRERAIALFESIBPGA 130 GTK------DADAYRRFVAVWSERSRHVWKAPST--PPTGSNLIGAFGGLATARGNSEL 170 171 SRQPIAPGDALLDEYFDSEALKAALAWFGAQSGPPM---SEPGTAPMVGFAALMHV-LPP 226 G--RAVGGSGALSAALASRMAVDGATVALGDGVTSIRRNSNHWTVTTESGREVHARKVIA 284 GVKYPIGGFTAVVNALHQLALENGVEFQLDSEVISINTASSRGNTSATGVSLLHNRKV-- 286 --GPGIGAVLRL--ATSALP 330 ----QNLDADLVVSAGDLHHTENKLLPRELRTYPERYWSNRNPGIGAVLILLGVKGBLP 341 331 SY-RGDATTRESTSGLOLLVSDRAHLRTAHGAALAGELPPRPAVLGMSFSGIDPTIAPAG 389 342 QLDHHNLFFSEDWTDDFAVVPDGPQLTRPHNAS-----NSIYVSKPSTSEDGVAPAG 393 390 RHQVTLWSQWQPYRLSGHRD-WASVAEAAADRIVGE-----MEAFAPGFTDSVLDRFIQ 442 : : : | | | | : | | : | | : | | 394 YENLFVLIPTKASSSIGKGDAYMQSASASVETIASHAINQIATQAGIPDLIVURRTI 453 7 AVVVGSGHNALVSAAYLAREGWSVEVLEKDTVLGGAVSTVE--RFPGYKVDRGSSAHLMI 64 14 AVVIGAÇVAGLATSALLARDĞWQYTVLEKNTDVGGRAGSLEISGFPGFRWDTGPSWYLMP 73 454 GPADFEHRYHSWVGSALGPAHTLRQSAFLR--GRNSSRKV---NNLFYSGATTVPGVGI 507 443 TPRDIESELGMIGGNVMHVEMSLDQMMLWRPLPELSGHRVPGADGLYLTGASTHPGGGV 501 Gaps 7.9%; Score 219.5; DB 4; Length 548; 25.8%; Pred. No. 1.6e-09; tive 68; Mismatches 243; Indels 89; 285 GCHILITILD --- LLGNGGFDRITLDHWRRKIRV-Query Match
Best Local Similarity 25.8
Matches 139; Conservative 227 (229 287 120

ch completed: February 29, 2004, 14:44:12 time : 66.9999 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		,	Description	Q8gcr9 pantoea ste	Q8vuj3 pantoea agg	Q9rlh6 paracoccus	P94792 flavobacter	Q88hv7 pseudomonas	Q97ut7 sulfolobus	Q9ltg@ arabidopsis	Q9fyl3 narcissus p	Q9spk6 haematococc	09fun2 citrus unsh	Q9fub9 citrus unsh	Q8lkv3 vitis vinif	Q8vxp2 crocus sati	049815 capsicum an	049814 capsicum an	Q9s6y0 lycopersico
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ALIGNMENTS

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R9 PRELIMINARY; PRT; 175 AA.		01-MAR-2003 (TrEMBLrel, 23, Created)	(TrEMBLrel, 25,	ne hydroxylase.			Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	Enterobacteriaceae; Pantoea.	NCBI_TaxID=66269;		SEQUENCE FROM N.A.		deSouza M.L., Kollmann S.R., Schroeder W.A.;		Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.			GO:0008152; P:metabolism; IEA.	IPR005596; Carote	6087; Sterol_des	03897; Carotene_hydrox; 1.	SEQUENCE 175 AA; 19884 MW; D7F1069562D83054 CRC64;	100.0%; Score 956;	ial Similarity 100.0%; Fred. No. 4.8e-89; 175; Conservative 0; Mismatches 0; Indels 0; Gaps	1 MIMINNALIVEVITVVGMEVVAALAHKYIMHGWGWGWHISHHEPRKGAFEVNDLYAVVFAI 60	1 MINIMALIVEVIVVGMEVVAALAHKYIMHGWGWELSHHEPRKGAFEVNDLYAVVFAI 60	61 VSIALIYEGSTGIWPLQWIGAGWTAYGLLYFWYHDGLVHQRWPFRYIPRKGYLKRLYWAH 120	61 VSIALIYFGSTGIWPLQWIGAGWTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYWAH 120
LT 1 R9 QBGCR9	QBGCR9;	01-M	01-0	Beta	CRIZ.	Pant	Bact	Ente	NCBI	Ξ	SEOU	STRA	deSo	"Car	Subm	EMBL	ġ	ġ	Inte	Inte	Pfam	SEOU	Query Match	Best Loc Matches				
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VSIALIYEGSTGIWPLQWIGAGMTAYGLLYFMVHDGLVHQRWPFRYIPRKGYLKRLYMAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LSILLIYLGSTGVWPLQWIGAGMTLYGLLYFIVHDGLVHQRWPFRYVPRRGYLRRLYMAH 120
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Kamiunten H., Hirata R.;
"Isolation and characterization of carotenoid biosynthesis genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLWIWNALIVFVTVVGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAPBVNDLYAVVPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RM:HHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDEQDGVDTSSSGK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RMFHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDEQDGVDTSSSGK 175
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                                                                                                                                                                                                               Pantoea agglomerans pv. milletiae.
Bacteria; Proteobacteria; Gammaproteobacteria; Snterobacteriales;
Enterobacteriaceae; Pantoea.
MCBI_TaxID=182454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carocene hydroxylase.
CRTZ.
Paracoccus marcusii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.
NCBI_TaxID=59779;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Indels
                                                                                                                                                                                                                                                                                                                                      Pantoea agglomerans pv. milletiae Wist 801.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB076662; BAB596602.1;
GO; GO:01003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR005596; Carotene hydrox.
InterPro; IPR005596; Carotene hydrox.
Fram: PF0187; Carotene hydrox.
Fram: PF0187; Carotene hydrox.
SEQUENCE 175 AA; 20222 MW; 4849DD4C61167845 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MH1.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15112; CAB56060.1; -.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR005596; Carotene_hydrox.
                                                                                                                                                      Last sequence update}
Last annotation update}
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Last annotation update)
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No. 1.9e-75;
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                                                                                                                                      Created)
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(TrEMBLrel. 13, I
(TrEMBLrel. 25, I
                                                                                                                  08-003;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-0CT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.38;
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                                                                                                        PRELIMINARY;
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                                                                                                                                                                                  Crtz protein.
CRTZ.
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01-MAY-2000 (
01-MAY-2000 (
01-OCT-2003 (
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65 LIYFGSTGIWP--LQWIGAGMTAYGLLYFMVHDGLVHQRWPFRYIPRKGYLKRLYMAHRM 122
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                                                                                                                                                                                                                                                               6 NALIVEVTVVGMEVVAALAHKYIMHG-WGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIA 64
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                                                                                                                                                                                                                                                                                                      5 WNALI-VFVTVVGMEVVAALAHKYIMHG-WGWGWHLSHH-BPRKGAFEVNDLYAVVFAIV
                                                                                                                                                                                            Gaps
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"Isolation and characterization of the carotemoid biosynthesis generate and characterization of the carotemoid biosynthesis generate 1 gene 185:35-41(1997).

I. Gene 185:35-41(1997).

R. GO; GO:0005509; R:catalytic activity; IEA.

GO; GO:000524; F:catalytic activity; IEA.

R. GO; GO:0005129; P:metabolism; IEA.

R. InterPro; IPR005596; Caroteme hydrox.

R. InterPro; IPR005049; EF-hand.

R. InterPro; IPR005049; EF-hand.

R. InterPro; IPR005049; FF-hand.

R. Pfam; FF03897; Caroteme hydrox; I.

R. Pfam; FF03897; Caroteme hydrox; I.

R. Pfam; FF03897; Caroteme hydrox; I.

R. PROSITE; PS00018; EF HAND; I.

S. SEQUENCE 169 AA; 19282 MW; 85334038DB3DAABI CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 169;
                                                                                                                                                                                            39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plavobacterium sp. ATCC 21588.
Bacteria; Bacteroidetes; Plavobacteria; Flavobacteriales;
Flavobacteriaceae; Plavobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 HHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDE 164
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InterPro; IPR006087; Sterol desat.
Pfam, PR03897; Carotene_hydrox; 1.
SRQUENCE 162 A4, 18882 WW; 798891BFP8743999 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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51.5%; Pred. No. 1.8e-41;
tive 31; Mismatches 44;
                                                                                                                            Ouery Match

51.5%; Score 492; DB 2;
Best Local Similarity 57.4%; Pred. No. 5.3e-42;
Matches 93; Conservative 20; Mismatches 39

Matches 93; Conservative 20; Mismatches 39
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MEDLINE=97186694; PubMed=9034310;
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Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Query Match
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                                                                                                                                                                                                                         MEDLINE-2242066; PubMed=12534463; Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Nartins Gos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nalson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lubber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Riewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                            01-UTM-2003 (TrEMBLrel. 24, Created)
01-UTM-2003 (TrEMBLrel. 24, Last sequence update)
01-UTM-2003 (TrEMBLrel. 25, Last annotation update)
Beta-caroteene hydroxylase.
CRTZ OR PP3246.
Pseudomonas putida (strain KT2440).
Pseudomonas putida (strain KT2440).
Pseudomonas putidases.
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STRAIR=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
EMBI, AEOLGYS, AANG8853.1; -.
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01-0CT-2001 (TrEMBirel. 18, Last sequence update)
01-0CT-2003 (TrEMBirel. 25, Last annotation update)
01-0CT-2003 (TrEMBirel. 25, Last annotation update)
01-0CT-2003 (TrEMBirel. 25, Last annotation update)
CRTZ on SSO2906.
Sulfolobus solfataricus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO: GO:0003824; F:catalytic activity; GO; GO:0008152; P:metabolism; IRA: InterPro; IPR005596; Carotene_hydrox. InterPro; IPR006087; Sterol desat. Pfam; PF03897; Carotene_hydrox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AA; 17522 MW;
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1es 82, Conservative
PRELIMINARY;
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                                                                                                                                                                           NCBI_TaxID=160488;
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Q88HV7
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61 VSVYLPPIGIQGSYVALSIAIGMSSYGIAYFFIHDMVIHDRHLHLRSWGLKHRP----FK 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLWIWNALIVFVTVVGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAI 60
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X., Thi-Mgoc H.P., Redder P., Schenk M.B., Theriault C., Tolstrup N., Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Garrett R.A., Ragan M.A., Sensen C.W., Van der Cost J.; Tolstrup T., Complete genome of the crenarchaeon Sulfolobus solfataricus P2.", Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

EMBL, AR006883; AAK43015.1; S.A. 98:7835-7840(2001).

ETR, H90469; H90469.

GO, GO:0008152; F:catalytic activity; IRA.

GO, GO:0008152; P:metabolism; IRA.

InterPro; IPR005596; Carotene_hydrox.

InterPro; IPR006087; Sterol Gesat.

Pfam; PF03897; Carotene_hydrox; 1.
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Yamada K., Banh J., Chan M.M., Chang C.H., Chang B., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 AA; 17602 MW; 66B61EB88EDD5BCS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.3%; Score 271; DB 17; 38.6%; Pred, No. 1.3e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 RLYMAHRMHHAVRGKEGCVSFGFLY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 DLILVHDIHH----KGGKGNWGFLF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative beta-carotene hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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268 NGVPYGLFLGP 278
                                                                                                                                                                                           PRELIMINARY;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 IWPLQWIGAGM--TAYGLLYFMYHDGLVHQRWPFRYIPRKGYLKRLYMAHRMHHAVRGKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 IWPLQWIGAGM--TAYGLLYFMVHDGLVHQRWPFRYIPRKGYLXRLYMAHRMHHAVRGKE 130
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Saki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Theologis A.; Theologis A.; Theologis A.; Theologis A.; Theologis A.; Theologis A.; Theologis A.; Theologis A.; Theologis A.; Theologis A.; Theologis A.; Theologis A.; Theologis A.; The EMBL/GenBank/DDBJ databases.

Expansion of the EMBL/GenBank/DDBJ databases.

Expansion of the EMBL/GenBank/DDBJ databases.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-carotene hydroxylase...
Narcissus pseudonarcissus (baffodil).
Bukaryota, Viridiplantae, Srreptophyra, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 VGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALIYFG--STG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.3%; Score 271; DB 10; Length 303; larity 42.0%; Pred. No. 2.9e-19; Conservative 26; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.2%; Score 270; DB 10; Length 308; 43.5%; Pred. No. 3.7e-19; ative 22; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Flower;
Schaub P., Beyer P., Al-Babili S.;
A cDNA encoding beta-carotene hydroxylase from Narcissus pseudonarcissus.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 GCVSFGFLYAP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- VPYGLFLGP 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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66 IYFGSTGIWPLQWIGA-----GMTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYM 118
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STRAIN=CV. Miyagawa; TISSUE=Fruit;
STRAIN=CV. Myagawa; TISSUE=Fruit;
Kim I., KO K., Kim C., Chung W.;
"Isolation of a cDNA encoding beta-carotene hydroxylase from Citrus.";
Submitted (OGT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP266158; AAG10793.1;
GO; GO:0003824; F:catalytic activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription of hydroxylase from Haematococcus pluvialis: cDNA sequence, regulation and functional complementation.";

Biochia. Biophys. Acta 1446:203-212(1999).

Biochia. Biophys. Acta 1446:203-212(1999).

GO: 0003824; F:catalyric activity; IEA.

GO: GO: 0003824; F:catalyric activity; IEA.

GO: GO: 0003825; P:metabolism; IEA.

InterPro; IPR0016408; Reg_chr_condens.

InterPro; IPR001608; Reg_chr_condens.

InterPro; IPR001608; Reg_chr_condens.

PER03897; Carotene hydrox.

InterPro; IPR016081: Seroul_desat.

PER03897; Carotene hydrox; 1.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Sapindales; Rutaceae; Citrus.
NCBI_TaxID=55188;
                                                                                                                                                                                    Haematococcus pluvialis.
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 AA; 34986 MW; 45100BA5ECBA13EC CRC64;
                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carotenoid hydroxylase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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42.0%; Pred. No. 3.9e-19;
tive 20; Mismatches 49;
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322 AA
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01-WAR-2001 (TrEMBLrel. 16, Last seqn
01-OCT-2003 (TrEMBLrel. 25, Last ann
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PRT;
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                                                                                                                                                                                                                                                    Haematococcaceae, Haematococcus
NCBI_TaxID=44745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.0*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 INPLOWIGACM--TAYGLLYFMYHDGIVHQRWPFRYIPRKGYLKRLYMAHRMHHAVRGKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 LVPGLCFGAGLGITVFGMAYMFVHDGLVHKRFPVGPIADVPYFRRVAAAHQLHBS--DKP 272
                                                                                                                                                                        72
                                                                                                                                                                                        15 VGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALIYFG--STG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 VGMEVVAALAHKYIMHGWGWGWGHLSHHEPRKGAFEVNDLYAVVPAIVSIALIYFG--STG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Citrus unshiu (Satsuma orange).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Sapindales; Rutaceae; Citrus.
NCBI_TaxID=55188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. Miyagawa;
Kim I.-J., Ko K.-C., Kim C.-S., Chung W.-I.;
"Isolation of cDNA showing polymorphism to GenBank Accession Number
                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                    Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.6%; Score 263.5; DB 10; Lengua
39.3%; Pred. No. 1.7e-18;
Mismarches 52; Indels
                                                                                                                                     52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP296158 from Citrus.";
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP215289; AAG33536.1;
GO:00008152; F:catalytic:activity; IEA.
GO: GO:0008152; P:metabolism; IEA.
InterPro; IPR005596; Garotene.hydrox.
InterPro; IPR005596; Sarotene.hydrox.
InterPro; IPR005087; Sterol desat.
Pfam; PP01897; Carotene.hydrox; 1.
SEQUENCE 311 AA; 34766 MW; E7868067P4A00AEB CRC64;
                InterPro; IPR005596; Carotene_hydrox.
InterPro; IPR06087; Sterol_deat.
Effan; PF03897; Carotene hydrox; SEQUENCE 311 AA; 34799 MW, 37083C01A303D4A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                    DB 10;
                                                                                              27.6%; Score 263.5; DB 1
39.3%; Pred. No. 1.7e-18;
                                                                                                                                                                                                                                                                                                                             273 HGVPYGLFLGPKELEEVGGLBELEKBISKR 302
                                                                                                               39.3%; Pred. av. ive 15; Mismatches
                                                                                                                                                                                                                                                                                                       131 GCVSFGFLYAPP-----LSKIQATLRER 153
                                                                                                                                                                                                                                                                                                                                                                                                                                311 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 HGVPYGLFLGPKELEEVGGLEELEKEISKR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 GCVSFGFLYAPP-----LSKLQATLRER 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
GO; GO:0008152; P:metabolism; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16,
                                                                                             Query Match
Best Local Similarity 39.33
Matches 59, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-carotene hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKV3
QBLKV3
QBLKV3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                           SULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SULT 12
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299 AA.

PRT;

PRELIMINARY;

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145 VGMEFWARWAHKALWHAALSHHRPREGPFELNDVFAIINAVPAISLLSYGLFNKG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 IWPLOWIGAGM--TAYGLLYFWYHDGLVHQRWPFRYIPRKGYLKRLYMAHRMHHAVRGKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 LVPGLCFGAGLGITVFGMAYMFVHDGLVHRRFPVGPIANVPYLRKVASAHQLHHS--DKF 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                STAIN=CV. Pinotage; TISSUE=Leaf;

STAIN=CV. Pinotage; TISSUE=Leaf;

Young P.R., Chen S.W., Vivier M.A.;

Talation, characterization and heterologous expression of a betaracterization of APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF499108; AAMT-107-1;

SUDMITTED (20:0003824; F:catalytic activity; IEA.

GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

RO; GO:0008152; P:metabolism; IEA.

InterPro; IPR006087; Sterol desat.

R Pfam; PF03897; Carotene hydrox, 1.

SRQUENCE 299 AA; 32997 WW; 0231906399D21037 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 VGMEVVAALAHKYIMHGWGWGLISHHEPRKGAFEVNDLYAVVFAIVSIALLYFG--STG
                                                                                                                                                                                                                                                   Eukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Vitaceae; Vitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sukaryota, Viridiglantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Asparagales, Iridaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Stigma;
Gonez-Gonez Lo.,
Itsolation and characterization of a carotenoid biosynthesis gene
coding for a carotenoid hydroxylase highly expressed in saffron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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TISSUB-Stigma;
Gonez Gonez L.;
Submitted (UL. 2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ416711; CAC95130.2; -.
SEQUENCE 305 AA; 34108 MW; 42FFBE4BD45F870B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stigmas.";
Submitted (DEC-2001) to the BMBL/GenBank/DDBJ databases
                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.5%; Score 263; DB 10;
41.2%; Pred. No. 1.8e-18;
iive 26; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 262.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305
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01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.5%;
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                                                                                                                              Beta-carotene hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-carotene hydroxylase.
BCH1CS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 GCVSFGFLYAP 141
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                                                                                                                                                                  BCH1.
Vitis vinifera (Grape)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=29760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 IWPLOWIGACM--TAYGLLYFMVHDGLVHORWPFRYIPRKGYLKRLYMAHRWHHAVRGKE 130
                                                                                                                                                                                                                                                                                                                               206 LLPGLCFGAGLGITLFCLAYMFVHDGLVHRRFPVGPIADVPYFQRVAAAHQIHHSEK-FE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 IVFVIVVCMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALIYF 68
                                                                                                                       75
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1993 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Beta-carotene hydroxylase 2 (Fragment).
Capsicum annuum (Bell pepper).
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capsicum annuum (Bell pepper).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spernatophyta, Magnoliophyta, eudicotyledons; core eudicots; asterids;
Isniids; Solanales; Solanaceae, Capsicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mention 1975, Keller Y., D'Harlingue A., Camara B.; Bouvier P., Keller Y., D'Harlingue A., Camara B.; "Xanthophyl biosynthesis : molecular and functional characterization of carotenoid hydroxylases from pepper fruits (Capsicum annuum L.)."; Blochim. Biophys. Acta 1391:320-328(1998).
                                                                                                                       VCMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALIYFG--STG
                                                                                                                                                                                  146 VGWEFWARWAHRALWHASLWHMHESHHRPRSGPFBLNDVFAIINAVPAIALNFGFFHRG
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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        1 Similarity 38.6%; Pred. No. 2.1e-18;
61; Conservative 29; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 AA; 35426 MW; F68792194297B3B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 GCVSFGFLYAPP-----LSKLQATLRERHAARSGAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-VPYGLFWGPXELEELGGLKELEKEVSRRIKAYNNSA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0TN-1998 (TrEMBLrel. 06, Created)
01-0TN-1998 (TrEMBLrel. 06, Last sequence update)
01-0TN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0008152; F:metabolism; IEA.
InterPro; IPR005596; Carotene hydrox.
InterPro; IPR006087; Sterol_desat.
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            Best Local
Matches 6
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15 VGMEVVAALAHKYIMMGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALIYFG--STG 72
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                                                               MEDGINE FROM N.A.

MEDGINE 98223452; PubMed=9555077;

Bouvier F., Keller Y., D'Harlingue A., Camara B.;

Bouvier F., Keller Y., D'Harlingue A., Camara B.;

Bouvier F., Keller Y., D'Harlingue A., Camara B.;

Examinophyll biosynthesis: molecular and functional characterization of carotenoid hydroxylases from pepper fruits (Capsicum annuum L.).";

Biochim. Biophys. Acta 1391:320-328(1998).

EMBL; Y09722; CAA70888.1; --
GO; GO:0003812; F:metalytic activity; IBA.

GO; GO:00038152; P:metalolium: IBA.

InterPro; IPR005596; Carotene hydrox.

InterPro; IRR006087; Sterol_desat.
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27.2%; Score 260.5; DB 10; Length
Best Local Similarity 38.0%; Pred. No. 3.5e-18;
Matches 57; Conservative 28; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 316 AA; 35792 MW; P59395B6DA552329 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 NGVPYGLFLGPKELREVGGLEELEKEVNRR 309
lamiids; Solanales; Solanaceae; Capsicum
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03897; Carotene_hydrox; 1.
                   NCBI_TaxID=4072;
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Search completed: February 29, 2004, 14:51:08 Job time : 18.3897 secs

34 71.5 7.5 654 35 71.5 7.5 654 36 71.5 7.5 946 37 70.5 7.4 452	70.5 7.4	00000000000000000000000000000000000000	0.00 0.00 0.00	, B 77000	CRIC PANAN CHANDAD	P21688;	DT 01-MAY-1991 (Rel. 18, 1 DT 10-OCT-2003 (Rel. 42, 1 DT 02-CT-2003 (R			RN 11J RP SEQUENCE PROM N.A. RC STRAIN=20D3; RX MEDLINE=91072214; PubMe	RA Misawa N., Nakagawa M., RA Nakamura K., Harashima		RL J. Bacteriol. 172:6704- CC -!- FUNCTION: Catalyzes CC beta-carotene to ze	CC -!- PATHWAY: Carotenoid		the Buro	use by non-pro modified and this	CC entities requires a lic	EMBE DOODR 7. B		InterPro; IPR006087;	DR Pfam; PF03897; Carotene KW Carotenoid biosynthesis		Query Match 93 Rest 1003 Similarity 93	vat	Qy 1 MEMIMALIVEVITY	Db 1 MLWIMNALIVEVIT	Oy 61 VSIALIYFGSTGIW	: OD QO	Oy 121 RMHAVRGKEGCVK
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen	protein search, using sw model	February 29, 2004, 14:27:18 ; Searc (without 3089.496	US-09-941-947A-36 956 I MLWIWNALIVEVITVGMEVVARS	BLOSUM62 Gapop 10.0 , Gapext 0,5	141681 segs, 52070155 residues	hits satisfying chosen parameters:	length: 0 length: 200000000	<pre>: Minimum Match 0% Maximum Match 100% Listing first 45 summaries</pre>	SwissProt_42:*	is the number of results prediter than or equal to the score rived by analysis of the total	SUMMARIES	f Query Match Length DB ID	93.3 175 1 CRTZ PANAN 68.4 176 1 CRTZ ERWHE	162 1 CRTZ	383	934	9.0 435 1 9.0 447 1	8.8 404 I	8.6 446 1 8.6 445 1	8.5	8.2 370 1	8.2 551	8.1 410 1	0.00	8.0 712 1	7.9 169 1 LEPA MICTO	7.8 350 1	7.7 1032 1	7.6 431 1 7.5 236 1	
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SEQUENCE FROM N.A.

NCBI_TaxID=549;

Erwinia herbicola,

01-APR-1993 01-APR-1993 ERWHE

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 YFGSTGIWP-LQWIGAGMTAYGLLYFMVHDGLVHQRWPFRYIPRKGYLKRLYMAHRMHHA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 TVGAYW-WPVLWWIALGMTVYGLIYPILHDGIVHQRWPFRYIPRRGYFRRLYQAHRLHHA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- FUNCTION: Catalyzes the hydroxylation reaction from beta-carotene to zeaxanthin via beta-cryptoxanthin (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LIVEVIVVGMEVVAALAHKYIMHG-WGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90062243; PubMed=7592436; Misawa N., Satcomi Y., Kondo K., Yokoyama A., Kajiwara S., Saito T., Misawa N., Miki W. Rondo R., Yokoyama A., Kajiwara S., Saito T., Satcomi Y., Miki W. Misawa and functional analysis of a marine bacterial carotemoid biosynthesis gene cluster and astaxanthin biosynthetic pathway
                                                                                                                                                                                                         MEDLINE-9525/715; PubMed=7733978;
Misawa N., Kajiwara S., Kondo K., Yokoyama A., Satomi Y., Saito T.,
Miki W., Ohtani T.;
                                                                                                                                                                                                                                                                             "Canthaxanthin blosynthesis by the conversion of methylene to keto groups in a hydrocarbon beta-carotene by a single gene."; Biochem. Biophys. Res. Commun. 209:867-876(1995).
                                                                                                       Betaproteobacteria; Burkholderiales;
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Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19157 MW; 0CA5235CBFEB33B5 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
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+ive 22; Mismatches
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InterPro; IPR005596; Carotene hydrox.
InterPro; IPR006087; Sterol_desat.
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                                                                                                                       Alcaligenaceae; Alcaligenes.
NCBI_TaxID=512;
                                            Beta-carotene hydroxylase.
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                                                                                         Alcaligenes sp.
Bacteria, Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                     biosynthetic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93; Conservative
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Best Local Similarity
Matches 93; Conserv
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SEQUENCE FROM N.A.
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01-OCT-1996
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P54973;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 NALIVEVIVVGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIAL
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 VRGREGCVSFGFIYARKPADLQAILRERHGRPPKRDAAKORPDAASPSS 173
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                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=EHO10;
MEDLINE=93138098; PubMed=8422926;
Hundle B.S., O'Brien D.A., Beyer P., Kleinig H., Hearst J.
In vitro expression and activity of lycopene cyclase and
beta-carotene hydroxylase from Erwinia herbicola.";
FEBS Lett. 315:329-334(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the hydroxylation reaction from beta-carotene to zeaxanthin.
-!- PATHWAY: Carotenoid blosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 AA; 19966 MW; BDE0A1C8A53F7BA8 CRC64;
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68.2%; Pred. No. 5.2e-56;
                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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InterPro; IPR005596; Carotene hydrox.
InterPro; IPR006087; Sterol_desat.
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Q44262;
01-NOV-1997 (Rel. 35, Created)
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CRTZ OR CRTH.
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Best Local Similarity 68.2
Matches 116; Conservative
                                                                                                                                     STANDARD;
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us-09-941-947a-36.rsp

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Query Match
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                                                                                                                                         This SMSS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 LIYFGSTGIWP--LQWIGAGMTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAHRM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 LFTVG--WIWAPVLWWIALGMTVYGLIYFVLHDGLVHQRWPFRYIPRKGYARRIYQAHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 NALIVEVIVVGMEVVAALAHKYIMHG-WGWGWHLSHHEPRKGAFGVNDLYAVVFAIVSIA 64
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Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,
Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,
Kinney A.U., Bliz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L.,
Allen S.M., Blackweil M., Reiter R.S., Carlson T.J., Russell S.H.,
Feldmann K.A., Plerce J., Browse J.;
"cloning of higher plant omega-3 fatty acid desaturases.";
Plant Physiol. 103-467-476(1993).
--- FUNCTION: ER (microsomal) omega-3 fatty acid desaturase introduces
the third double bond in the biosynthesis of 18:3 fatty acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.8%; Score 495; DB 1; Length 162;
58.0%; Pred. No. 9.7e-41;
iive 19; Mismatches 39; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             948624; P46311;
01-NVV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Omega-3 fatty acid desaturase, endoplasmic reticulum (BC 1.14.19.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; peprantophyta; Magnoliophyta; eudicotyledons; core eudicots; rosida; eurosids II; Brassicales; Brassicaceae; Brassica.
proposed at the gene level.";
J. Bacteriol. 177:6575-6584(1995).
-!- FUNCTION: Catalyzes the hydroxylation reaction from
beta-carotene to zeaxanthin via beta-cryptoxanthin.
-!- PATHWAY: Carotenoid biosynthesis. Involved in astaxanthin
biosynthetic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MRDBG-1455229; MRDLINE-99088059; PubMed-1455229; MRDLINE-99088059; PubMed-1455229; Somerville C.R.; Somerville C.R.; Map-based cloning of a gene controlling omega-3 fatty acid deaturation in Arabidopsis."; Science 258:1353-1355(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 HHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 HHAVEGRDHCVSFGFIYAPPVDKLKQDLK-----MSGVLRAE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carotenoid biosynthesis. SEQUENCE 162 AA; 18926 MW; FB8891AA12A92C6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 AA
                                                                                                                                                                                                                                                                                                                                                                           Interpro, IPR005596; Carotene hydrox.
InterPro, IPR066087; Sterol desat.
Pfam, PF03897; Carotene hydrox; 1.
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es 94, Conservative
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Best Local Si
Matches 94,
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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AC P48623;
DT 1-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 31, Last annotation update)
DT 01-FEB-1996 (Rel. 31, Last annotation update)
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DT 01-FEB-1996 (Rel. 31, Last annotation update)
DT 01-FEB-1996 (Rel. 31, Last annotation update)
DT 01-FEB-1996 (Rel. 31, Last annotation update)
CM Set All C20980 OR P23F1.10.
CM Arabidopsis thaliana (Mouse-ear cress)
CM Arabidopsis thaliana (Mouse-ear cress)
CM Arabidopsis thaliana; Streptophyta; Embryophyta; Tracheophyta;
CM Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
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                                                                                                                                                                                                                                                        -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
-1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
-1- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.
-1- SIMILARITY: Belongs to the fatty acid desaturase family.
important constituents of plant membranes. It is thought to u cytochrome b5 as an electron donor and to act on fatty acids esterified to phosphatidylcholine and, possibly, other phospholipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L01418; AAA32994.1; -.
EMBL; L22662; AAA61775.1; -.
BIR; A44227; A44227; A44227; A44227; A44227; A44227; A44227; A44227; A44227; A46224.1; FA_desat_fam.
InterPro: IPR00480; FA_desat_fam.
ProdDom; P0001081; FA_desat_fam; 2.
Oxidoreductase; Patty_acid_biosynthesis; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 10.6%; Score 101.5; DB 1; Length 383; Local Similarity 25.5%; Pred. No. 0.018; les 26; Conservative 20; Mismatches 29; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 RKGAFEVNDLYAVVFAIVSIALIYFGSTGIMPLOWIGAGMTAYGLLYFMVHD-
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333 AA;
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detectable in root tissue.
-!- DOMAIN: The histidine base domains may contain the active site and/or be involved in metal ion binding.
-!- SIMILARITY: Belongs to the fatty acid desaturase family.
                        TISSUE SPECIFICITY: Abundant in leaves and seedlings. Barely
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SEQUENCE
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C STRAINE-C. Columbia,

MEDIJINE-22954850; BubMed=14593172;

A Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Phan P.K., Cheuk R.P.,

A Kalin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Tange C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Chan M.M., Tange C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A rakawa T., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A rakawa T., Donnson-Eppson C., Hsuan V.W., Itda K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A Satou M., Tamse R., Vaysberg M., Wallender B.K., Wong C., Yamamura Y.,

A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Microsomal (ER) omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 1813 fatty acids, important constituents of plant membranes. It is thought to use cytochrome b5 as an electron donor and to act on fatty acids esterified to phosphatidylcholine and, possibly, other phospholipids.

PATHWAY: Polyunanturated fatty acid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAINS-C. Columbia.
STRAINS-C. Columbia.
STRAINS-C. Columbia.
Lin X. Kaul S., Rounsley S.D., Shea T.P., Benitco M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Fujii C.Y., Mason T.M., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams N.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia,
MEDLINE=94345020; PubMed=8066143;
Nishiuchi T., Nishimura M., Arondel V., Iba K.,
Genomic nucleotide sequence of a gene encoding a microsomal omega-3
fatty acid desaturase from Arabidopsis thaliana.",
Plant Physiol. 105:767-768(1994).
                                                                                                                                     STRAIN=CV. Columbia, TISSUE-Seedling, MEDLINE=94302147; PubMed=8029334; Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L., Kinney A.J., Hitz M.D., Booth J.R. Jr., Schweiger B., Stecca K.L., Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H., Fedmann K.A., Pierce J., Browse J.; "Cloning of higher plant omega-3 fatty acid desaturases."; "Cloning of higher plant omega-3 fatty acid desaturases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Columbia, TISSUB=Hypocotyl;
Watahiki M.C., Yamamoto K.I.; Vamamoto Submitted (62P-1993) to the EMBL/GenBank/DDBJ databases.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Columbia, TISSUE=Hypocotyl;
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Science 302:842-846[2003].
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                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 RSMSYVVRDIIAV--AALAIAAVYVDSWFEMPLYWAAGG-TLFWAIFVLGHDCGHGSFSD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                         27;
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AC P46710; Q9CCN5;

DT 01-NOV-1995 (Rel. 32, Dat sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DF Resphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 RKGAFEVNDLYAVVPALVSIALIYFGSTGIWPLQWIGAGMTAYGLLYFMVHD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.8%; Score 93.5; DB 1; Length 386; 26.5%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith D.R., Robison K.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 -----GLVHQRWPFRYIPRKGYLXRLYMAHRWHAVRG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6A7EA2A692B85164 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 HISTIDINE BOX-1.
HISTIDINE BOX-2.
HISTIDINE BOX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Mismatches
                                                                                                                                                                                                                                                                         PIR; JQ2335; JQ2335.
InterPro; IPR005804; FA desat fam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                              EMBE; D17579; BAA04505.1; -.
EMBE; D26508; BAA05514.1; -.
EMBE; AC004680; AAC31854.1; -.
EMBE; AX063966; AAL36322.1; -.
EMBE; AX06462; AAM20102.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44076 MW;
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27; Conservative
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262
105
141
308
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386 AA;
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SEQUENCE
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                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the ERBL outstation the Buropean Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               810 ORWPFFRSVLSNMAQVLAKSDLGLAARYABLVVDEALRRRVFDKIADBHRRTIAIHKLIT 869
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                                                                                                        -!- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PRP) it forms oxaloacetate, a four-carbon dicarboxylic acid source for the tricarboxylic acid cycle.
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.; Moodward J.R., "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             948622;
01-FBB-1996 (Rel. 33, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
Temperature-sensitive omega-3 fatty acid desaturase, chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,,
O.S.
                                                                                                                                                        CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)0 + phosphoenolpyruvate + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.1%; Score 87; DB 1; Length 934;
23.5%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 161 BY SIMILARITY.
593 593 BY SIMILARITY.
934 AA, 102515 MW, 3EE8FD762EC45180 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       870 GHDDLLADNPALARSVFNRPPYLEPLNHLQVELLRRY--RSG 909
                                                                                                                                                                                                 -!- PATHWAY: Tricarboxylic acid cycle.
-!- SIMILARITY: Belongs to the PEPCase family.
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FADB OR ATSG05580 OR MOPIO.12.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U00013; AAA17132.1; ALT INIT.
PIR; B86981. B8691.
HSSP; P00864; JFT;
Leproma; ML0578; ---
InterPro; JPR001449; PRPcase.
Pfam, PF00311; PEPcase.
Pfam, PF00311; PEPcase.
PROSITE; P800393; PEPCAREIASE.
PROSITE; P800391; PEPCASE 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
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SEQUENCE FROM N.A.
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FD3D ARATH
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-!- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 16:3 and 18:3 fatty acids, important constituents of plant membranes. It is thought to use ferredoxin as an electron donor and to act on fatty acids seterified to galactolipids, sulfolipids and phosphatidylglycerol. PATHWAY: Polyunsaturated fatty acid biosynthesis.
-!- FATHWAY: POLYUNBARIATHURE.
-!- INDUCTION: BY LOW TEMPERATURE.
-!- DOWAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MBDLINE=97471969; PubMed=9330910;
Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
Miyajima N., Tabata S.,
"Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned PI clones."
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STRAIN=cv. Columbia, TISSUE-Aerial parts;
MEDLINE=95148742; PubMed=7846164;
Gibson S., Arondel V., Iba K., Somerville C.R.;
"Cloning of a temperature-regulated gene encoding a chloroplast omega-3 desaturase from Arabidopsis thaliana.";
Plant Physiol. 106:1615-1621(1994).
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ProDom; PD001081; FA desat fam; 2.
Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 435;
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                                                                                                                                                                                                                                                                         STRAIN=cv. Columbia; TISSUE=Hypocotyl;
Watahiki M.C., Yamamoto K.T.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
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196 HISTIDINE BOX-2.
363 HISTIDINE BOX-3.
50136 MW, 3D77A8035A6214E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 LNSVAGHILHSS---ILVPYHGW----RISHRITHHQNHG 200
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26.3%; Pred. No. 0.56;
ative 17; Mismatches 29;
                                                                                                                                                                                                                                                                      Columbia; TISSUE=Hypocotyl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U08216; AAB60302.1; -. MBML; D1778; BAA04504!; -. EMBL; AB005241; BAB11547.1; -. InterPro; IPR005804; FA_desat_fam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L27158; AAA65621.1; -.
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192
359
3435 AA;
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RESULT 9 FD3C_SESIN

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Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-)
                                                                                                                       SEQUENCE FROM N.A.
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NON TER 1
TRANSIT <1
                                                                               eurosids II, Bra
NCBL_TaxID=3708;
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P27544;
                 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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LSS1 HUMAN
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Matches
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                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the BMBL outstation the Buropean Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 AYGLLYFMVHD-----GLVHORWPRYIPRKGYLKRLYMAHRWHAVR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 MFWALFVLGHDCGHGSFSNDPKLNSVVGHILHSS---ILVPYHCW----RISHRTHHONH 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 HCWVKDPW-------RSMGYVVRDV-AVVFGLAAVA-AYFNNWVVWPLYWF-AQST 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                           -!- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the third double bond in the blosynthesis of 16:3 and 18:3 fatty acids, important constituents of plant membranes. It is thought to use ferredoxin as an electron donor and to act on fatty acids esterified to galactolipids, sulfolipids and phosphatidylglycerol. PATHWAY: Polyunsaturated fatty acid blosynthesis.
-- SUBCELFULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
-- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.
                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamids, Lamiales, Pedaliaceae, Sesamum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HKYIMHGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALIYFGSTGIWPLQWIGAGMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Gaps
                                                                 Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U25817; AAA70334.1; -.
InterPro; IRR005804; FA desat fam.
Pfam; PF00487; FA desaturase; 1.
ProDom; PD001081; FA desat fam; 2.
Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane; Transit peptide.

RANSII : PCHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMEGA-3 FATTY ACID DESATURASE.
HISTIDINE BOX-1.
HISTIDINE BOX-2.
HISTIDINE BOX-3.
4E76250DDD6DA6B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.0%; Score 86; DB 1; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.64;
ches 36; Indels
                                                                                                                                                                                                   Shoji K., Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
                                                        update)
                                                                                             Sesamum indicum (Oriental sesame) (Gingelly)
     447 AA
                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 24.0%; Pred. No. 0.64 tes 29; Conservative 18; Mismatches
                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CV. 4294; TISSUE=Cotyledon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51116 MW;
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447
171
207
374
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203
370
347 AA;
                                                                                                                                            NCBI_TaxID=4182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211
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01-FEB-1996
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FD3C_BRANA
P48618;
    SESIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESULT 10
D3C BRANA
D FD3C B
C P48618
T 01-FEB
T 28-FEB
               P48620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 QWICAGWTAYGLLYFMVHD------GLVHQRWPPRYIPRKGYLKRLYMA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 YWIAQG-TMFWALFVLGHDCGHGSFSNDPRLNSVVGHLHSS---ILVPYHGW----RIS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 DIRAAIPKHCWVKNPW------KSMSYVVREL-AIVFALAAGA-AYLNNWLVWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 EVVAAL-AHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALIYFGSTGIWPL
Brassica napus (Rape).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
Probom; PD001081; FA_desat_fam; 2.
Oxidoreductase; Fatty acid blosynthesis; Chloroplast; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 8.8%; Score 84.5; DB 1; Length 404; Similarity 24.0%; Pred. No. 0.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMEGA-3 FATTY ACID DESATURASE.
HISTIDINE BOX-1.
HISTIDINE BOX-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4B58FB2F36B2EDE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLOROPLAST (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HISTIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 122963; AAA61774.1; ALT_INIT.
PIR; PQ0812; PQ0812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46617 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404
125
161
328
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157
157
324
3404 AA;
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103
148
176
239
287
97
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P46310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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TISSUE=Hypothalamus;

REDLINE=2238827; PubMed=12477932;

REDLINE=2238827; PubMed=12477932;

StraubBeag R.L., Feingold E.A., Ghemen C.M., Schuler G.D.,

Klauener R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Browneteln M.J., Usdin T.B., Toshiyaki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., McZley M.M., Scotengen E.J., Lu X., Gibbs R.A.,

Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myrzs R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marza M.A.,

Generation and initial analysis of more than 15,000 full-length

Human and mouse CDNA sequences ";

Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad Sci. U.S.A. 99:16899-16903(2002).

-! - ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                         Expression of growth/differentiation factor 1 in the nervous system:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=99091901; PubMed=9872981;
Jiang J.C., Kirchman P.A., Zagulski M., Hunt J., Jazwinski S.M.;
"Homologs of the yeast longevity gene LAGI in Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Lamerdin J. E., McCready P.M., Skowronski E., Adamson A.W.,
Lamerdin J. E., McCready P.M., Kyle A., Ramirez M., Stilwagen S.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
Submitted (JUN-1998) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Longevity assurance homolog 1 (UGG-1 protein) (LAG1 protein)
LASS1 OR UGG1 OR LAG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P27544-2; Sequence=VSP 003049;
Note=No experimental confirmation available;
-:- SIMILARITY: Contains 1 TLC (TRAM/LAG1/CLN8) domain.
                                                                                                                                                                                                                                                                                                                                                                    conservation of a bicistronic structure.";
Proc. Natl. Acad. Sci. U.S.A. 88:4250-4254(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P27544-1; Sequence=Displayed;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=91239545; Pubmed=2034669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 8:1259-1272(1998)
                                                                                                                                   (Human)
                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=2
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 FMVHD----GLVHQRWPFRYIPRKGYLKRLYMAHRMHHAVRGKEGCVSFGF-----LYA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---VGILV
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01-NOV-1995 (Rel. 32, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
FORGE3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
PAD7 OR FADD OR AT3G11.17 OR F9F8.4 OR F1189.10.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Exptophyta; Embryophyta; Core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%; Score 83; DB 1; Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 WIWNALIVEVT--------VVGMBVVAALAHKYIMHGWGWG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform 2).

/FTId=VSP 003049.

G -> C (IN REF. 4).

F102C12C47DB4162 CRC64;
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                                                                                                      EMBL, M62302; AAAS88500.1, -...
EMBL, AF105009; AAD16892.1; -...
EMBL, AF105009; AAD16892.1; -...
EMBL, AF105006; AAD16892.1; JOINED.
EMBL, AF105006; AAD16892.1; JOINED.
EMBL, AF105009; AAD16892.1; JOINED.
EMBL, AF105009; AAD16892.1; JOINED.
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
EMBL, AC003972; -...
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STRAIN=cv. Columbia; TISSUE=Hypocotyl;
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SEQUENCE FROM N.A.
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or send an email to license@isb-sib.ch)
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203
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                                                                                                                                                                                               STRAIN=cv. Columbia; TISSUE-Aerial parts;
STRAIN=cv. Columbia; TISSUE-Aerial parts;
MEDILINE-94043239; Pubmed-8226956;
Iba K., Gibson S., Nishiuchi T., Fuse T., Nishimura M., Arondel V.,
Hugly S., Somerville C.R.;
"A gene encoding a chloroplast omega-3 fatty acid desaturase
coppies alterations in fatty acid desaturase
copy number of the fad7 mutant of Arabidopsis thaliana.";
J. Biol. Chem. 268:24099-24105(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watahiki M., Yamamoto K.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-cv. Columbia; TISSUE-Hypocotyl;
Watahiki M., Yamamoto K.;
            MEDLINE=94302147; PubMed=8029334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 YWLAQG-TMFWALFVLGHDCGHGSFSNDPKLNSVVGHLLKSS---ILVPYHGW----RIS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 selection (Rel. 40, Least subunit 1)
(Oxidase BO(3) subunit 1) (Cytochrome O ubiquinol oxidase subunit 1).
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Nature 407:81-86[2000].

-!- FUNCTION: Cytochrome O terminal oxidase complex is the component of the aerobic respiratory chain that predominates when cells are grown at high aeration. This ubiquinol oxidase shows proton pump activity across the membrane in addition to the electron transfer (By similarity).
-!- CAPALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
-!- COPACTOR: Contains two protoheme IX (heme B55 and B562) and copper B (By similarity).
-!- PATHMAX: Ubiquinol oxidase catalyzes the terminal step in the electron transport chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 EVVAAL-AHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVPAIVSIALIYFGSTGIWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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STRAIN=Toxyo 1998;
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Genome sequence of the endocellular bacterial symbiont of aphids
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Bacteria; Broteobacteria; Gammaproteobacteria; Enterobacteriales;
EMBL; 122961; AAA61773.1; -.
EMBL; D14007; BAA03106.1; -.
EMBL; D26019; BAA05040.1; -.
EMBL; AC009991; AAF01508.1; -.
EMBL; AC073395; AG50977.1; -.
PIR; JQ2336; JQ2336.
PIR; JQ236; FA desat_fam.
Pfam; PF00487; FA desat_fam.
Probom; PD001081; FA desat_fam.
Probom; PD001081; FA desat_fam.
Propom; PO01081; FA desat_fam; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.6%; Score 82.5; DB 1; Length 446;
23.3%; Pred. No. 1.4;
tive 24; Mismatches 36; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                               OMEGA-3 FATTY ACID DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 167 HISTIDINE BOX-1.
199 203 HISTIDINE BOX-2.
366 370 HISTIDINE BOX-3.
446 AA; 51174 MM; 121125F634553D35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  CHLOROPLAST (POTENTIAL)
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NCBI_TaxID=118099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 MESSILWTLGFLVTFSIGGWTGVLLSVPPADFVLHNSLFLVAHFHNVIIGGVVFGCPAGI 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 LIWIWGHPEVYILVLPVFGVFSEVVATFSKRRLFGYVSLVWATLSITILSFIVW----EH 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 QR----WPFRY------IPRKGYL--KRLYMAHRMHAVRGKE--GCVS-- 134
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IRON (HEME B AXIAL LIGAND) (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
IRON (HEME D AXIAL LIGAND) (PROBABLE).
IRON (HEME D AXIAL LIGAND) (PROBABLE).
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                                                                                                                                                                                                                                                                                                             Complete proteome.

EXTRACELLULAR (POTENTIAL).
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3F502A628133EA65 CRC64;
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PROSITE; PS00077; COX1; 1.
Oxidoreductase; Respiratory cl
                                                                                                                                                                                                       InterPro; IPR000883; COX1. Pfam; PF00115; COX1; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 YWFCQG-TMFWALFVLGHDCGHGSFSNNPKINSVVGHLLHSS---ILVPYHGW----RIS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                                                              18 EVVAAL-AHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALIYFGSTGIWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 DIRAAIPKHCWVKNPW-------RSMSYVLRDV-VVVFGLAAVA-AYFNNWVAWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                               Ricinus communis (Castor bean).
Bukaryota, Viridiplantae, Streeptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Malpighiales, Euphorblaceae, Acalyphoideae, Acalypheae,
                                                                                                                                                      Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
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PIR; T10063; T10063.
FinterPro; IPR005804; FA desat fam.
Pfan; PF00487; FA desaturase; 1.
Probom; Pf00487; FA desat fam; 2.
Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
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TY ACID DESATURASE.
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HISTIDING BOX-2.
HISTIDINE BOX-3.
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Last annotation update)
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Pred. No. 1.
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MEDLINE=94302177; PubMed=8029360;
                                                                                                                 (Rel. 33, Created)
(Rel. 33, Last seq
(Rel. 41, Last ann
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                         437 NYWFPKLFGFV 447
                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (By similarity).

CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CORACTOR: Contains two protoheme IX (heme B55 and B562) and
copper B (By similarity).
PATHWAY: Ubiquinol oxidase catalyzes the terminal step in the
electron transport chain.
SUBCELULAR LOCATION: Integral membrane protein (By similarity).
SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
                                                                                                              Q8K994;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Ubiquinol oxidase polypeptide I (EC 1.10.3.-) (Cytochrome O subunit 1)
(Oxidase EO(3) subunit 1) (Cytochrome O ubiquinol oxidase subunit 1).
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE_220484549; PubMed=12089438;
MEDLINE_22048549; PubMed=12089438;
MEDLINE_22048549; PubMed=12089438;
Pernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
"50 million years of genomic stasis in endosymbiotic bacteria.";
Science 256:2376-2379 (2002).
-!- FUNCTION: Cytochrome O terminal oxidase complex is the component of the aerobic respiratory chain that predominates when cells are grown at high aeration. This ubiquinal oxidase shows proton pump activity, across the membrane in addition to the electron transfer
                                                                                                                                                                                                                 Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam: PF00115; COXI; 1.
PRINES: PROLES; CYCOXIDASEI.
PROSITE: P801007; COXI; 1.
Oxidoreductase; Respiratory chain; Transmembrane; Heme; Copper;
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                           213 HRTHHONHG 221
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                                                                                                                                                                                                                                                                                                              74; Gaps
                                                                                                                    POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IRON (HEWE AXIAL LIGAND) (PROBABLE).

COPPER B (PROBABLE).

COPPER B (PROBABLE).

COPPER B (PROBABLE).

COPPER B (PROBABLE).

IRON (HEME D AXIAL LIGAND) (PROBABLE).

IRON (HEME B AXIAL LIGAND) (PROBABLE).
                                                                                                                                                                                                                                     1'-histidyl-3'-tyrosine (His-Tyr)
                                                                                                                                                                                                                                                                                  8.4%; Score 80; DB 1; Length 659; 20.9%; Pred. No. 3.6; tive 23; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                     1 MINIMIALIVEVIV-----VGMEVVAALAHK----YIMHGWG-----
                                                                                                                                                                                                                                               (By similarity).
23D6FB4B04732D23 CRC64;
         SXTRACELLULAR (POTENTIAL)
                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                         EXTRACELLULAR (POTENTIAL)
                                  CYTOPLASMIC (POTENTIAL).
                                                                                   CYTOPLASMIC (POTENTIAL).
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Best Local Similarity 20.9
Matches 40; Conservative
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659 AA;
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Search completed: February 29, 2004, 14:45:17 Job time : 5.94944 secs

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

using sw mode] protein search, protein

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February 29, 2004, 14:34:14; Search time 4.87104 Seconds (without alignments) 3455.835 Million cell updates/sec on:

US-09-941-947A-36 956 itle: erfect score:

1 MLWIWMALIVFVTVVGMEVV.....ARSGAARDEQDGVDTSSSGK 175 equence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 coring table:

283366 seqs, 96191526 residues sarched: stal number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed inimum DB s iximum DB s

Listing first 45 summaries ost-processing: Minimum Match 100%

PIR 78:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:* tabase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description H90469 T09562 A44227 DB Length Query Score ssult Š.

crtZ protein - Erw beta-carotene hydr beta-carotene hydr omega-3 fatty acid omega-3 fatty acid hypothetical prote NADH2 dehydrogenas GDF-1 embryonic gr omega-3 fatty acid omegyge-1 fatty acid bo-type ubiquinol omega-3 fatty acid probable phosphoen hypothetical membr omega-3 fatty acid putrescine/ornithi omega-3 fatty acid stearcyl-CoA 9-des conserved hypothet probable cytochrom nypothetical prote hypothetical prote hypothetical prote fatty acid hypothetical prote phosphoenolpyruvat ootassium-transpor JQ2337 S75695 JQ2335 JQ2335 JC7872 AF2615 B97397 G83556 G83556 AG3586 AG3586 D39364 T03029 JQ2336 T10063 AB3023 r44519 H84984 888888 888 89.00 18.00 1

30 78 8.2 751 2 DB1062 31 77.5 8.1 228 2 AB3510 32 77.5 8.1 416 2 T19435 34 77.5 8.1 489 2 E84229 35 77 8.1 222 1 D69991 37 77 8.1 3473 1 56991 37 77 8.1 3473 2 527927 38 76.5 8.0 342 2 40 76.5 8.0 453 1 QQBE39 41 76.5 8.0 651 2 544257 42 76 7.9 208 2 H87631 44 76 7.9 300 2 H87631 45 76 7.9 542 2 C70732	nitric oxide reduc	molybdenum transpo	hypothetical prote	probable NADH2 deh	DNA damage-inducib	conserved hypothet	genome polyprotein	polyprotein - rice	BGLF3 protein - hu	N-acetyl-gamma-glu	omega-3 fatty acid	phosphotransferase	12K protein mla12A	hypothetical prote	integral membrane	probable integral
777 55 58 81 777 77 77 77 77 77 77 77 77 77 77 77 7	D81062	AB3510	T19435	A70648	E84229	D69991	A46112	S27927	QQBE39	872490	JQ2339	544257	508427	T23328	H87631	C70732
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	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	<b>4</b> .

## ALIGNMENTS

CITE Protein - Erwinia uredovora
C;Species: Brwinia uredovora
C;Species: Brwinia uredovora
C;Species: Brwinia uredovora
C;Species: Brwinia uredovora
C;Accession: F37802
R;Misawa, N.; Nakagawa, M.; Kobayashi, K.; Yamano, S.; Izawa, Y.; Nakamura, K.; Harashim
J. Bacteriol. 172, 6704-6712, 1990
A;Title: Elucidation of the Erwinia uredovora carotemoid biosynthetic pathway by function
A;Reference number: A37802
A;Accession: F37802
A;Accession: F37802
A;Accession: Preliminary
A;Accession: Preliminary
A;Accession: Preliminary
A;Accession: C;Accession: 
ö Gaps ò Query Match 93.3%; Score 892; DB 2; Length 175; Best Local Similarity 91.4%; Pred. No. 1.8e-81; Matches 160; Conservative 6; Mismatches 9; Indels

61 VSIALIYFGSIGIWPLOWIGAGWIAYGLLYFWYHDGLVHQRWPFRYIPRKGYLKRLYMAH 120 120 셤 ઠે

121 RMHHAVRGKEGCVSFGFLYAPPLSKLQATLRBRHAARSGAARDEQDGVDTSSSGK 175 ଚ

RESULT 2 \$52982

Deta-carotene hydroxylase - Erwinia herbicola
C;Species: Erwinia herbicola
C;Species: Erwinia herbicola
C;Species: Erwinia herbicola
C;Accession: 852982
R;Hundle, B.; Alberti, M.; Nievelstein, V.; Beyer, P.; Kleinig, H.; Armstrong, G.A.; Bur Mol. Gen. Genet. 245, 406-416, 1994
A;Title: Functional assignment of Erwinia herbicola Eho 10 carotenoid genes expressed in A;Reference number: 852976; MUID:95107236; PMID:7808389

A,Accession: S52982 A,Status: preliminary A,Molecule type: DNA A,Residues: 1-176 <HUN>

A; Cross-references: EMBL: M87280; NID: 9148404; PIDN: AAA64983.1; PID: 9148414

Gaps 'n 68.4%; Score 654; DB 2; Length 176; 68.2%; Pred. No. 9e-58; tive 21; Mismatches 31; Indels Conservative Best Local Similarity Matches 116; Conserv Query Match

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Cyaccession: A44227
Ayaronelu V.; Lemieux. B.; Hwang, I.; Gibson, S.; Goodman, H.M.; Somerville, C.R.
Science 258, 1153-1155, 1992
A;Title: Map-based cloning of a gene controlling omega-3 fatty acid desaturation in Aral
A;Reference number: A44227; MUID:93088059; PMID:1455229
A;Accession: A44227
A;Status; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Yadav, N.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J., J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browse, J.
Plant Physiol. 103, 467-476, 1993
A;Title: Cloning of higher plant omega-3 fatty acid desaturases.
A;Reference number: JQ2335; MUID:94302147; PMID:8029334
A;Accession: JQ2337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:L22962; NID:g408491; PIDN:AAA61775.1; PID:g408492
C;Comment: This enzyme introduces the third double bond in the biosynthesis of 18:2 and
C;Superfamily: omega-3 fatty acid desaturase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ທີ່
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                            73 IMPLOWIGAGM--TAYGLLYFNVHDGLVHORWPFRYIPRKGYLKRLYMAHRMHHAVRGKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Brassica napus (rape)
C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C.Accession: JQ2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Brassica napus (rape)
Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                           15 VGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALIYFG--STG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:L01418; NID:g167147; PIDN:AAA32994.1; PID:g167148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  omega-3 fatty acid desaturase (BC 1.14.99.-) BN3 [similarity] - rape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 RKGAFEVNDLYAVVFAIVSIALIYFGSTGIWPLOWIGAGMTAYGLLYFMVHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 383;
                                                                                                                                                                                                                                                                                                                                                                                            omega-3 fatty acid desaturase (BC 1.14.99.-) [similarity] - rape N,Alternate names: omega-3 linoleate desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: manA
A; Residues: 1-383 <ARO.
A; Cross-references: GB:L01418; NID:g167147; PIDN:AAA32994.1;
A; Experimental source: developing seed
A; Note: sequence extracted from NCBI backbone (NCBIP:119842)
C; Superfamily: omega-3 fatty acid desaturase
C; Reywords: oxidoceductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 -----GLVHQRWPFRYIPRKGYLKRLYMAHRMHHAVRG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 IPLLINSVVGHILLES---FILVPYHGW----RISHRTHHQNHG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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26.3%; Pred. No. 0.032;
tive 17; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.6%; Score 101.5; DB
25.5%; Pred. No. 0.021;
tive 20; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.4%
Best Local Similarity 26.3%
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Conservative
                                                                                                                                                                                                                    131 GCVSFGFLYAP 141
                                                                                                                                                                                                                                                                     265 NGVPYGLFLGP 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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A;Residues: 1-377 <YAD>
A;Cross-references: GR:1
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;Species. Arabidopsis thaliana (mouse-ear cress)
;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
;Accession: T09562
;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuel
ubmitted to:the Protein Sequence Database, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              She, O.; Singt, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, rrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
ubmitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VSVYLFFLGIQGSYVALSIAIGMSSYGIAYFFIHDMVIHDRHLHLRSWGLÄKHRP----FK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: GB:AE006641; NID:g13816278; PIDN:AAK43015.1; GSPDB:GN00155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSIALIYFGSTGIWPLQWIGAGWTAYGLLYFWVHDGLVHQR-----WPFRYIPRKGYLK 114
                                                                                                              IYFGSTGIWPLQWIGAGMTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAHRMHA 125
                                                                                                                                                65
                                                           63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eta carotene hydroxylase (crt2) [imported] - Sulfolobus solfatarious
;Species: Sulfolobus solfatarious
;Date: 24-May_2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
                                       NALIVEVIVVGMBVVAALAHKYIMHGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Gaps
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                                                                                                                                                                                                                          VRGKEGCVSFGFLYAPPLSKLQATLRERHA--ARSGAARDEQDGVDTSSS 173
                                                                                                                                                                                                                                                         9
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.;Cross-references: EMBL:AL050400; GSPDB:GN00062; ATSP:L73G19.80
.;Experimental source: cultivar Columbia; BAC clone L73G19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.5%; Score 253; DB 2; Length 310; Best Local Similarity 41.2%; Pred. No. 1.4e-17; Matches 54; Conservative 24; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.3%; Score 271; DB 2; Length 151
38.6%; Pred. No. 1e-19;
ive 26; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description: Sulfolobus solfataricus complete genome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \(\text{Map position: 4}\)
\(\text{introns: 126/3; 146/3; 170/3; 215/3; 257/3; 276/3\)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 RLYMAHRMEHAVRGKBGCVSFGFLY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 38.6%
Marches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reference number: A99139
Accession: H90469
Status: preliminary
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Residues: 1-151 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Gene: ATSP:L73G19.80
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A; Cross-references: EMBL: AC004680; NID: 93420043; PIDN: AAC31854.1; PID: 93420053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 26.5
tes 27, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: At2g29980; F23F1.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ents of plant membranes.
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                    Species: Synechocystis sp.

'Warier, PCC 6803

Bate: 25-Apr-1997 #text_change 08-Oct-1999

Bate: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

Baccession: 575695

Raceko, T.; 38to, 8.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Kaneko, T.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda B. Res. 3, 109-136, 1996

Bate: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Residues: 1-410 <KAN>
Cross-references: EMBL:D90912; GB:AB001339; NID:g1653228; PIDN:BAA18256.1; PID:d101898
Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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Species: Arabidopsis thaliana (mouse-ear cress)

Bace: 20-Apr-2000 #sequence revision 20-Apr-2000 #text_change 02-Feb-2001

Accession: UQ2335; T02487; A84703

Russell, Nierzbicki, A.; Agerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J., AR Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browse, J.

Title: Cloning of higher plant omega-3 fatty acid desaturases.

Accession: UQ2335; MUID:94302147; PMID:8029334
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*Residues: 1-386 < YAD>

*Cross-references: GB:D17579; NID:g1030693; FIDN:BAA04505.1; FID:g471091

*Cross-references: GB:D17579; NID:g1030693; FIDN:BAA04505.1; FID:g471091

*Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; I

*Indicted to the EMBL Data Library, August 1998

*Exercite in Exabidopsis thaliana chromosome II BAC F23F1 genomic sequence.

*Reference number: 214675

*Accession: T02487
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   45 RSMSYVARDIPAVV--ALAVAAVYFDSWFFWPLYWAAQG-TLFWAIFVLGHGSFSD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 TEIYQKAHWYNDVPEALVMLAF-----GIWPPLLTWMWQGFSQWPLILAASAGWYYTLG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 FLESAIARGVGLPNADEITDLTHRPGPFLTPPAPWMVNRTY--HWRHHFDDPNAYFCGTL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLWIWNALIVFVTVVGMEVVA----ALAH----KYIMHGWGWGWHLSHHEPRKGAPEV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FMVH------DGLVHQRWPFRYI PRKGYLKRLYMAHRMHH-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                       pothetical protein sll1376 - Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.3%; Score 98.5; DB 2; Length 410; 22.6%; Pred. No. 0.044; cive 27; Mismatches 51; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: nucleic acid sequence not shown; translation not shown Molecule type: DNA
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                                                                                                              ----GLVHQRWPFRYIPRKGYLKRLYMAHRMHHAVRG 128
                                                                                                                                                                             102 IPLINTAVGHILHSFILVÞYHGW----RISHRTHHONHG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reference number: S74322; MUID:97061201; PMID:8905231
Accession: S75695
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Molecule type: DNA
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Best Local Similarity 22.6%
Matches 51; Conservative
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A;Molecule type: DNA Askesidues: 1-38 csrp. Askesidues 1-38 csrp. Askesidues (SPDB:GN00139 A;Ross-references: GB:AR002093; NID:G3420053; PIDN:AAC31854.1; GSPDB:GN00139 C;Comment: The omega-6 and omega-3 fatty acid desaturases introduce the second and the t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stearoyl-CoA 9-desaturase (EC 1.14.19.1), FAD3 - Chlorella vulgaris
N,Alternate names: acyl-CoA desaturase, delta9-desaturase, omega-3 stearoyl-CoA desatura
C;Species: Chlorella vulgaris
C;Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 31-Mar-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: JC7872
R;Suga, K.; Honjoh, K.; Furuya, N.; Shimizu, H.; Nishi, K.; Shinohara, F.; Hirabaru, Y.; Biosci. Biotechnol. Biochem. 66, 1314-1327, 2002
A;Title: Two low-temperature-inducible Chlorella genes for deltal2 and cmega-3 fatty aci s crevisiae, and expression of omega-3 fad in Nicotiana tabacum.
A;Reference number: JC7871; MUID:22152188; PMID:12162554
A, Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Rui, S., Moder, M.; C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-418 <-85UG>
A;Cross-references: DDBJ:AB075527
C;Comment: This enzyme is involved in low temperature adaptation and the development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 RKGAFEVNDLYAVVFALVSIALIYFGSTGIWPLQWIGAGMTAYGLLYFMVHD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 386;
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2.jntrons: 103/2; 133/2; 155/3; 186/3; 248/3; 275/3; 321/3
C;Superfamily: omega-3 fatty acid desaturase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YAPPLSKLQATLRERHAARSGAARDEQDGVDTSSSG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---PLFAYPFYLLNRSPGKNGSHYDPKSDLFTASEG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.8%; Score 93.5; DB 1; 26.5%; Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
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Dypothetical protein PA0702 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G8356
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; BrStover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brady, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path) A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reterence number: Dya A;Reterence preliminary
A;Residues: 1-301 <STO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE004506; GB:AE004091; NID:g9946584; PIDN:AAG04091.1; GSPDB:GN00
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 AIVSIALIYFGSTGIWPLQWIGAGWTAYGLLYFWWHDGLVHQRWPFRYIPRKGYLKRLYM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---RYIP-----RKGYLKRLYMAHR----MHHAVR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphoenolpyruvate carboxylase (BC 4.1.1.31) ppc - Mycobacterium leprae N;Alternate names: B1496 C3_207 C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Accession: S72765
R;Smith, D.R.; Robison, K.
Submitted to the EMEL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid B1496.
A;Reference number: S72695
A;Accession: S7276
A;Accession: S7276
A;Accession: S7276
A;Accession: S7276
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A;Accession: S7276
A;Accession: SMI>
A;Accession: SMI>
C;Genetics: SMEL:U00013; NID:G466868; PIDN:AAA17132.1; PID:G466887
C;Genetics:
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9.1%; Score 87; DB 2; Length 907;
Best Local Similarity 23.5%; Pred. No. 1.4;
Matches 38; Conservative 21; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
9.2%; Score 88; DB 2; Length 301;
Best Local Similarity 24.8%; Pred. No. 0.35;
Matches 36; Conservative 24; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Gene: ppc
C;Superfamily: phosphoenolpyruvate carboxylase
C;Keywords: carbon-carbon lyase; carboxy-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 ---AHRMHHAVRGKEGCVSFGFLYA 140
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                                               114 KRLYMAHRMHHAVRGKEGCVSFG 136
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                                                              Conserved hypothetical protein Atu0318 [imported] - Agrobacterium tumefaciens (strain CE ') Species: Agrobacterium tumefaciens

[] Species: Agrobacterium tumefaciens

[] Species: Agrobacterium tumefaciens

[] Accession: AF2615

[] Wood, D.W.; Sectubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I Karp, P.; Romero, P.; Zhang, S.

[] Karp, P.; Romero, P.; Zhang, S.

[] Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ter, E.W.

[] Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.

[] Accession: AF2615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .Residues: 1-304 <KUR>
.Cross-references: GB:AE008688; PIDN:AAL41340.1; PID:g17738653; GSPDB:GN00186
.Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 ALAVTIABFGLYWAHRIAHBTVFF---WRFHALHHSVVRLWVVNTGRFHVADSLFKITLS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 --OIPLYFMGA----PLQVFWWLGAVTAFIGIL---THCNVDWKTGLLDYIFSTPR---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 IVSIALIYFGSTGIWPLQ---WIGAGMTAYGLLYFMVHDGLVHQRWPFRYI---PRKGYL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:AE007869; PIDN:AAKB6134.1; PID:g15155221; GSPDB:GN00169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 ALIVEVIVVGMEVVAALAHKYIMHGWGWGWHLSHHE-----PRKGAFEVND-LYAVVFA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ALIVEVIVVGMEVVAALAHKYIMHGWGWGWHLSHHE-----PRKGAFEVND-LYAVVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 9.5%; Score 91, DB 2; Length 313; Local Similarity 26.6%; Pred. No. 0.18; es 38; Conservative 19; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.5%; Score 91; DB 2;
Best Local Similarity 26.6%; Pred. No. 0.18;
Matches 38; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 KRLYMAHRWHHAVRGKEGCVSFG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LHRWHHSKOLPEGNTNYG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: AGR C_556
Map position: circular chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;Status: preliminary
.;Molecule type: DNA
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Matches
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62 PCRHEVALGWIGHYAVGILYGVIFALYGGA-AWFANPIFLP-AWI-----FGILTIAAG 113
                                                                                                                                                                     43 PRK-----GAFEVNDLYAVVFALVSIALIYFGSTGIWPLOWIGAGMTAYGLL---- 89
     : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

Colession: B86981

Colession: B86981

Davies, R.M.; Englmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc; Davies, R.M.; Batherford, K.M.

M. M.A.; Rutherford, K.M.

ture 409, 1007-1011, 2001

Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squitle: Massive gene decay in the leprosy bacillus

Fitle: Massive gene decay in the leprosy bacillus

Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pothetical membrane spanning protein BMBII0616 [imported] - Brucella melitensis (strai
Species: Brucella melitensis
Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: AG3586
DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Coltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess oc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
Ittle: The genome sequence of the facultative intracellular pathogen Brucella melitens Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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Accession: B86981
Status: preliminary
Wolecule type: DNA
Residues: 1-934 cSTO>
Cross-references: GB:AL450380; NID:913092776; PIDN:CAC30086.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     810 QRWPFFRSVLSNMAQVLAKSDLGLAARYABLVVDBALRRRVFDKIADEHRRITAIHKLIT 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RYIP-----RKGYLKRLYMAHR----MHHAVR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          esidues: 1-162 <KUR>
Loss-references: GB:AE008918; PIDN:AAL51858.1; PID:g17984795; GSPDB:GN00191
Myperimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 RKGAFEVNDLYAVVFALV----SIALIYFGSTGIWPLOWIGAGMTAYGLLYFMVHDGLVH 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
9.1%; Score 87; DB 2; Length 934;
Best Local Similarity 23.5%; Pred. No. 1.5;
Watches 38; Conservative 21; Mismatches 53; Indels
                                                                                                                                                         128 GKEGCVSFG-----FLYAPPLSKLQATLRERHAARSG 159
                                                                                                                                                                                                                                      128 GKEGCVSFG-----FLYAPPLSKLQATLRERHAARSG 159
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Superfamily: phosphoenolpyruvate carboxylase
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Tolecule type: DNA
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Sest Local Simi
Natches 41;
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

I protein - protein search, using sw model

February 29, 2004, 14:51:24 , Search time 11.619 Seconds (without alignments) 3180.293 Million cell updates/sec in on:

.tle:

US-09-941-947A-36 956 1 MIWIWNALIVFVTVVGMEVV.....ARSGAARDEQDGVDTSSSGK 175

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BLOSUM62 coring table:

Gapop 10.0 , Gapext 0.5

809742 stal number of hits satisfying chosen parameters: 809742 segs, 211153259 residues :arched:

nimum DB seq length: 0 ximum DB seq length: 200000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

tabase :

Published Applications AA:*

1: \cgn2_6/prodated/2/pubpaa/US07_PUBCOMB.pep:*
2: \cgn2_6/prodated/2/pubpaa/PCT_NEW_PUB_pep:*
3: \cgn2_6/prodated/2/pubpaa/PCT_NEW_PUB_pep:*
4: \cgn2_6/prodated/2/pubpaa/US06_NEW_PUB_pep:*
5: \cgn2_6/prodated/2/pubpaa/US06_PUBCOMB.pep:*
6: \cgn2_6/prodated/2/pubpaa/US08_NEW_PUB_pep:*
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17: \cgn2_6/prodated/2/pubpaa/US08_PUBCOMB.pep:*
18: \cgn2_6/prodated/2/pubpaa/US08_NEW_PUB.pep:*
19: \cgn2_6/prodated/2/pubpaa/US08_NEW_PUB.pep:*
11: \cgn2_6/prodated/2/pubpaa/US08_NEW_PUB.pep:*
11: \cgn2_6/prodated/2/pubpaa/US08_NEW_PUB.pep:*
11: \cgn2_6/prodated/2/pubpaa/US08_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 36, Appl	Sequence 12, Appl	Sequence 7, Appli	Sequence 6, Appli	Sequence 5, Appli	Sequence 34, Appl	Sequence 8, Appli	Sequence 9, Appli	Sequence 6, Appli	Seguence 183, App	Sequence 4, Appli	Sequence 398, App	Sequence 3, Appli	Sequence 10, Appl	Sequence 1, Appli
OI	US-09-941-947A-36	US-10-218-118-12	US-09-323-998D-7	US-09-323-998D-6	US-09-323-998D-5	US-09-920-923-34	US-09-323-998D-8	US-09-547-267-9	US-09-920-923-6	US-10-166-225A-183	US-09-323-998D-4	US-10-259-194A-398	US-10-115-571A-3	US-10-115-571A-10	US-10-115-571A-1
DB	10	74	σı	σ	o,	10	Ф	σ,	10	14	σ,	15	14	14	14
% Query Match Length DB ID	175	175	175	175	162	162	162	169	169	169	294	309	383	383	380
% Ouery Match	100.0	100.0	93.3	68.4	52.2	51.8	51.0	50.9	50.9	50.9	25.8	25.6	10.6	10.6	10.5
Score	926	926	892	654	499	495	488	487	487	487	247	245	101.5	101.5	100.5
sult No.	1	7	m	4	Ś	φ	7	Φ	σ	10	11	13	13	14	1.5

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US-09-837- US-10-115 US-10-115 US-10-115 US-10-115 US-10-115 US-10-115 US-10-115 US-10-115 US-10-115 US-10-115 US-10-115 US-10-115 US-10-115 US-10-115	US-10-115- US-10-115- US-10-310- US-10-115- US-10-369- US-10-125- US-09-885-1 US-09-885-1 US-09-885-1 US-09-885-1 US-09-885-1 US-09-885-1 US-10-115-
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; ORGANISM: Erwinia uredovora
US-09-323-998D-7
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US-09-323-998D-6
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GENERAL INFORMATION:
FRANCIS X.
APPLICANT: CUNINGRAM JR., FRANCIS X.
APPLICANT: CUNINGRAM JR., FRANCIS X.
APPLICANT: CUNINGRAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENERS OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 199172-0919
CURRENT FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 09/088,724
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1997-09-25
PRIOR FILING DATE: 1997-09-25
PRIOR FILING DATE: 1997-09-25
PRIOR FILING DATE: 1997-09-25
PRIOR APPLICATION NUMBER: 08/624,125
PRIOR APPLICATION NUMBER: 08/624,125
PRIOR APPLICATION NUMBER: 08/624,125
PRIOR APPLICATION NUMBER: 08/624,125
PRIOR APPLICATION NUMBER: 08/624,125
PRIOR APPLICATION NUMBER: 08/624,125
PRIOR FILING DATE: 1995-03-29
NUMBER OF SEQ ID NOS: 61
  61 VSIALIYFGSTGIWPLQWIGAGMTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAH 120
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                                                                                     RMHHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDEQDGVDTSSSGK 175
                                                                                                                  121 RMHHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDEQDGVDTSSSGK 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 956; DB 14; Length 175; Best Local Similarity 100.0%; Pred. No. 9e-101; Matches 175; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brostowicz, Patricia
APPLICANT: Rouviere, Pierre
APPLICANT: Rouviere, Pierre
APPLICANT: Rouviere, Pierre
APPLICANT: Rouviere, Pierre
APPLICANT: Chord Grees Encoding Carotenoid Compounds
TITHE OF INVENTION: Genes Encoding Carotenoid Compounds
FILE REFERENCE: CL1876 US NA
CURRENT APPLICATION NUMBER: 08/10/218,118
PRIOR APPLICATION NUMBER: 60/312,646
PRIOR PILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 175
                                                                                                                                                                                                                                                                           Sequence 12, Application US/10218118
Publication No. US20030148319A1
GENERAL INFORMATION:
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SEQ ID NO 7
LENGTH: 175
TYPE: PRT
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ORGANISM: Pantoea
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S-10-218-118-12
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S-09-323-998D-7
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Sequence 6, Application US/0932399BD
Parent No. US20020102631A1
GENERAL INFORMATION:
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENERO OC CAROTENDID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 108172-09019
CURRENT FILING DATE: 1999-06-02
FRIOR FILING DATE: 1998-06-02
FRIOR PPLICATION NUMBER: 09/088,725
FRIOR APPLICATION NUMBER: 09/088,725
FRIOR APPLICATION NUMBER: 08/6-02
FRIOR APPLICATION NUMBER: 08/6-02
FRIOR APPLICATION NUMBER: 08/6-02
FRIOR PLING DATE: 1997-09-25
FRIOR PLING DATE: 1996-03-29
FRIOR FILING DATE: 1996-03-29
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APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RMHHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDEQDGVDTSSSGK 175
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        Length 175;
Score 892; DB 9; Length 17
Pred. No. 1.8e-93;
6; Mismatches 9; Indels
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        Query Match
Best Local Similarity 91.4%;
Matches 160; Conservative
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ORGANISM: Erwinia herbicola
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Best Local Similarity 68.2
Matches 116; Conservative
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TITLE OF INVENTION: GENES OF CAROTEMOID BIOSYNTHESIS AND METABOLISM AND TITLE OF INVENTION: GENES OF USE THEREOF FILE REPRENCE: 108172-0919

TITLE OF INVENTION: METHODS OF USE THEREOF FILE REPRENCE: 108172-0919

CURRENT APPLICATION NUMBER: 05/088,724

PRIOR APPLICATION NUMBER: 09/088,725

PRIOR PELING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 09/088,725

PRIOR PLING DATE: 1998-06-02

PRIOR PLING DATE: 1998-06-02

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Patent No. US20020147371A1
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FREMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
GRRESPET: 340 Kingsland Street
COTTY: Nutley
                                     ----TSGVLRAE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 HHAVBGRDHCVSFGFIYAPPVDKLKQD1K-----MSGVLRAE 157
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.0%; Score 488; DB 9;
57.4%; Pred. No. 1.7e-47;
tive 19; Mismatches 40;
121 HHAVEGRDHCVSFGFIYAPPVDKLKQDLK-
                                                                                                                                                                     Sequence 8, Application US/09323998D Patent No. US20020102631A1
GENERAL INFORMATION:
APPLICANT: CUNNINGHAM UR., FRANCIS X. APPLICANT: SUN, ZAIREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Agrobacterium aurianticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93; Conservative
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                                                                                                                                                         -09-323-998D-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 TVGAYW-WPVLWWIALGMTVYGLIYFILHDGLVHQRWPFRYIPRRGYFRRLYQAHRLHHA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TENGRALOW, YALT
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
TITLE OF INVENTION: Improved Fermentative Carotenoid
CURRENT APPLICATION NUMBER: US/09/920,923
CURRENT FILING DATE: 2001-08-02
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
ENOTH: 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 HHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDE 164
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58.0%; Pred, No. 2.7e-48;
tive 19; Mismatches 39;
TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 1081'2-09019 CURRENT PREPLICATION NUMBER: US/09/323,998D CURRENT FILING DATE: 1999-06-02 PRIOR APPLICATION NUMBER: 09/088,724 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1997-09-25 PRIOR PRIOR FILING DATE: 1997-09-25 PRIOR PREPLICATION NUMBER: 08/624,125 PRIOR FILING DATE: 1996-03-29 NUMBER OF SEQ ID NOS: 61 SOFTWARE: PATENTIN VET: 2.1 SSQ ID NOS: 61 LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.2%; Score 499; DB
57.8%; Pred. No. 9.6e
iive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34, Application US/09920923
Publication No. US20030022273A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 57.8%
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pasamontes, Luis
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ORGANISM: Alicalgenes sp.
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Best Local Similarity
Matches 94; Conserva
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ORGANISM: E-396
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APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
TITLE OF INVENTION: GRAPE OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REPRESENCE: 106112-09019
CURRENT APPLICATION NUMBER: US/09/323,998D
CURRENT FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR FILING DATE: 1998-66-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1997-09-25
PRIOR FILING DATE: 1997-09-25
PRIOR FILING DATE: 1997-09-25
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                     Sequence 183, Application US/10166225A

Publication No. US20030148416A1

GENERAL INFORMATION:
APPLICANT: BEREY, Alan
APPLICANT: BEREY, Alan
APPLICANT: BREYEL, Merner
APPLICANT: BREYEL, Merner
APPLICANT: IOPEZ-ULIBARH, Rual
APPLICANT: MAYER, Anne F.
APPLICANT: MAYER, Anne F.
APPLICANT: MAYER, Anne F.
APPLICANT: MAYER, Anne F.
APPLICANT: MAYER, Anne F.
APPLICANT: MAYER, Anne F.
APPLICANT: MAYER, Anne F.
APPLICANT: MAYER, ANNE F.
APPLICANT: MAYER, ANNE F.
APPLICANT: MAYER, ANNE F.
APPLICANT: MAYER, ANNE F.
APPLICANT: MAYER, ANNE F.
APPLICANT: MAYER: US/10/166,225A
CURRENT FILING DATE: 2002-06-05
NUMBER: PatentIn Version 3.1
SEQ ID NO 183
LEWOTH: 169

"WAYER. F.
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50.9%; Score 487; DB 14;
Best Local Similarity 51.5%; Pred. No. 2.3e-47;
Matches 88; Conservative 31; Mismatches 44;
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US-10-166-225A-183
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                                                                                                        RESULT 10
US-10-166-225A-183
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US-09-323-998D-4
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Sequence 6, Application US/09920923
Publication No. US20030022273A1
GENERAL INNORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygamicay. Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentive Carotenoid
CURRENT PRILING DATE: 105/09/20,923
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.9%; Score 487; DB 9;
51.5%; Pred. No. 2.3e-47;
tive 31; Mismatches 44
                                                                                                                                                                            NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELEPHONE: (201) 235-5801
TELEPHONE: (201) 235-5801
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
               US/09/547,267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Flavobacterium sp. R1534
                                                                                                              08/660,645
                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 169 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 51.5%
Matches 88; Conservative
                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
S-09-547-267-9
                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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Gaps

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APPLICANT: HER MAJESTY IN RIGHT OF CANADA as represented by THE MINISTER OF APPLICANT: AGRICUTURE AND AGRI-FOOD CANADA APPLICANT: SOMERS, Daryl APPLICANT: SOMERS, Daryl APPLICANT: RAKOW, Cerhard TITLE OF INVENTION: PLANT FATTY ACID DESATURASES AND ALLELES THEREFOR FILE REFERENCE: 81601-28 CURRENT APPLICATION NUMBER: US/10/115,571A CURRENT APPLICATION NUMBER: CA 2,284,246 PRIOR FLING DATE: 1999-10-01 NUMBER: CA 2,284,246 PRIOR FLING DATE: 1999-10-01 SOFTWARE: Patentin version 3.1 SOFTWARE: Patentin version 3.1 SOFTWARE: Patentin version 3.1 SOFTWARE: Patentin version 3.1
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APPLICANT: ACRICULTURE AND AGRI-FOOD CANADA
APPLICANT: SOWERS, Daryl
APPLICANT: RAKOW, Gerhand
TITLE OF INVENTION: PLANT FATTY ACID DESATURASES AND ALLELES THEREFOR
TITLE OF INVENTION: PLANT FATTY ACID DESATURASES AND ALLELES THEREFOR
TITLE OF INVENTION: PLANT FATTY ACID DESATURASES AND ALLELES THEREFOR
TITLE OF INVENTION OF PLANT FATTY ACID DESATURASES AND ALLELES THEREFOR
THING DATE: 2000-09-29
REIOR PPLICATION WUMBER: CA 2,284,246
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PRETENT VERSION 3.1
SEQ ID NO 10
LENGTH: 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::| | ::| | ::| | ::| | | ::| | | : ::| | | : ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 RKGAFEVNDLYAVVFAIVSIALIYFGSTGIWPLOWIGAGMTAYGLLYFMVHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.6%; Score 101.5; DB 14; Length 383; 25.5%; Pred. No. 0.0052; Live 20; Mismatches 29; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 RKGAFEVNDLYAVVFALVSIALIYFGSTGIWPLQWIGAGMTAYGLLYFMVHD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 IPLINSVVGHILHS----FILVPYHGW----RISHRTHHQNHG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 -----GLVHQRWPPRYIPRKGYLKRLYMAHRMHAVRG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 IPLLNSVVGHILHS---FILVPYHGW----RISHRTHHONHG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Brassica napus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/L01418
DATABASE ENTRY DATE: 1993-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank/P48624;
DATABASE SUTRY DATE: 1996-02-01
RELEVANT RESIDUES: (1)..(383)
US-10-115-571A-10
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US-10-115-51A-10
US-10-115-571A-10
Sequence 10, Application US/10115571A
Publication NO. US20030150020A1
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Best Local Similarity
Matches 26, Conserva
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                                                                <u>ب</u>
                                                                                                                                                                                                      73 IMPLOWIGAGM--TAYGLLYFMYHDGLVHQRWPFRYIPRKGYLKRLYMAHRMHHAVRGKE 130
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                                                                                                                                          15 VGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAREVNDLYAVVFAIVSIALIYFG--STG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhu, TOSTANI ALLAR, TOSTANI AND CHARACTERIZATION OF PLANT GENES TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES FILE REPERENCE: 10029-NP
CURRENT APPLICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
PRIOR PELICATION NUMBER: US 60/325,277
PRIOR PELING DATE: 2002-04-06
PRIOR PELING DATE: 2002-04-06
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
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                                                                     6; Gaps
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; Pred. No. 1.8e-19;
23; Mismatches 48; Indels
                                                            47; Indels
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SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
SEQ ID NO 398
LENGTH: 309
                     Pred. No. 1e-19;
41.2%; Pred. Northes
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Publication No. US20040010815A1
SENERAL INFORMATION:
APPLICANT: Lange, Markus B.
APPLICANT: Glassemian, Majid
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
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Publication No. US20030150020A1
SENERAL INFORMATION:
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ilarity 41.2%;
Conservative 23
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Goff, Stephen A.
Katagiri, Fumiyaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moughamer, Todd
Provart, Nicholas
Ricke, Darrell
                                                        54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 GCVSFGFLYAP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 NGVPYGLFLGP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 G-VPYGLFLGP 286
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10-259-194A-398
        Best Local Similarity
Matches 54; Conserv
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Best Local Similarity
Matches 54, Conserv
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-10-259-194A-398
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APPLICANT: APPLICANT: APPLICANT:

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us-09-941-947a-36.rapb

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NAME/KEY: SITE
LOCATION: (213)...(213)
COTHER INFORMATION: Pects of the invention acid substitution in accordance with various as OTHER INFORMATION: pects of the invention
FRATURE:
NAME/KEY: SITE
LOCATION: (275)...(275)
OTHER INFORMATION: Position of amino acid substitution in accordance with various as OTHER INFORMATION: pects of the invention
FRATURE:
NAME/KEY: SITE
LOCATION: (347)...(347)
OTHER INFORMATION: Position of amino acid substitution in accordance with various as OTHER INFORMATION: Position of amino acid substitution in accordance with various as OTHER INFORMATION: Position of amino acid substitution in accordance with various as S-10-115-571A-1
                                                           Sequence 1, Application US/10115571A
Publication No. US20330150020A1
Publication No. US20330150020A1
GENERAL INFORMATION.
APPLICANT: HER MAJESTY IN RIGHT OF CANADA as represented by THE MINISTER OF APPLICANT: ACKNY, GETHART
APPLICANT: RAKOW, GETHART
TITLE OF INVERTY PATTY ACID DESATURASES AND ALLELES THEREFOR FILE REFERENCE: 81601-28
CURRENT APPLICATION NUMBER: US/10/115,571A
CURRENT FILING DATE: 1999-10-01
SOFTWARE: PATENTING DATE: 1999-10-01
SOFTWARE: PATENTING DATE: 1999-10-01
SOFTWARE: PATENTING DATE: 1999-10-01
SOFTWARE: PATENTING DATE: 1999-10-01
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10.5%; Score 100.5; DB 14; Length 380;
Best Local Similarity 26.3%; Pred. No. 0.0067;
Matches 26; Conservative 17; Mismatches 35; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: SITE
LOCATION: (95)...(99)
OTHER INFORMATION: Histadine box sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Brassica napus
ESULT 15
S-10-115-571A-1
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learch completed: February 29, 2004, 15:28:06
 ob time : 12.619 secs

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93.3%; Score 892;
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
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1698.885 Million cell updates/sec
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                                                                                                                                                                   February 29, 2004, 14:35:44 ; Search time 5.31793 Seconds
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1 MLWIWNALIVEVTVVGMEVV.....ARSGAARDEQDGVDTSSSGK 175
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1: /cgr2 6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2 6/ptodata/2/iaa/5B_COMB.pep.*

4: /cgn2 6/ptodata/2/iaa/6A_COMB.pep.*

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5: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep.*

6: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep.*

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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-624-125-7
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US-09-323-99BE-7
US-08-623-15-6
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US-08-623-10-11
US-08-623-10-11
US-08-623-10-11
US-09-315-918-11
US-09-315-918-11
US-09-315-919-11
US-09-315-919-11
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 4
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Sequence 6, Application US/07783705A

Patent No. 542939

GENERAL INFORMATION:
APPLICANT: Misawa, No. 5429939iniko
APPLICANT: Kobayashi, Kazuo
APPLICANT: Yamano, Shigeyuki
TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
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TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
TITLE OF INVENTION SYNTHESIS OF CAROTENOIDS
TOWNTER READABLE FORM:
MEDIUCATION TYPE: Diskette, 3.50 inch, 720KD storage
COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: NS-DISKET OF CAROTENOIDS
TILING DATE: 19911023
CLASSIPICATION NUMBER: US 07/519,011
FILING DATE: 1-1940-1959
ATTORNEY/AGRIT INFORMATION:
REGISTRATION NUMBER: US 07/519,011
FILING DATE: 1-19-ARK-1990
ATTORNEY/AGRIT INFORMATION:
REGISTRATION NUMBER: US 07/519,011
TELEPHONE: 212-708-1935
TELEPHONE: 212-46-5939
INFORMATION PATA NOW.
US-09-920-923B-6
US-09-674-529B-14
US-09-674-529B-15
US-09-674-529B-16
US-09-674-529B-16
US-09-674-529B-16
US-09-674-529B-13
US-09-674-529B-13
US-08-674-529B-13
US-08-937-155-4
US-09-323-99BB-4
US-09-674-529B-12
US-09-674-529B-12
US-09-674-529B-12
US-09-674-529B-12
US-09-674-529B-12
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US-09-674-529B-12
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121 RMHHAVRGKEGCVSFGFLYAPPLSKLQATLRERHGARAGAARDAQGGEDEPASGK 175
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APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-323-998E-7; Application US/09323998E; Patent No. 6642021
                                                                                                                 Sequence 7, Application US/08937155
Patent No. 6524811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: KELBER, STEVEN B. REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 27,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703-413-3000
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acid
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-937-155-7
                                                                                                                                                                       GENERAL INFORMATION:
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US-08-937-155-7
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5-08-624-125-7
Sequence 7, Application US/08624125
Sequence 7, Application US/08624125
Patent No. 5744341
GENERAL INFORMATION:
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                           1 MEWIWNALIVEVTVICHEVIAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAA
                                                                               1 MEMIWNALIVEVTVVGMEVVAALAHKYIMHGWGWGWHESHHEPRKGAFEVNDEYAVVFAI
                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Indels
                              Indels
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MEDIUM TYPE: PLOPPY disk
COMPUTER: LBM PC compatible
ODREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,125
FILING BATE: 29-MAR-1996
CLASSIFICATION:
          91.4%; Pred. No. 1.1e-101;
ive 6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 892; DB 1; I
Pred. No. 1.1e-101;
6; Mismatches 9;
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NAME: KELBER, STEVEN B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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INFORMATION FOR SEQ.ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 91.4
Matches 160; Conservative
          Best Local Similarity 91.4
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
IS-08-624-125-7
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STRANDEDNESS: si
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61 VSIALIYFGSTGIWPLOWIGAGWTAYGLLIYFWVHDGLVHORWPFRYIPRKGYLKRLYMAH 120
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APPLICANT: GUNINCHAM JR., PRANCIS X.
APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENES OF CARCTENOID BIOSYNTHESIS AND
TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
CORRESPONDENCE: 21
CORRESPONDENCE: 0BLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,155 FILING DATE: CLASSIFICATION:
APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/624,125 FILING DATE: 29-MAR-1996 ATTORNEY, AGENT IN PROPARATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.3%; Score 892; DB 4; 1
Best Local Similarity 91.4%; Pred. No. 1.1e-101;
Matches 160; Conservative 6; Mismatches 9;
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us-09-941-947a-36.rai

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MOLECULE TYPE: protein
             TOPOLOGY: linear
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TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND KETABOLISM AND FITLE OF INVENTION: METHODS OF USE THEREOF FILES FERENCE: 108172-09099 UP 108 THEREOF CURRENT APPLICATION NUMBER: US/09/323,998E CURRENT FILING DATE: 1999-06-02 PRIOR APPLICATION NUMBER: 09/088,724 PRIOR PILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 NUMBER: PARCHING DATE: 1998-06-02 NUMBER: PARCHING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-0
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Patent No. 5744341
GENERAL INFORMATION:
APPLICANT: CUN, ZAIREN
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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Pred. No. 1.1e-101;
6; Mismatches 9; Indels
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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
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COMPUTER: IBM PE Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624-7--
FILING DATE:
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29-MAR-1996
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NAME: KELBER, STEVEN B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 91.4%;
Xatches 160; Conservative
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ORGANISM: Erwinia uredovora
09-323-998E-7
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TYPE: amino acid
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CLASSIFICATION:
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66 IYFGSTGIWPLQWIGAGWTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAHRMHHA 125
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APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
NUMBER OF SEQUENCES: 21
CORRESCEDIBNEE ADDRESS: 2
ADDRESSES: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
                                                                                                                                 6 NALIVEVTVVGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVPAIVSIAL
                                                       Gaps
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Query Match 68.4%; Score 654; DB 1; Length 175; Best Local Similarity 68.2%; Pred. No. 2e-72; Matches 116; Conservative 21; Mismatches 31; Indels
                        2e-72;
~hes 31; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,155
FILING DATE:
FILING DATE:
PLING DATE:
PLING DATE: 29-MAR-1996
ATFORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,073
REGISTRATION NUMBER: 30,073
REGISTRATION NUMBER: 30,073
REGISTRATION NUMBER: 37,073
REGISTRATION NUMBER: 37,073
REGISTRATION NUMBER: 37,073
RELECHMENCE/POCKET UNBER: 2747-063-27
TELECOMMUNICATION:
TELESPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08937155
Patent No. 6524811
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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Best Local Similarity 68.2%
Matches 116; Conservative
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COMPUTER READABLE FORM:
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APPLICANT: Ausich, Rodney L.
APPLICANT: Ausich, Rednelm L.
APPLICANT: Abstract Mukhariji, Indrani
APPLICANT: Profitit, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huel-Che B.
APPLICANT: Yen, Huel-Che B.
APPLICANT: Yarger, James G.
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APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METHODS OF USE THEREOF
FILE RFFERENCE: 104012-091019
CURRENT APPLICATION NUMBER: 09/088,724
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR PILING DATE: 1998-06-02
RIOR APPLICATION NUMBER: 09/088,725
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 6
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                                                                                      66 IYFGSTGIWPLOWIGAGMTAYGILYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAHRA 125
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Best Local Similarity 68.2%; Pred. No. 2e-72;
Matches 116; Conservative 21; Mismatches 31; Indels
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STREET: 120 S. Riverside Plaza, 22nd Floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/08096623A Patent No. 5684238 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-09-323-998E-6
Sequence 6, Application US/09323998E
Patent No. 6642021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 175
TYPE: PRT
ORGANISM: Erwinia herbicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90909
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S-08-096-623A-18
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ZIP: 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-09-323-998E-6
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STATE:
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WASTION TYPE: PROPERLY
COMPATER: TANK COMPATIBLE
COMPATER: TANK COMPATIBLE
COMPATER: TANK COMPATIBLE
COMPATER: TANK COMPATIBLE
COMPATER: TANK COMPATIBLE
COMPATER: TANK COMPATIBLE
CLASSIFICATION NUMBER: 10 0/1662, 214
FILING DATE: 12 + 129
FILING DATE: 12 + 129
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FILING DATE: 12 + 129
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FILING DATE: 12 + 129
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,491
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTOKEY/ASTRY INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-663-310-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: MISARA, No. 58112731hiko
APPLICANT: KONDO, Keiji
APPLICANT: KONDO, Keiji
APPLICANT: KAJIWARA, Susumu
APPLICANT: YOKOYAMA, Akihiro
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
NUMBER OF SEQUENCES:
ADDRESSE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LIVEVIVVGMEVVAALAHXYIMHG-WGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.2%; Score 499; DB 1; Length 162; Best Local Similarity 57.8%; Pred. No. 2.1e-53; Matches 93; Conservative 22; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 VRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDEQD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Inh PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATION SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATION DATE: 99-MAR-1996
CLASSIFICATION NUMBER: US/08/624,125
FILING DATE: 29-MAR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KELBER, STEVEN B.
REGISTRATION NUMBER: 30,073
REPERENCE/DOCKET NUMBER: 2747-063-27
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3000
INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08663310
Patent No. 5811273
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-09-006-491-11
US-09-006-691-11
Sequence 11, Application US/09006491
Satent No. 5972690
GENERAL INFORMATION
APPLICANT: MISAWA, No. 5972690iniko
APPLICANT: MISAWA, No. 5972690iniko
APPLICANT: XONDO, Kelji
APPLICANT: XONOYAWA, Akihiro
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS
TITLE OF INVENTION: XANTHOPHYLLS
TITLE OF INVENTION: XANTHOPHYLLS
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER FOLDY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP.
                                                                                                                                                                          67 YFGSTGIWP-LOWIGAGMTAYGLLYFMVHDGLVHQRWPFRYIPRKGYLKRLYMAHRM-125
                                                                                                                                                                                                    8 LIVEVIVVGMEVVAALAHKYIMHG-WGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALI
Length 162;
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us-09-941-947a-36.rai

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23-SEP-1996
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  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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Patent No. 6150130
Batent No. 6150130
GENERAL INFORMATION:
APPLICANT: MISANA, No. 61501301niko
APPLICANT: KONDO, Keiji
APPLICANT: KONDO, Keiji
APPLICANT: KONDO, Keiji
APPLICANT: YOKOYAMA, Akhibro
TITLE OF INVENTION: TANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCES: 12
COUNTRY: USA
ZIP: D.C.
COUNTRY: USA
ZIP: D.C.
COUNTRY: USA
ZIP: D.C.
COMPATION: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION:
OFFRATING SYSTEM: PC-DOS/MS-DOS
OFFRATING SYSTEM: PC-DOS/MS-DOS
OFFRATING SYSTEM: PC-DOS/MS-DOS
OFFRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 52.2%; Score 499; DB 2; Length 162;
Best Local Similarity 57.8%; Pred. No. 2.1e-53;
Matches 93; Conservative 22; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 VRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDEQD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
RESERENCE/DOCKET NUMBER: 49441/109
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,919
                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SRQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                            DENCTH: 162 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein S-09-006-491-11
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67 YFGSTGIMP-LQWIGAGMTAYGLLYFMVHDGLVHQRWPFRYIPRKGYLKRLYMAHRMHHA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 TVGAYW-WPVLWWIALGAYTVYGLIYPILHDGLVHQRWPFRYIPRRGYFRKLYQAHKLHHA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 LIVEVTVVGMEVVAALAHKYIMHG-WGWGWHLSHHEPRKGAFEVNDLYAVVPAIVSIALI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CUNNIGHAM JR., FRANCIS X.
APPLICANT: CUNNIGHAM JR., FRANCIS X.
APPLICANT: CUNNIGHAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
NUMBER OF SEQUENCES: 21
CORRESSED: D.C.
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LIVVATVLVMELTAYSVHRWIMHGPLGMGWHKSHHEEHDHALEKNDLYGVVFAVLATILF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRET APPLICATION DATA: APPLICATION NUMBER: US/08/937,155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.2%; Score 499; DB 3; 57.8%; Pred. No. 2.1e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Mismatches
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DBC-1994
RIOR APPLICATION DATE: 36-DBC-1994
APPLICATION NUMBER: UP 6-235917
FILING DATE: 05-SBP-1994
PRIOR APPLICATION DATE: 3-348737
FILING DATE: 27-DBC-1993
ATTORNEY/AGBAT INPORMATION:
NAME: BEAT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 49441/109
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
        PCT/JP94/02220
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/624,125
FILING DATE: 29-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08937155
Patent No. 6524811
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 904136
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 162 amino acids
amino acid
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Matches 93; Conservative
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Washington
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TELEX: 9
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CITY: Wa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CUNNINGEAM JR., FRANCIS X.
APPLICANT: CUNNINGEAM JR., FRANCIS X.
APPLICANT: CUNNINGEAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENES OF CARCTEMOID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 10812-09019
CURRENT APPLICATION NUMBER: US/09/32,998E
CURRENT APPLICATION NUMBER: 09/088,724
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 5
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 YPGSTGIWP-LQWIGAGMTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAHRMHHA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 YFGSTGIWP-LOWIGACMTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAHRMHHA 125
                                                                                                                                                                                                                                                                                                                                                                                                                          8 LIVEVIVVGMEVVAALAHKYIMHG-WGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALI 66
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60
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57.8%; Pred. No. 2.1e-53;
ive 22; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 VRGKEGCVSFGFLYAPPLSKLOATLRERHAARSGAARDEOD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 VEGRDHCVSFGFIYAPPVDKLKQDLK-----RSGVLRPQDE 159
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52.2%; Score 499; DB 4;
Best Local Similarity 57.8%; Pred. No. 2.1e-53;
Matches 93; Conservative 22; Mismatches 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/0932399BE Patent No. 6642021
GENERAL INFORMATION:
NAME: KELBER, STEVEN B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
                                                                                                                                                                                 : 162 amino acids
amino acid
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MOLECULE TYPE: protein
-08-937-155-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Alcaligenes sp.:-09-323-998E-5
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Best Local Similarity
Matches 93; Conserv
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65 LIYPGSTGIWP--LOWIGAGWIAYGLLYFMVHDGLVHQRWPFRYIPRKGYLKRLYMAHRM 122
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Sequence 4, Application US/00663310
Sequence 4, Application US/00663310
Sequence 4, Application US/00663310
Setting 1 MISAMATION:
APPLICANT: MISAMA, No. 58112731hiko
APPLICANT: KANIWARA, Susumu
APPLICANT: YOKOYAMA, Akihira
APPLICANT: YOKOYAMA, Akihira
APPLICANT: YOKOYAMA, Akihira
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZITE: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THEN PC COMPATIBLE
COPERATIONS SYSTEM: PC-DOS/MS-DOS
CURERIT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-SEP-1996
CLASSIFICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
FILING DATE: 26-DEC-1994
FILING DATE: 06-SEP-1996
FILING DATE: 06-SEP-1996
FILING DATE: 06-SEP-1997
FILING DATE: 18-DEC-1994
PRIOR APPLICATION NUMBER: US 6-235917
FILING DATE: 18-DEC-1994
PRIOR APPLICATION NUMBER: US 6-235917
FILING DATE: 18-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION WIMBER: 29-768
PREGISTRATION WIMBER: 29-768
PREGISTRATION WIMBER: 29-768
PREGISTRATION WIMBER: 29-768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 495; DB 2;
; Pred. No. 6.5e-53;
19; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: February 29, 2004, 14:55:05
Job time : 6.31793 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.0%;
Matches 94; Conservative 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-663-310-4
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February 29, 2004, 14:26:38; Search time 20.6908 Seconds (without alignments) 2389.754 Million cell updates/sec
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956
1 MIMIMNALIVFVTVVGMEVV......ARSGAARDEQDGVDTSSSGK 175
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                               1586107 segs, 282547505 residues
                                                                                      protein - protein search, using sw model
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nimum DB seq length: 0 ximum DB seq length: 2000000000

1586107

tal number of hits satisfying chosen parameters:

st-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* geneseqp1990s:* geneseqp1980s:* geneseqp2004s: tabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description			Pantoea	8	Aaw87892 Protein e	0	œ.	o ы		9	9 3 3	o o	Aaw69536 crtE2396	m			4		4			. Her	1 H. pluvi	3322 Soybean	Aay32321 Soybean b
	ID	AAB22316	AA016023	ABP96690	AAR07468	AAW87892	ABG93890	AAR13988	ABG93889	AAR79061	AAW87886	AAR79059	AAW82259	AAW69536	AAW87883	AAW98197	AAG78480	ABG93888	AAW06518	AAW69534	ABU97245	ABG93891	ABB93795	AAB11111	AAY32322	AAY32321
	8													Ċ												
	Length DB	175	175	175	175	175	175	176	175	162	162	162	162	162	162	219	219	162	169	169	169	162	O	CV	. 255	
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sult	No.		7	m	4	S	Ó	7	00	σ	10	11	12	13	4	15	16	17	18	13	20	21	22	23	24	25

Aay22110 Beta-caro	Aay32318 Corn beta	Aag31290 Arabidops							Ada48532 Rice prot		Ric	Ą	Aay15198 A. aestiv	Aay15197 A. aestiv	Aay15194 A. aestiv	Aay15196 A. aestiv	Aay32323 Wheat bet		Aag15971 Arabidops
AAY22110	AAY32318	AAG31290	AAG31289	AAY90227	AAW35347	AAG31288	ABB93101	ABG93887	ADA48532	AAY54284	ADA48506	AAY15195	AAY15198	AAY15197	AAY15194	AAY15196	AAY32323	AAG26754	AAG15971
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311	223	199	208	291	294	310	310	294	292	294	309	306	309	315	306	315	131	125	150
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263.5	259	253	253	253	253	253	253	248	247	247	24.5	240.5	240.5	240.5	234.5	234.5	228	227	130
26	27	20	5 6	90	31	3 8	33	. S.	35	9 6	37	38	36	4	4	4	, 4 , W	4 4	45

### ALIGNMENTS

Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; beta-carotene hydrolase; CrtZ. Pantoea stewartii beta-carotene hydrolase (CrtZ) enzyme. AAE22316 standard; protein; 175 AA. (first entry) Pantoea stewartii. WO200218617-A2. 25-JUL-2002 07-MAR-2002. AAE22316; RESULT 1 

04-SEP-2001; 2001WO-US027420.

01-SEP-2000; 2000US-0229858P.

(DUPO ) DU PONT DE NEMOURS & CO E I.

Koffas M, Miller ES; Dicosimo DJ, Rouviere PE; Brzostowicz PC, Cheng Q, Odom JM, Picataggio SK,

WPI; 2002-351711/38. N-PSDB; AAD35514.

Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon the caroten substrates.

Claim 23; Page 146; 156pp; English.

The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopertenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by using microorganism having a nucleic acid molecule encoding enzymes in

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the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Pantoea stewartii beta-carotene hydrolase (CrtZ) enzyme used in the invention

Sequence 175 AA;

1 MIMINNALIVEVTVVGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDIYAVVPAI Gaps ö Length 175; Indels Score 956; DB 5; I Pred. No. 9.7e-108; ; Mismatches 0; ò 100.0%; 175; Conservative Similarity Query Match Best Local S Matches

ö

61

AA016023 standard; protein; 175 AA A016023 ESULT

AA016023

(first entry 20-FEB-2003 Pantoea stewartii Beta-carotene hydroxylase.

Carotenoid; crt.

Pantoea stewartii

WO200279395-A2.

10-OCT-2002

26-JAN-2001; 2001US-0264329P. 04-MAY-2001; 2001US-0288984P.

25-JAN-2002; 2002WO-US002124

(CRGI ) CARGILL INC

De Souza ML, Kollmann SR,

Schroeder WA;

May CA,

2003-075455/07. WPI; 2003-075455, N-PSDB; ABT14195

****************

Novel isolated mucleic acid useful e.g. to engineer host cells with the ability to produce particular carotenoids and polypeptides useful in cell-free systems to make particular carotenoids.

Claim 38; Page 65-66; 74pp; English.

The invention comprises the amino acid and coding sequence of a number of carotenoid (crt)-related proteins. The crt-related DNA and protein agequences of the invention are useful for engineering cells which are able to produce carotenoids. The present amino acid sequence represents a crt-related protein of the invention

Sequence 175 AA;

Length 175; Score 956; DB 6; Pred. No. 9.7e-108; 100.0%; 100.0%; Query Match Best Local Similarity

ö 120 120 9 9 61 VSIALIYFGSTGIWPLQWIGAGMTAYGLLXFWVHDGLVHQRWPFRYIPRKGYLKRLYMAH 61 VSIALIYFGSTGIWPLQWIGAGMTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAH 1 MLMIWNALIVEVIVVGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAI 1 MIMIWNALIVEVTVVGMEVVAALAHKYIMHGWGWHLSHHEPRKGAFEVNDLYAVVFAI 121 RMEHAVRGKEGGVSFGFLYAPPLSKLQATLRERHAARSGAARDEQDGVDTSSSGK 175 Gaps ö Indels ö Mismatches ö Conservative 175; Matches 셤 8 g ð 셤 Š

ABP96690 standard; protein; 175 RESULT 3 ABP96690

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ABP96690;

(first entry 03-JUN-2003 Pantoea stewartii beta-carotene hydroxylase SEQ ID NO:12

crtY; Pantoea stewartii; carotenoid biosynthetic enzyme; crtE; crtX; crtI; crtB; crtZ; beta-carotene hydroxylase; enzyme; phytoene; carotenoid

Pantoea stewartii.

WO2003016503-A2.

27-FEB-2003

15-AUG-2002; 2002WO-US026647.

15-AUG-2001; 2001US-0312646P.

(DUPO ) DU PONT DE NEMOURS & CO E I.

Rouviere Q, Picataggio SK, Cheng Brzostowicz PC,

WPI; 2003-268323/26. N-PSDB; ACC44764.

encoding nucleic acid molecule isolated from Pantoea stewartii encoenoid biosynthetic enzyme, useful for regulating carotenoid biosynthesis in an organism Novel 

Claim 4; Page 67-68; 68pp; English.

The present invention describes Pantoea stewartii carotemoid biosynthetic enzymes (1). More specifically described are the geranylgeranyl pyrophosphate synthase (crtE), zeaxanthin glucosyl transferase (crtX), lycopene cyclase (crtZ), phytoene gyuthase (crtZ) and beta-carotene hydroxylase (crtZ) enzymes (see ABP96685 to ABP96690) encoded by ACC44759 to ACC44764. (1) can be used for regulating carotemoid biosynthesis in an organism, (1) can be used for regulating organism, such that the carotemoid biosynthesis is altered in the organism. (1) and the genes encoding (1) are useful for converting phytoene to the carotemoids, for creating recombinant organisms that have the ability to produce various carotemoid compounds, and also for enhancing or manipulating carotemoid compounds, and also for enhancing or manipulating encodends. (1) can also be used for producing gene products having enhanced or altered activity

Sequence 175 AA;

Gaps Length 175; Indels 'Match 100.0%; Score 956; DB 6; I Local Similarity 100.0%; Pred. No. 9.7e-108; es 175; Conservative 0; Mismatches 0; Query Match Matches

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9 1 MINIMNALIVEVTVVGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAI

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us-09-941-947a-36.rag

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The present sequence represents a protein involved in carotenoid biosynthesis. The specification describes astaxanthin diglucosides and adonixanthin-3'-glucosides. The specification also describes a method for the preparation of a carotenoid glycoside, in which all, or part of, carotenoid biosynthesis genes crtE, crtB, crtI, crtY, crtZ, crtX or crtW are introduced to a microbe or plant and expressed. The transformed organism is cultured and astaxanthin diglucosides, adonixanthin-3'-glucosides, and/or astaxanthin monoglucoside are collected. The carotenoid glucosides are used as food additives. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ESILLIYLGSTGWWPLQWIGAGWTAYGLLYFWYHDGLVHQRWPPRYIPRKGYLKRLYMAH 120
                                                                                                                                                                                               Carotenoid biosynthesis; astaxanthin diglucoside, crtE gene; crtB gene; crtI gene; adonixanthin-3'-glucoside; astaxanthin monoglucoside; carotenoid glycoside; crtY gene; crtZ gene; crtX gene; crtW gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLWIMNALIVEVIVIGMEVIAALAHKYIMHGWGWGWILSHHEPRKGAFEVNDLYAVVFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MINIMNALIVEVTVVGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VSIALIYFGSTGIWPLQWIGAGMTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RM-HHAVRGKEGCVSFGFLYAPPLSKIQATLRERHAARSGAARDEQDGVDTSSSGK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 892; DB 2; Length 175;
Pred. No. 6e-100;
6; Mismatches 9; Indels
                                                                                                                                                         Protein encoded by the carotenoid biosynthesis gene crtz.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New carotenoid glucoside(s) - used as food additives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KIRI ) KIRIN BREWERY KK.
(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 23-24; 26pp; Japanese.
                            AAW87892 standard; protein; 175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG93890 standard; protein; 175 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             97JP-00140460
                                                                                                                                                                                                                                                                                                                                                                                                                                                    97JP-00140460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 93.3%;
Local Similarity 91.4%;
es 160; Conservative
                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-099030/09.
                                                                                                                                                                                                                                                                                              Pantoea ananatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV84084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 175 AA;
                                                                                                                                                                                                                                                          food additive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIRI ) KIRIN
                                                                                                                                                                                                                                                                                                                                 JP10327865-A.
                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2003
28-NOV-2002
                                                                AAW87892:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG93890;
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Matches
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ABG93890
ID ABG9
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AC ABG9
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DT 29-A
            AAW87892
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                                                          VSIALIYFGSIGIWPLQWIGAGMTAYGLLYFMVHDGLVHQRWPFRYIPRKGYLKRLYMAH 120
                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VSIALIYFGSTGIWPLQWIGAGWTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLWINNALIVFVTVVGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with enzymatic activity for the conversion of beta-carotene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A sequences encoding enzymes for carotenoid biosynthesis - for prodn. carotenoid cpds. e.g. beta-carotene, lycopene, phytoene, etc.
61 LSILLIYLGSTGWWPLQWIGAGMTAYGLLYFWUHDGLVHQRWPERYIPRKGYLKRIYMAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful as
of cancer.
                                                                                                                                                         RMHHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDEQDGVDTSSSGK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RWHHAVRGKEGCVSFGFLYAPPLSKLOATLRERHAARSGAARDEQDGVDTSSSGK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene products are useful for the synthesis of carotenoids, useful coloring, vitamin A precursor, and possibly in prevention of cancalso AAQ06293-9. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 93.3%; Score 892; DB 2; Length 175; Local Similarity 91.4%; Pred. No. 6e-100; Loss 160; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carotenoid biosynthesis; vitamin A; cancer; food coloring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura K;
                                                                                                                                                                                                                                                                    AAR07468 standard; protein; 175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Fig 6; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90EP-00107493,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89JP-00103078
90JP-00053255
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misawa N, Kobayashi K,
                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KIRI ) KIRIN BEER KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-322212/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pantoea ananatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ06298
                                                                                                                                                                                                                                                                                                                                                                                                                            into zeaxanthin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 175 AA;
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21-APR-1989; 05-MAR-1990; 20-APR-1990;

24-0CT-1990. EP393690-A.

24-OCT-2003 28-JAN-1991 Polypeptide

AAR07468;

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120

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Query Match

Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of producing or enhancing production of a carotenoid in a host cell. The method comprises inserting into the cell a vector comprising a hetrologous nucleic acid sequence encoding a protein with epsilon-cyclase enzyme activity operably linked to a promoter, and expressing the heterologous sequence to produce the protein. ABG93886.ABG93914 represent epsilon-cyclase, isopentenyl pyrophosphate isomerase and beta-carotene hydroxylase proteins of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VSIALIYFGSTGIWPLQWIGAGMTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LSILLIYLGSTGWWPLQWIZAGMTAYGLLYFWVHDZLVHQRWPFRYIPRKGYLKRLYMAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MIMINALIVEVIVIZMBVIAALAHKYIMHGWGWGWFLSHHBPRKGAFEVNDLYAVVPAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLWIWNALIVFVTVVGMEVVAALAHKYIMHGWGWGWHLSHHEPRKGAFEVNDLYAVVFAI 60
                                                                                                                                                                                                                                                                                                                                                            Producing, or enhancing production of a carotenoid in a host cell by transforming the cell with a vector encoding a epsilon cyclase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMHHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDEQDGVDTSSSGK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Epsilon-cyclase; carotenoid; isopentenyl pyrophosphate isomerase; beta-carotene hydroxylase; plant; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Score 860; DB 5; Length 17: 89.1%; Pred. No. 4.7e-96; Arive. 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGPP; carotenoid; phytoene; zeaxanthin; lycopene; ss.
            Erwinia uredovora beta-carotene hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-carotene hydroxylase - variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR13988 standard; protein; 176 AA
                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 6; 85pp; English.
                                                                                                                                                                                         96US-00624125.
97US-00937155.
98US-00088724.
98US-00088725.
                                                                                                                                                               99US-0032399B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 156; Conservative
                                                                                                                                                                                                                                                              CUNNINGHAM F X.
                                                                                                                                                                                                                                                                                                        Sun Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
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                                                                                 Pantoea agglomerans.
                                                                                                                                                                                                                                                                                                                                  WPI; 2:002-690609/74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 175 AA;
                                                                                                         US2002102631-A1.
                                                                                                                                                                                                                                                                                                       Cunningham FX,
                                                                                                                                                               02-JUN-1999;
                                                                                                                                                                                          29-MAR-1996;
                                                                                                                                                                                                      25-SEP-1997;
02-JUN-1998;
                                                                                                                                                                                                                                     02-JUN-1998;
                                                                                                                                                                                                                                                                            SUS
                                                                                                                                    01-AUG-2002
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                                                                                                                                                                                                                                                             (CUNN/)
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AAR13988
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coli celle to produce GGPP and the carotenoids phytoene through
zeaxanthin diglucoside, which is the final prod. identified in the
carotenoid pathway contd. in plasmid pakers (cong a ca. 13 kb
carotenoid pathway contd. in plasmid pakers (cong a ca. 13 kb
chromosomal DNA fragment isolated by Perry et al., J. Bacteriol., 168.607
(1986). The genes for geranylgeranyl pyrophosphate (GGPP) synthase,
phytoene synthase, phytoene dehydrogenase-44, lycopene cyclase, beta-
carotene hydroxylase, and zeaxanthin glycoplase are represented in
AAQ13716, AAQ13718, AAQ13792, AAQ13724 and AAQ13726
respectively. The native sequence (AAQ13724) was genetically engineered.
At the 5' and of the agene, codons encoding the native second and third
amino acid have been changed from Leu-Val to Val-Leu. Recombinant
expression plasmids can be used to produce large amts. of the enzymes and
thence large amts. of the carotenoids which they synthesise. (Updated on
25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biosynthesis of carotenoid(s) in genetically engineered hosts - using DNA encoding enzymes from Erwinia herbicola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 ALIYPGSTGIWPLOWIGAGNTAYGLLYFMVHDGIVHQRWPRYIPRKGYLKRLYMAHRMH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ALIANGTAGYWPIQMIGCGMTVYGLLYFLVHDGLVHQRWFFHWIFRRGYLKRLYVAHRLH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are a total of six relevant genes in a 7900 bp region that cause coli cells to produce GGPP and the carotenoids phytoene through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 INNALIVEVTVVGMEVVAALAHKYIMHGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VLNSLIVILTVIAMEGIAAFTHRYIMAGWGWRWHEPHHTPRKGVFELNDLFAVVFAGVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 HAVRGKEGCVSFGFLYAPPLSKLOATLRERHA--ARSGAARDBQDGVDTSSS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAVRGREGCVSFGFIYARKPADLQALLRERHGRPPKRDAAKDRFDAASPSSS 173
                                                                                                                                                                                                                                                                                                                                  Ausich RL, Brinkhaus FL, Mukharji I, Proffitt JH, Yarger JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Indels
Pantoea agglomerans; EHO-10 (E. vulneris - ATCC 39368).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.4%; Score 654; DB 2;
67.4%; Pred. No. 5.5e-71;
tive 21; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erwinia herbicola beta-carotene hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 21(1-3); 313pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG93889 standard; protein; 175 AA.
                                                                                                                                                                       9008-00487613.
9008-00525551.
9008-00562674.
9108-00662921.
                                                                                                                                  91WO-US001458
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(first entry)
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Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-281410/38.
                                                                                                                                                                                                                                                                                      (STAD ) AMOCO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ13725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 176 AA;
                                                                                                                                  04-MAR-1991;
                                                                                                                                                                         02-MAR-1990;
18-MAY-1990;
                                                                                                                                                                                                                                           28-FEB-1991;
                                           WO9113078-A.
                                                                                                                                                                                                                       -AUG-1990;
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28-NOV-2002
                                                                                       05-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 IYFGSTGIWPLONIGAGWTAYGLLYFMVHDGLVHQRWPRRYIPRKGYLKRLYMAHRA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            production of
into the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of producing or enhancing production a carotennid in a host cell. The method comprises inserting into the ce a vector comprising a heterologous nucleic acid sequence encoding a protein with epsilon-cyclase enzyme activity operably linked to a promoter, and expressing the heterologous sequence to produce the protein. ABC91386-ABG93914 represent epsilon-cyclase, isopentenyl pyrophosphate isomerase and beta-carotene hydroxylase proteins of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 NALIVEVTVVGMEVVAALAHKYIMHGWGWGHHLSHHEPRKGAFEVNDLYAVVFAIVSIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 hydroxy-beta-ionone ring methylene to keto group converting peptide.
                                                                                                                                                                                                                                                                                                             Producing, or enhancing production of a carotenoid in a host cell by transforming the cell with a vector encoding a epsilon cyclase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Epsilon-cyclase, carotenoid, isopentenyl pyrophosphate isomerase, beta-carotene hydroxylase; plant; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRGKEGCVSFGFLYAPPLSKLQATLRERHA--ARSGAARDEQDGVDTSSS 173
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N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.2%; Score 642; DB 5;
66.5%; Pred. No. 1.6e-69;
iive 23; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR79061 standard; peptide; 162
                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 6; 85pp; English.
                                                                                                                                                 96US-00624125.
97US-00937155.
98US-00088724.
98US-00088725.
                                                                                                                         99US-00323998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-hydroxy-beta-ionone ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.5
Matches 113; Conservative
                                                                                                                                                                                                                    (CUNN/) CUNNINGHAM F X. (SUNZ/) SUN Z.
                                                                                                                                                                                                                                                            Ζ;
                                                                                                                                                                                                                                                              Sun
                                         Pantoea agglomerans
                                                                                                                                                                                                                                                                                        WPI; 2002-690609/74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 175 AA;
                                                                     US2002102631-A1.
                                                                                                                                                                                                                                                            Cunningham FX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9518220-A1
                                                                                                                         02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-1996
                                                                                                                                                   29-MAR-1996;
                                                                                                                                                                             02-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alcaligenes
                                                                                                                                                                25-SEP-1997;
                                                                                               01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR79061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AR79061
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AAR79058-R790629 are xanthophyll polypeptides. These polypeptides are capable of converting the 4-methylene group of a 3-hydroxy-beta-ionone ring to a 4-keto group in doing so these peptides also add a hydroxyl group to the 3-position carbon-atom of the 4-keto-beta-ionone ring. The DNA sequences may be used in the production of astaxanthine and other keto gp. contg. xanthophylls, the sequences may also be used to transform certain yeasts and other microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 YPGSTGIWP-LQWIGAGMTAYGLLYFMVHDGLVHQRWPFRYIPRKGYLKRLYMAHRMFHA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carotenoid biosynthesis; astaxanthin diglucoside; crtE gene; crtI gene; adomixanthin-3'-glucoside; astaxanthin monoglucoside; carotenoid glycoside; crtY gene; crtZ gene; crtX gene; crtW gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LIVEVTVVGMEVVAALAHKYIMHG-WGWGWHLSHHEPRKGAFEVNDLYAVVFAIVSIALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ÷.
                                                                                                                                                                                                                                                                                                                                         DNA's encoding xanthophyll(s) - esp. asta:xanthin and other xanthophyll(s) using e.g. E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by the carotenoid biosynthesis gene crtZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 VRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDEQD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 VEGRDHCVSFGFIYAPPVDKLKQDLK-----RSGVLRPQDE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.2%; Score 499; DB 2;
57.8%; Pred. No. 3.6e-52;
ive 22; Mismatches 38
                                                                                                                                                                                                                              ď
                                                                                                                                                                                                                              Yokoyama
                                                                                                                                                        (KIRI ) KIRIN BERR KK.
(MARI-) MARINE BIOTECHNOLOGY INST CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22; Page 95-96; 131pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z
                                                                                                                                                                                                                              Kajiwara S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW87886 standard; protein; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97JP-00140460.
                                          94WO-JP002220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97JP-00140460.
                                                                                    93JP-00348737.
94JP-00235917.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KIRI ) KIRIN BREWERY KK.
                                                                                                                                                                                                                              Kondo K,
                                                                                                                                                                                                                                                                        WPI; 1995-246386/32.
N-PSDB; AAQ99488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alcaligenes sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP10327865-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-1997;
                                            26-DEC-1994;
                                                                                       27-DEC-1993;
05-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAR-1999
06-JUL-1995.
                                                                                                                                                                                                                              Misawa N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW87886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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                                                                                                  The present sequence represents a protein involved in carotenoid biosynthemis. The specification describes astaxanthin diglucosides and admixanthin-3'-glucosides. The specification also describes a method for the preparation of a carotenoid glycoside, in which all, or part of, carotenoid biosynthesis genes crtB, crtB, crtI, crtY, crtZ, crtK or are introduced to a microbe or plant and expressed. The transformed organism is cultured and astaxanthin diglucosides, adonixanthin-3'-glucosides, and/or astaxanthin monoglucoside are collected. The carotenoid glucosides are used as food additives
                                                                                                                                                                                                                                                                                                                                         67 YFGSTGIWP-LOWIGAGMIAYGLLYFWYHDGLVHQRWPFRYIPRKGYLXRLYMAHRMHHA 125
                                                                                                                                                                                                                                                                                                                                                      65 TVGAYW-WPVLWWIALGMTVYGLIYPILHDGLVHQRWPFRYIPRRGYFRRLYQAHRLHHA 123
                                                                                                                                                                                                                                                                                                           8 LIVFVTVVGMEVVAALAHKYIMHG-WGWGWHLSHHEPRKGAFEVNDLYAVVPAIVSIALI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydroxy-beta-ionone ring methylene to keto group converting peptide.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                      ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthophyll; astaxanthine; methylene; keto group; conversion;
3-hydroxy-beta-ionone ring.
                                                                                                                                                                                                                                             Query Match 52.2%; Score 499; DB 2; Length 162; Best Local Similarity 57.8%; Pred. No. 3.6e-52; Matches 93; Conservative 22; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA's encoding xanthophyll(s) - esp. asta:xanthin and other xanthophyll(s) using e.g. E. coli.
                                                                                                                                                                                                                                                                                                                                                                                       126 VRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDEQD 166
                                                                                                                                                                                                                                                                                                                                                                                                     124 VEGRDHCVSFGFIYAPPVDKLKQDLK-----RSGVLRPQDE 159
                                                       New carotenoid glucoside(s) - used as food additives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yokoyama A;
(KALY-) KALYO BIOTECHNOLOGY KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MARI-) MARINE BIOTECHNOLOGY INST CO LID.
                                                                             Disclosure; Page 14-15; 26pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR79059 standard; peptide; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kajiwara S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-JP002220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agrobacterium aurantiacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misawa N, Kondo K,
                      WPI; 1999-099030/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-246386/32.
                                  N-PSDB; AAV84078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ99486
                                                                                                                                                                                                                         Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIRI ) KIRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09518220-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-2003
28-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR79059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR 79059
 4×∝∝×₽×∞×0000000000000
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AAR79058-R796629 are xanthophyll polypeptides. These polypeptides are capable of converting the 4-methylene group of a 3-hydroxy-bera - ionone ring to a 4-keto group in doing so these peptides also add a hydroxyl group to the 3-position carbon-atom of the 4-keto-bera- ionone ring. The DNA sequences may be used in the production of astaxanthine and other etero group to ontg. xanthophylls, the sequences may also be used to transform certain yeasts and other microorganisms. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 LFTVG--WIWAPVLWWIALGWTVYGLIYFVIHDGLVHQRWPFRYIPRKGYARRLYQAHRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel method for the preparation of carotenoids using genes and proteins isolated from Candida utilis. The invention specifically describes the isolation of a 3-bydroxy-3 methylglutaryl coenzyme A (HWG-CoA) reductase protein. This sequence represents the Candida utilis crtZ protein which is used in the method of the invention. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 LIYFGSIGIWP--LQWIGAGWTAYGLLYFMVHDGLVHQRWPFRYIPRKGYLKRLYMAHRM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene useful for increase in carotenoid production - and preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 NALIVFVTVVGMEVVAALAHKYIMHG~WGWGHLSHHEPRKGAFEVNDLYAVVFAIVSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 NFLIVVATVLVMELTAYSVHRWIMHGPLGWGWHXSHHEBHDHALEKNDLYGLVFAVIATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HMG-CoA; 3-hydroxy-3-methylglutaryl coenzyme A reductase; crtZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 HHAVRGKEGCVSFGFLYAPPLSKLOATLRERHAARSGAARDE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 HHAVEGRDECVSFGFIYAPPVDKLKODLK----MSGVLRAE 157
                                                                                                                                                                                                                                                                                                                                                                                                              51.8%; Score 495; DB 2;
58.0%; Pred. No. 1.1e-51;
iive 19; Mismatches 39.
Claim 20; Page 79-80; 131pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 18-19; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW82259 standard; protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97JP-00058012.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KIRI ) KIRIN BREWERY KK.

 utilis crtZ protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                      Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-560727,
N-PSDB; AAV73183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pichia jadinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP10248575-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L2-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-0CT-2003
16-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW82259;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Query Match Best Local S: Matches 94

65

123

AAW69536;

AW69536

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The present sequence represents a protein involved in carotenoid biosynthesis. The specification describes astaxanthin diglucosides and adonixanthin-3'-glucosides. The specification also describes a method for the preparation of a carotenoid glycoside, in which all, or part of, carotenoid biosynthesis genes crtE, crtE, crtI, crtY, crtZ, crtX or crtW are introduced to a microbe or plant and expressed. The transformed organism is cultured and astaxanthin diglucosides, adonixanthin-3'-glucosides, and/or astaxanthin monoglucosides, adonixanthin-3'-glucosides are used as food additives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 LIYFGSTGIWP--LØWIGAGMTAYGLLYFMVHDGLVHQRWPFRYIPRKGYLKRLYMAHRM 122
                       63 LPTVG--WIMAPVLMWIALGMTVYGLIYFVIHDGLVHQRWPFRYIPRKGYARRLYQAHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 LFTVG--WIWAPVLWWIALGMTVYGLIYFVIHDGLVHQRWPFRYIPRKGYARRLYQAHRL 120
65 LIYFGSTGIWP--LOWIGAGMTAYGLLYFWVHDGLVHORWPFRYIPRKGYLKRLYMAHRM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NFLIVVATVLVMELTAYSVHRWIMHGPLGWGWHKSHHEEHDHALEKNDLYGLVFAVIATV 62
                                                                                                                                                                                                                                                                                                                                                                                                                        Carotenoid biosynthesis; astaxanthin diglucoside; ortE gene; ortE gene; crtI gene; adonixanthin-3'-glucoside; astaxanthin monoglucoside; carotenoid glycoside; crtY gene; crtZ gene; crtX gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 NALIVEVIVVGMEVVAALAHKYIMHG-WGWGHLSHHEPRKGAFEVNDLYAVVFAIVSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.8%; Score 495; DB 2; Length 16; 58.0%; Pred. No. 1.1e-51; ive 19; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by the carotenoid biosynthesis gene crtz.
                                                                                                             123 HHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 HHAVRGKEGCVSFGFLYAPPLSKLOATLRERHAARSGAARDE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New carotenoid glucoside(s) - used as food additives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KIRI ) KIRIN BREWERY KK.
(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 11-12; 26pp; Japanese.
                                                                                                                                                                                                                                                      Ź
                                                                                                                                                                                                                                                   AAW87883 standard; protein; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97JP-0014046D.
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                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agrobacterium aurantiacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-099030/09.
N-PSDB; AAV84075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     food additive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP10327865-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-1997;
                                                                                                                                                                                                                                                                                                                                            10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998.
                                                                                                                                                                                                                                                                                                 AAWB7883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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Matches
                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                   AAW87883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes the preparation of carotenoid pigments e.g. canthaxanthins using a cell transformed by a vector having DNA sequences (a) to (e) or substantially homologous sequences. (a) a DNA sequence (crtE) coding GGPP synthase of Plavobacterium sp. R1534; (b) a DNA sequence (crtI) coding prephytoene synthase of Flavobacterium sp. R1534; (c) a DNA sequence (crtI) coding phytoene desaturase of Plavobacterium sp. R1534; (d) a DNA sequence (crtY) coding lycopene cyclase of Plavobacterium sp. R1534, and (e) a DNA sequence (crtY) coding lycopene cyclase of Plavobacterium sp. R1534, and (e) a DNA sequence (crtV) coding lycopene cyclase of Plavobacterium sp. R1534, and sequence (crtV) coding lycopene cyclase of Plavobacterium sp. R1534, and sequence (crtV) coding lycopene cyclase of carotenoid mixture can also be used in preparation of food products. The method is an improved method of fermentation for carotenoid
                                                                                                                                                                                                             LIYFGSTGIWP--LQWIGAGMTAYGLLYFMVHDGLVHQRWPFRYIPRKGYLKRLYMAHRM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 NALIVFVTVVCMEVVAALAHKYIMHG-WGWGHLSHHEPRKGAFBVNDLYAVVFAIVSIA 64
                                                                                                                                     3 NFLIVVATVLVMELTAYSVHRWIMHGPLGWGWHKSHHEEHDHALEKNDLYGLVFAVIATV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of carotenoid - comprises fermentation with transformed cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carotenoid; pigment; canthaxanthin; R1534; crtB; prephytoene synthase; crtI; phytoene desaturase; crtY; lycopene cyclase; crtW2396; beta-carotene beta-oxygenase; food product; fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 NALIVEVIVVGMEVVAALAHKYIMHG-WGWGWHLSHHBPRKGAFBVNDLYAVVFAIVSIA
                                               Gaps
                                                  10;
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       DB 2; Length 162;
                          1.1e-51;
Thes 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39; Indels
                                                                                                                                                                                                                                                                              HHAVRGKEGCVSFGFLYAPPLSKLQATLRERHAARSGAARDE 164
                                                                                                                                                                                                                                                                                                     51.8%; Score 495; DB 2;
58.0%; Pred. No. 1.1e-51;
iive 19; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        crtE2396 gene product beta-carotene hydroxylase.
    51.8%; Score 495; DB
58.0%; Pred. No. 1.1e
ive 19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW69536 standard; protein; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-00348653
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                               | Simflarity 58.0 94; Conservative
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Best Local Similarity
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production

Best Loc Matches

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Length 162;

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60 NFLIVVATVLVMELTAYSVHRWIMHGPLGWGMHKSHHEEHDHALERNDLYGLVPAVIATV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 LIYFGSTGEWP--LQWIGAGWTAYGLLYFWVHDGLVHQRWPFRYIPRKGYLKRLYMAHRM 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a fusion between the SSU leader and a beta-carotene hydroxylase encoded by the crtZ gene (see AAX25067) of A. auriantiacum. The xanthophyll content of seeds can be altered by transforming cells of a host plant with at least one construct containing: (i) a transcription initiation region of a gene that is preferentially expressed in seeds; (ii) the sequence for a plastid transit peptide; (iii) DNA from a carotenoid synthesis gene coding region, and (iv) a transcription terminator. The transformed cells are regenerated to plants and these, or their progeny, grown to produce seeds. The method is especially used to increase the carotenoid content in oilseed plants. Coexpression of beta-carotene hydroxylase and beta-carotene ketolase (see AAW8198) results in increased astaxanthin and zeaxanthin content in the seeds of transformed plants
                                                                                                                                                                                                                                                                                      Btea-carotene hydroxylase; crt2 gene; carotenoid; xanthophyll; pigment; astaxanthin; zeaxanthin; transgenic plant; oilseed plant; seed oil; A. auriantiacum.
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51.8%; Score 495; DB 2; Length 219;
Best Local Similarity 58.0%; Pred. No. 1.6e-51;
Matches 94; Conservative 19; Mismatches 39; Indels 10; Gaps
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178 HHAVEGRDHCVSFGFIYAPPUDKLKQDLK-----MSGVLRAE 214
                                                                                                                                                                                                                   SSU/beta-carotene hydroxylase fusion.
AAM98197 standard; protein; 219 AA
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                                                                                                                                             05-JUL-1999 (first entry)
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N-PSDB; AAX25067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
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                                                                      AAW98197;
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Q93ci 6 xanthobacte
Q9xxx1 bradyrhizob
P94789 flavobacter
Q9rlh3 paracoccus
Q8rt2 uncultured
Q91pb3 rhodocyclus
Q91pb3 rhodocyclus
Q91vv07 deinococcus
Q95057 rhodocyclus
Q95044 tagetes ere
Q95044 tagetes ere
Q97v419 synechococc
Q9m608 citrus para
Q7v419 synechococc
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GenCore version 5.1.6
Copyright (a) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q47846
Q87014
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Q9371X1
P9471X1
P9471X1
Q971H3
Q971H3
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### ALIGNMENTS

RSULT	LT 1									
SGCS0	08									
<u>.</u>	08950	PRELIMINARY;		PRT;	296 AA.	AA.				
: E	01-MAR-2003	(TrEMBLrel.	23.	Created)						
Ħ	01-MAR-2003			Last seq	sence.	sequence update)				
Ħ	01-OCT-2003	(TrEMBLrel.	25,	Last ann	stati	annotation update)	(a)			
œ :	Phytoene synthase.	thase.								
Z,	CKTB.	:								
ģ	Pantoea stewartii.	artii.								
ŭ	Bacteria; Pr	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales	; Gar	mmaprote	pact	eria, En	terobact	eriale		
ö	Enterobacteriaceae;	iaceae; Pantoea.	oea.							
×	NCBI_TaxID=66269;	6269;								
z	[=									
ę,	SEQUENCE FROM N.A.	M N.A.								
ပ္က	STRAIN=ATCC 8200;	8200;								
5	deSouza M.L.	deSouza M.L., Kollmann S.R., Schroeder W.A.;	я.	Schroed	er w.	A.;				
닭	"Carotenoid	Biosynthesis	(M	02/0793	35 A2	, , ,				
귀	Submitted (C	Submitted (OCT-2002) to the EMBL/GenBank/DDBJ	the 1	EMBL/Gen	3ank/	ь	databases.			
굕	EMBL; AY1667	13; AAN85600	1.							
굕	GO; GO: 00167	GO; GO: 0016740; F:transferase activity; IEA.	eras	activi	Y:	EA.				
뽔	GO; GO:00090	58; P:biosyn	thes	is, IEA.						
ĸ	InterPro; IP	R002060; Squ	/phy	synths						
æ	InterPro; IP	InterPro; IPR008949; Terpenoid synth.	peno	id synth						
œ	Pfam; PF0049	4; SOS PSY;	, i	l						
뜻	PROSITE; PSO	1044; SQUALE	He	YTOEN SY	,, ,, ,,,	H				
æ	PROSITE; PSD	1045; SQUALE		TOEN SY	,       	٦.				
ģ	SEQUENCE 2	SEQUENCE 296 AA; 33108 MW; B2294BI6D8513FC2 CRC64;	8 MW	; B2294]	31608	513FC2 C	RC64;			
8	Query Match	100	100.0%;	Score	1535;	Score 1535; DB 2;	Length 296;	296;		
M Be	Best Local Similarity Matches 296; Conserv	ů T	*	Pred. No. 4 0; Mismatches	No. 4	Pred. No. 4.2e-126; Mismatches 0;	Indels	0	Gaps	0;
Ż:	A MAV	MAVGSKSPATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPBQRLQQ	DAKT	RESTEMENT	AWCRE	CDDVIDDO	TLGFHAD	PSSOME	EORLOO	09
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Matches 243; Conservative
                         PRELIMINARY;
                                                QBVUJ4;
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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CRTB.
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                                                                               121 YCYHVAGVVGIMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
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                                                                                                                                                                                        YCYHVAGVVGIAMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
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LEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEWKTROAYAGSOMHEPAFAEOEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94236237; PubMed=8180698;

MEDLINE=94236237; PubMed=8180698;

MEDLINE=94236237; PubMed=8180698;

A TO K.Y., Lai B.M., Lee L.Y., Lin T.P., Hung C.H., Chen C.L.,

Chang Y.S., Liu S.T.;

"Analysis of the gene cluster encoding carotenoid biosynthesis in

Erwinia herbicola 810-13.";

Microbiology 140:331-339 (1994).

R Microbiology 140:331-339 (1994).

R PIRS, 552587; S52587; S52587; S52587; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; S52697; 
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                                                                                                                                                         EEEGLTKANYAAPENROALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQVYR
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                                                                                                                                                                                                                                                                                              KIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRWKTYPPRPAHLWQRPI 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Prephytoene pyrophosphate synthase.
CRTB.
CRTB.
Bantoea agglomerans.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Pantoea.
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88.5%; Pred. No. 9.5e-112;
.ive 12; Mismatches 22; Indels (
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Matches 262, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 EEEGLIKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQVYR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL
                                                                                                                                                                                                                                                                                                                biosynthesis genes from
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                                                                                                                                           Pantoea agglomerans pv. milletiae.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 296;
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TGOJation and characterization of carotemoid biosynthesis
Troolation and characterization of carotemoid biosynthesis
Pantoea agglomerans pv. milletiae Wist 801.";
E Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; ABOT6662; BABT9604.1;
GOJ GO:0016740; Fitransferase activity; IEA.
R GO; GO:0016740; Fitransferase activity; IEA.
R InterPro; IPR002069; Fitransferase activity; IEA.
R InterPro; IPR002069; Farpenoid_synthse.
R InterPro; IPR003049; Terpemoid_synth.
R FROITE; PS01044; SQS RSY; 1. Perpenoid_synth.
R PROSITE; PS01044; SQS MENY PHYTORN SYN 2; 1.
SRQUENCE 296 AA; 32696 MW; C28FC3EC03C3CE56 CRC64;
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Hyphomicrobiaceae; Kanthòbacter.
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                                         Created)
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Last annotation update)
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Last annotation update)
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82.1%; Pred. No. 1.2e-100;
ive 12; Mismatches 41;
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Larsen R.A., Metcalf W.W.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
SHEL, AF408848; AAL02001.1; -.
GO: GO:0016740; F:transferase activity; IEA.
296
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62 EMKTROAYAGSOMHEPAFAAFOEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLRY 121
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01-MAY-1997 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phytoene synthase
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                                                                                                                                                                                                      4 GSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTEGFHADQPSSQMPEQRLQQLEM
                                                                                                                                                                                                                                        19 GSKSFÄAAARLFGPRMREDAVMLYAWCRHCDDVVDGQBEG-HGRVSSAASPABRLDGLYB
                                                                                                                                                                                                                                                                          64 KTRQAYAGSQMHBPAFPAAFQEVAMAHDIAPAYAFDHIBGFAMDVRETRYLTLDDTLRYCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hannibal L., Lorquin J., Angles d'Ortoli N., Garcia N., Chaintreuil C., Masson-Boivin C., Dreyfus B., Giraud S.; Isolation and characterization of the canthaxanthin biosynthesis genes from the photosynthetic bacterium Bradyrhizobium sp. strain ORS278.";
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48.4%; Score 743.5; DB 2; Length 335;
Best Local Similarity 51.7%; Pred. No. 9.6e-57;
Matches 156; Conservative 40; Mismatches 87; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bradyrhizobium sp. CRS278.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiacee; Bradyrhizobium.
NCBI_TaxID=114615;
                                                                                                                                       Length 311;
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EMBL, AP218415, AAP78202.1; -
GO: GO:0016740; F:transferase activity; IBA.
GO: GO:001678058; P:biosynthesis; IBA.
GO: GO:0090898; P:biosynthesis; IBA.
InterPro; IPR002060; Squ/pht, synthe.
InterPro; IPR008949; Terpenoid_synth.
Pfam; PP00494; SQS PSY; 1.
PROSITE; PS01044; SQUALEN PHYTOEN SYN 1; 1.
PROSITE; PS01045; SQUALEN PHYTOEN SYN 2; 1.
SEQUENCE 335 AA; 36869 FM; 6010A5B12014FDD2 CRC64;
GO; GO:0009058; P:biosynthesis; IEA.
InterPro; IPR002060; Squ/bpht. synthse.
InterPro; IPR008949; Terpenoid_synth.
Pfam; PF00494; SQS_PSY; 1.
PROSITE; PS01044; SQUALEN HYTOEN SYN_1; 1.
SEQUENCE 311 AA; 33279 MN; 77527659568099CAA CRC64;
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Last annotation update)
                                                                                                                                  %; Score 804; DB 2;
%; Pred. No. 4.4e-62;
37; Mismatches 93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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MEDLINE=20309720; PubMed=10851005;
                                                                                                                                       52.48;
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                                                                                                                                                                        161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                    Query Match
Best Local Similarity
Matches 161; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phytoene synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                           198
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                                                                                                                                                                                          BEGLIKANYAAPENROALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQVYRK 241
                                                                                                                                                                                                                                                                                                         242 IGVKVEQAGKQAWDHRQSTSTAEK-----LTLLLTASGQAVTSRMKTYPPRPAHLWQ 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 PADWLAEAG---ATVEGPVPSDALYSVIIRLLDAAEPYYASARQGLPHLPPRCAWSLAAA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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61 LEMKTRQAYAGSQMHE-----PAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 IAQGSQSFAQAAKLMPPGIREDTVMLYAWCRHADDVIDGQVMGSAPEAGGD--PQARLGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 PESWLEEEGLTKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPBQRLQQ
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Gene 185:35-41(1997),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
Flavobacteriaceae; Flavobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32616 MW; 536CCC680B4D99D0 CRC64;
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Last annotation update)
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PROSITE; PS01044; SQUALEN PHYTOEN SYN 1; 1.
PROSITE; PS01045; SQUALEN PHYTOEN SYN 2; 1.
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Q9RLH3

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MEDLINE=21822632; PubMed=11832943;
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 38.0
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                        DILAALQGDGPVTPPPAALRAVARRHDFPQAWPMDLIEGPAIDVBARDYRTLDDVLEYSY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 KTROAYAGSOMHEPAFAAFOEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLRYCY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 HVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWLEBB 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 GLTKANYAAPENRQALSRIAGRLVREAEPYYVSSMACLAQLPLRSAWALATAKQVYRKIG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 G---ARVDGFVPSPELYTVILRLLDAAEPYYPSARVGLADLPPRCAWSIPPAFRIYRAIG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEM 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MH1; Harker M., Hirschberg J.; Harker M., Hirschberg J.; "Carotenoid biosynthesis genes in the bacterium Paracoccus marcusii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae; Paracoccus.
NCBI_TaxID=59779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 42.1%; Score 645.5; DB 2; Length 304; Best Local Similarity 46.9%; Pred. No. 3.2e-48; Matches 137; Conservative 35; Mismatches 115; Indels 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHILT, Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. Sylba; Y15112; CAB56063.1, ...
GO; GO:0001640; F:transferase activity; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
InterPro; IPR002060; Sq1/phyt synthse.
InterPro; IPR006949; Terpenoid synth.
Pfam; PF00494; SOS PSY; 1.
SEQUENCE 304 AA; 33185 MW; OCOBA7CEDC30828A CRC64;
                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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Bacteria, Proteobacteria, environmental samples
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                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paracoccus marcusii,
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01-OCT-2002 (TrEMBI
01-OCT-2003 (TrEMBI
Phytoene synthase.
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CRTB.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 GL----TKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQV 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GSKSFATASTIFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEM 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 GSLSFHAASKLLPASVRDPALALYAFCRLADDEVDE------GQNKTRAVIELQE
Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
Hamada T., Eisen J.A., Praser C.M., DeLong B.F.;
"Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 RVASAVGAMMCVIMRVRDADALARACDLGVAMQLINIARDVGEDARAGRIYLPLEWIDAE
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SEQUENCE FROW N.A.

MEDLINE-2182232; PubMed-11832943;

Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,

Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;

"Unsuspected diversity among marine aerobic anoxygenic phototrophs.";

Nature 415:630-633(2022)

EMBL, AE008919; ALL76346.1;

EMBL, AE008919; ALL76346.1;

EMBL, Processer Sequence activity; IEA.

GO, GO:0016740; Fitzmanferase activity; IEA.

GO, GO:001679; Priosynthesis; IEA.

InterPro; IPR002060; Squ/phyt synthse.

InterPro; PR008949; Perpenoid synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.1%; Score 446.5; DB 2; Length 346; 38.0%; Pred. No. 1e-30; ive 35; Mismatches 120; Indels 33
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                                                                                                                                                                                                                                                                                                             Pfam; PF00494; SQS_PSY; 1.

PROSITE; PS01044; SQUALEN PHYTOEN SYN 1; 1.

SROSITE; PS01045; SQUALEN PHYTOEN SYN 2; 1.

SROUNCE 346 AA, 37857 WW, 13AGC6E82PAC1237 CRC64;
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PROSITE: PS01045; SQUALEN PHYTOEN SYN 2; 1.
SROUENCE 379 AA; 41383 MN; 3AĀ160ĒS61C3CC6D CRC64;
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Last sequence update)
Last annotation update)
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NCBL TaxID=153809;
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                                                                                                Nature 415:630-633 (2002).

EMBL, AB008921; AAM48647.1; -
GO; GO:0016740; F:transferase activity; -
GO; GO:0099058; P:biosynthesis; IEA.
InterPro; IRR002060; Squ/phyt, synthe.
InterPro; IPR004949; Terpenoid_synth.
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Rubrivivax gelatinosus.";
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                                                                                            4 GSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEM
                                                                                                                                                             41 GSRSFWVASQLLPPTIRNDACGLYAFCREADDLIDE---GDDADAALAQLHE-RLDGI--
                                                                                                                                                                                                                          64 KTROAYAGSOMHEPAFAAFOBVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLRYCY
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                                         Gaps
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Menin L., Yoshida M., Jaquinod M., Nagashima K.V., Matsuura K.,
Parot P., Vermeglio A.;
"Dark aerobic growth conditions induce the synthesis of a high
midpoint potential cytochrome c8 in the photosynthetic bacterium
                                         12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Comamonadaceae, Rubrivivax.
NCEL_TaxID=28068;
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STRAIN=11144;
Magashima K.V., Shimada K., Matsuura K.;
Phylogenetic analysis of photosynthetic genes of Rhodocyclus gelatinosus: Possibility of horizontal gene transfer in purple
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Photosynthetic gene cluster in purple bacterium, Rubrivivax
gelatinosus.";
(In) Garab G. (eds.);
                                     Indels
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
Best Local Similarity 38.4%; Pred. No. 7.3e-27; Matches 103; Conservative 38; Mismatches 115;
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 BEEGL-TKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL
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STRAINER! / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE=20036896; PubMed=10567266;
Minite O., Eisen J.A., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wamathevan J.J., Lam P., McDanald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Pleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 RKIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKTY---PPRPA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 AEIGRMLEROGLDSVNHRVVVPARRKAALMARAASAAFNTPGRAYISMPPLPA 299
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5
                                                                                                                                                                                                                                                                                                                                                             25.8%; Score 395.5; DB 2; Length 344; 36.2%; Pred. No. 2.9e-26; Ive 32; Mismatches 140; Indels 15;
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WCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                37551 MW; CCC7F8AD52AA4570 CRC64;
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Last annotation update)
Biochemistry 38:15238-15244 [1999].
EMBL, AB034704; BAA94048.1; -
PIR, T50895; T50895.
GO, GO:0016740; F:transferase activity; IEA.
GO; GO:0005058; P:biosynthesis; IEA.
InterPro; IPR002060; Squ/phyt. synthse.
InterPro; IPR004949; Terpenoid_synth.
PR00494; SQS PBY; I.
PR0041E: PS01045; SQUALEN_PHYTORN SYN 2; I.
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TIGR, DROBG2, ...

G0, G0:0016740; F:transferase activity; IEA

G0, G0:0019058; P:biosynthesis; IEA...

InterPro; IPR002060; Squ/phyr synthse.

InterPro; IPR00849; Terpenoid_synth.

Pfam; PF04944; SQS PSY; 1.

PROSITE; PS010445; SQUALEN_PHYTOEN_SYN_2; 1.
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EMBL; AB001940; AAF10440.1; -.
PIR; D75466; D75466.
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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DR0862.
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182 PRGWLVEAGLDVDAWLQNPVHCPPVAQTVRKLLRAADBLYERSEHGIAALPRDCRPAIRA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phytoene synthase (Fragment) and auniotation update)
Tagetes erecta (African marigold).

Eukaryota, Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; astericampanulids; Asterales; Asteraceae; Asteroideae; Tageteae; Tagetee; Tagetee; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagetees; Tagete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.4%; Score 313.5; DB 10; Length 28.3%; Pred. No. 5.8e-19; ive 59; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 QVYRKIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       petal development.";
Submitted (ARR-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AR251.015; AAG10427.1;
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0009058; P:blosynthesis; IEA.
InterPro; IPR002060; Squ/phyt synthse.
InterPro; IPR002949; Terpenoid_synth.
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                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                       235 AKQVYRKIGVKVBQAGKQAWDHRQSTSTAEKLTLLTA
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PROSITE; PSO1044; SQUALEN PHYTOEN SYN 1; 1.
PROSITE; PSO1045; SQUALEN PHYTOEN SYN 2; 1.
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01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
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01-JUN-2001 (TEMBLE) 17,
01-OCT-2003 (TEMBLE) 25,
Phytoene synthase.
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tes 80; Conservative
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01-MAR-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 TRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHL-EGFAMDVRETRYLTLDDTLRYCY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 HVAGVVGLMMAQIMGVRDN-ATLDRACDIGLAFQLTNIARDIVDDAQVGRCYLPESWLEE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 EGLTKA-----NYAAPENRQALSRIAGRLVREAEPYYVSSWAGLAQLPLRSAWAIAT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 YGLSRAALERWGQGEPLSPAYRALMTHIGG-LARB---WYAAGRAGIPQLDGRGPLAVLT 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDTLRYCYHVAGVVGLAMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYL 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 IRTRLDGVYAGT----PAPIA-ADRALACTVHRYGVPRVLLDALLBGPLWDADGRRYDTI 121
                                                                                                                                                                                                                                                                                 5 SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK 64
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                                                                                                                                                                                                       Gaps
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"Photooxidative stress stimulates illegitimate recombination and mutability in carotenoid-less mutants of Rubrivivax gelatinosus.";

EMBO J. 16:4777-4787(1997).

EMBL; AY234384; AAB87738.1; -.

EMBL; AY234384; P.transferase activity; IEA.

GO; GO:0009058; P.biosynthesis; IEA.

InterPro; IPR00260; Squ/phyt synthse.
                                                                                                                                                                                                       24;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Comamonadaceae; Rubrivivax.
                                                                                                                         Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 343;
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                                                                                                                     Match
Local Similarity 37.5%; Pred. No. 2.3e-23;
es 103; Conservative 37; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Incerto,
Pfan, PF00494; SQS PSY; 1.
PROSTIE; PS01045; SQUALEN PHYTOEN SYN 2; 1.
PROSTIE; P343 AA; 37509 MW; C7CA4F5228B9CBAF CRC64;
                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 AKOVYRKIGVKVEQAGKOAWDHROSTSTAEKLTLL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 AARAYEGILDDLERAGYDNFGRRAYVSGRRKLIML 310
                                       35972 MW; 52B3ADB66C65853F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                           325 AA;
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SEQUENCE 325 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 YHVAGVVGLMMAQIMGVRDN-----ATLDRACDIGLAFQLTNIARDIVDDAQVGRCYLP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESWLEEEGLTKANYAAPENRQALSRIAGRIVREAEPYYVSSMAGLAQLPIRSAWAIATAK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | : | : | | : : | 325 QDELAQAGLSDDDIFAGEVTIKWRNFWKNQIKRARMFFDMAENGVTELSEASRWPVWASI 384
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           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Sapindales; Rutaceae; Citrus.
NCBI_TaxID=37656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                 COSTA M.C., Moreira C.D., Melton J.R., Otoni W.C., Moore G.A., "Developmental expression of carotenoid genes in Citrus.", Bubmitted (APP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF152892; AD38051.2; -
GO, GO:0016740; F:transferase activity; IEA.

GO, GO:0016740; F:transferase activity; IEA.

GO, GO:0009058; P:biosynthesis; IEA.

InterPro; IPR008949; Terpenoid synth.

PROSITE; PS01044; SQS, PSY; 1.

PROSITE; PS01044; SQUALEW PHYTORN SYN 1; 1.

PROSITE; PS01044; SQUALEW PHYTORN SYN 2; 1.

SRQUENCE 436 AA; 49360 NW; 87F7C8D79EFA83B1 CRC4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 OVYRKIGVKVEQAGKQAWDHRQSTSTABKLFLLLTASGQAVTSRMKTY 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56; Mismatches 132; Indels
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01-0CT-2003 (TrEMBirel. 25, Last sequence update)
01-0CT-2003 (TrEMBirel. 25, Last sequence update)
Phycone synthases (EC 2.5.1.-).
CRIB.PYS OR SYNW2256.
Synechococcus sp. (strain WH8102).
Bacteria, Cyanobacteria, Chrococcales, Synechococcus.
NOBI_TaxID=84588;
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Citrus paradisi (Grapefruit)
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81; Conservative
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Conservative

Best Local Similarity Matches 87; Conserv

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123
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                                                                                                                                                                                                                                                                                                                                                                                           138 RVAGTVGLMTQGVMGV-DGAYTSAPWSDRPDTSDAAVALGIANQLTNILRDVGEDRGRGR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 CYLPESWLEEEGLIKANYAAPERRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 IYLPLBDLERFGYSEDDLAAGRINSAWCELAQFQLKRARDWFARSEAGVRWLSRDARWPV 256
5 SKSPATASTLÆDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPBQRLQQLEMK 64
                                                                       24 AKTEVLGTLLLPPAKRRAIWAIYVWCRRTDELMDSPEA---QSRPVAELAS-RLDRWEBK
                                                                                                                                                           65 TRQAYAGSQMHE-PAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLRYCY
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257 WTSLRLYRGILDAIERVDYDVFNNRAYVGKVSKL 290
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Search completed: February 29, 2004, 14:51:04 Job time : 27.3391 secs

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                                           ; Search time 4.98876 Seconds (without alignments) 3089.496 Million cell updates/sec
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                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                        1 MAVGSKSFATASTLFDAKTR......VTSRMKTYPPRPAHLWQRPI 296
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                            otal number of hits satisfying chosen parameters:
                                                                                                                              141681 segs, 52070155 residues
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PSY_MAIZE
PSY1_EYCES
PSY_NEUCR
PSY_CUCME
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CRTB_STRGR
CRTB_MCTU
YAAC_HISN
FDFT_HUMAN
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FDFT_RAT
Y4AD_RHISN
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TRME SYNY3	KIT MOUSE	FLT3 HUMAN	TRME_ANASP	SPCP RAT	ISPA_ECOLI	CAPP STRPY	CAPP_STRP8	CAPP_STRP3	LA AEDAL	KIT CANFA	KIT_BOVIN
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# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misawa N., Nakagawa M., Kobayashi K., Yamano S., Izawa Y.,
Nakamura K., Harashima K.,
Elucidation of the Erwinia uredovora carotenoid biosynthetic pathway
by functional analysis of gene products expressed in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXVISIONS TO N-TERMINUS.
Misawa N., Nakagawa M., Kobayashi K., Yamano S., Izawa Y.,
Nakamura K., Harashima K.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Catalyzes the reaction from prephytoene diphosphate to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phytoene.
-!- PATHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: Belongs to the phytoene/squalene synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pantoea ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBITE; PS01044; SQUALEN PHYTOEN SYN 1; 1.
PROSITE; PS01045; SQUALEN PHYTOEN SYN 2; 1.
PROSITE; PS01045; SQUALEN PHYTOEN SYN 2; 1.
SROUTH CHOCLIONAL CHONNE; Carotenoid biosynthesis; Transferase.
SRQUENCE 309 AA; 34472 MW; 9AA381A7376BBFC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 309;
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                                       01-MAY-1991 (Rel. 18, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
Phytoene synthase (BC 2.5.1.-).
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309
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InterPro; IPR002060; Squ/phyt_synthse.
InterPro; IPR008949; Terpenoid_synth.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 172:6704-6712(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=20D3;
MEDLINE=91072214; PubMed=2254247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D90087; BAA14128.2; -. PIR; E37802; E37802.
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Terpenoid_synth.

InterPro; IPR008949;

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                                                                                                         61 LEMKTRQAYAGSQMHEPAPAPQEVAMAHDIAPAYAFDHLEGPAMDVRETRYLTLDDTLR 120
                                                                                                                           YCYHVAGVVGIAMAQIMGVRDNATLDRACDIGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
                                                                                                                                                                                                   134 YCYHVAGVVGLAMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAHAGRCYLPASWL 193
                                                                                                                                                                                                                                   BEEGLIKANYAAPENRQALSRIAGRIVREAEPYYVSSMAGLAQLPIRSAWAIATAKQVYR 240
                                                                                                                                                                                                                                                    73
                                              1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ
                                                             14 MAVGSKSFATASKLFDAKTRRSVLMLYAWCR-CDDVIDDQTLGFQARQPALGTFBQRLMQ
                                                                                                                                                                                                                                                                                                                241 KIGVKVEQAGKQAWDHRQSTSTAEKLTLLTASGQAVTSRMKTYPPRPAHLWQRPI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 89:6761-6764(1992).
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Armstrong G.A., Alberti M., Hearst J.B., Conserved enzymes mediate the early reactions of carotenoid biosynthesis in nonphotosynthetic and photosynthetic prokaryotes."; Proc. Natl. Acad. Sci. U.S.A. 87:9975-9979(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: Carotenoid biosynthesis.
SIMILARITY: Belongs to the phytoene/squalene synthetase family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
NCBL_TaxID=549;
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-!- CATALYTIC ACTIVITY: Prephytoene diphosphate = diphosphate
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; Pred. No. 5.6e-115;
11; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene synthase (EC 2.5.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                               309
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EMBL; M87280; AAA64982.1; -.
PIR; B39273; B39273; B39273; LIRECEPTC; PRO02060; SQU/phyt_synthse.
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=EH010;
MEDLINE=91088634; PubMed=2263648;
   88.98;
   il Similarity 88.9%
263; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 KIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPPRPAHLWQRPI 296
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96062243; PubMed=7592436; Misawa N., Saliwara S., Salto T., Misawa N., Satomi Y., Kondo K., Yokoyama A., Kajiwara S., Salto T., Obtani T., Miki M.; S., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto T., Salto 
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J. Bacteriol. 177:6575-6584(1995).
-!- FUNCTION: Catalyzes the reaction from prephytoene diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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.!- PATHWAY: Carotenoid biosynthesis. Involved in astaxanthin
                  Pfam; PF00494; SQS P8Y; I. PROSTE; PROSTE; P801044; SQUALEN PHYTORN SYN 1; 1.
PROSTIE; P801045; SQUALEN PHYTORN SYN 2; 1.
Multifunctional pryme; Carotemoid biosynthesis; Transferase.
SEQUENCE 309 AA; 34123 MW; B64235C9E0C06F38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium. NCBI TaxID=44155;
                                                                                                                                                                                                                                                     68; Indels
                                                                                                                                                                                                                            1.46-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Phytoene synthase (EC 2.5.1.-).
                                                                                                                                                                         67.0%; Scott No. 1. 64.0%; Pred. No. 1. 36; Mismatches
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                                                                                                                                                                                                                            Best Local Similarity 64.9
Matches 192; Conservative
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                                                                                                                                                                                                                                                                                                                                                 HVAGVVGLAMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWLEEE 183
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                                                                                                                                                                                                            4 GSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSOMPEORLOOLEM
                                                                                                                                                                                                                                            GSOSFATAAKLMPPGIRDDTVMLYAWCRHADDVIDGQALGSCPEAVND--PQARLDGLRA
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                                                                                                                                                                                                                                                                                                       DILAALQGDGPVTPPFAC--AVARRHDFPQAMPMDLIEGFAMDVBARDYRTLDDVLEYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 VKVEQAGKQAMDHRQSTSTARKLTLL-----LTASGQAVTSRMKTYPPRPAHLMQR
                                                                                                                                                                             Gaps
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MEDLINE=94292403; PubMed=8021167;
Lang H.P., Coddell R.J., Gardiner A.T., Hunter C.N.;
Lang H.P. are carcinoid biosynthesis: sequences and transcriptional analysis of the crt1 and crtB genes of Rhodobacter sphaeroides and overexpression and reactivation of crt1 in Escherichia coli and R. sphaeroides.";
J. Bacteriol. 176:3859-3869(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECURICE FROM N.A.
STRAINE-BYS 1273 / 2.4.1 / NCIB 8253 / DSM 158;
STRAINE-95238278; Pubmed-7721699;
LANG H.P., Cogdell R.J., Takaichi S., Hunter C.N.;
"Complete DNA sequence, specific In5 insertion map, and gene assignment of the carotenoid biosynthesis pathway of Rhodobacter
                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
WCBI_TaxID=1063;
   InterPro; incompage of Terpenoid Synch.

InterPro; IPR00894; JGS BSY; 1.

PROSITE; PR01044; SQUALEN PHYTORN SYN 1; 1.

PROSITE; PR01045; SQUALEN PHYTORN SYN 2; 1.

PROSITE; PR01045; SQUALEN PHYTORN SYN 2; 1.

PROSITE; PR01045; SQUALEN PHYTORN SYN 2; 1.

PROSITE; PR01045; SQUALEN PHYTORN SYN 2; 1.

All As; 32697 MW; SPA306D3868CD357 CRC64;
                                                                                                                                        Length 301;
                                                                                                                                                                           99; Indels
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STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE=20115911; PubMed=10648776;
                                                                                                                                        Score 648; DB 1;
Pred. No. 1.3e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene synthase (SC 2.5.1.-).
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                                                                                                                                                                         34; Mismatches
ogu/phyt_synthse.
Terpenoid_synth.
3y: 1
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01-0CT-1996 (Rel. 34, Last seq
10-0CT-1996 (Rel. 34, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                    42.28;
                                                                                                                                    Query Match
Best Local Similarity 47.2%
Matches 142; Conservative
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 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 SFSGVLDÝSARVAAAVGAMMCVLMRVRDPDVLARACDLGLAMQLTNIARDVGTDARSGRI
                                                                           Nucleic Acids Res. 28:862-867(2000).
-!- FUNCTION: Catalyzes the reaction from prephytoene diphosphate to

    -!- SIMILARITY: Belongs to the phytoene/squalene synthetase family.

                                                                                                                                      phytoene.
CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate
Kaplan S.; analysis of the photosynthesis region of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                       prephytoene diphosphate.
CATALYTIC ACTIVITY: Prephytoene diphosphate = diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 YAARHIYAGIGDELARNGYDSVTRRAFTTRROKLVWLGLSSTRAALS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 ATAKOVYRKIGVKVBQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 219 L -> Q (IN REF. 3).
286 286 S -> A (IN REF. 3).
324 S -> A (IN REF. 3).
355 AA, 39002 MW; E338PA4BDEF7E6045 CRC64;
                                                                                                                                                                                                                                                                         PATHWAY: Carotenoid and chlorophyll biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodobacter capsulatus (Rhodopseudomonas capsulata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002060; Squ/phyt_synthse.
InterPro; IPR008949; Terpenoid_synth.
Pfam; PP00494; SQS_PSY; 1.
PROSITE; PS01044; SQUALEN PHYTORN SYN_1; 1.
PROSITE; PS01045; SQUALEN PHYTORN SYN_2; 1.
PROSITE; PS01045; SQUALEN PHYTORN SYN_2; 1.
Chlorional enzyme; Carotenoid biosynthesis; Chlorophill biosynthesis.
Chlorophill biosynthesis. L -> Q (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.7%; Score 394; DB 1; 36.6%; Pred. No. 8.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ010302; CAB38740.1; -. EMBL; AF195122; AAF24290.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S71770; AAB31139.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S49621; S49621.
PIR; T50746; T50746.
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  dhary M.,
sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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P17056;
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Phytoene synthase, chloroplast precursor (EC 2.5.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47805 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X78814; CAA55391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S54135; S54135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 AA;
                                                                                                                                             TISSUE=Paracorolla;
                                                                                 Narcissus.
NCBI_TaxID=39639;
                                                                                                                                                                                                                                            phytoene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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PSY CAPAN
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                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by another is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 KTROAYAGSOMHEP---AFAA-FOEVAMAHDIAPAYAFDHIEGFAMDVRETRYLTIADDTL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 RLEDIYAGRPRNAPSDRAFAAVVEEFEMPRELPEAL----LEGFAWDAEGRWYHTLSDVQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 RYCYHVAGVVGIMMAQIMGVRDNATLDRACDIGLAFQLTNIARDIVDDAQVGRCYLPBSW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 LEEEGL-TKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEM 63
                                                                                                            Ambanacong G.A., Alberti M., Leach F., Hearst J.E.,
"Nucleoting G.A., Alberti M., Leach F., Hearst J.E.,
"Nucleoting G.A., Alberti M., Leach P., and nature of the protein
products of the carotenoid biosynthesis gene cluster of Rhodobacter
capsulatus.";
Mol. Genet. 216:254-268(1989).
-i- FUNCTION: Catalyzes the reaction from prephytoene diphosphate to
                                                                                                                                                                                                               phytoene.
-!- CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate
                                                                                                                                                                                                                                                                                     PATHWAY: Carotenoid and chlorophyll biosynthesis. SIMILARITY: Belongs to the phytoene/squalene synthetase family.
   Proteobacteria; Alphaproteobacteria; Rhodobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 YRKIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPPR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAAIGAEVAKAKYDNITRRAHTIKGRKLWLVANSAMSATATSMLPLSPR 293
                                                                                                                                                                                                                                             prephytoene diphosphate.
-!- CATALYTIC ACTIVITY: Prephytoene diphosphate = diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pir; Suggus; Suggus; Suggust synthse.
InterPro; IPR002060; Squ/phyt synthse.
InterPro; IPR008949; Terpenoid synth.
Pfam; PP00494; SQS PSY; 1.
PROSITE; PS01044; SQUALEN PHYTOEN SYN 1; 1.
Multifunctional enzyme; Carotenoid biosynthesis; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       blosynthesis.
339 AA; 37301 MW; 6D7052994934BF4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.6%; Score 393.5; DB 1 35.6%; Pred. No. 9.1e-28;
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(Rel. 34; Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 AA
                                                                FROM N.A. and BEC404; and BEC404;
                                                                                                  MEDLINE=89313663; PubMed=2747617
                    Rhodobacteraceae; Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X52291; CAA36534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z11165; CAA77541.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Sest Local Similarity 35.6
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlorophyll biosynthes
SEQUENCE 339 AA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S04403; S04403
                                   NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                            phytoene.
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01-OCT-1996
28-FEB-2003
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P53797;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 ESWLBEEGLTKANYAAPENROALSRIAGRLVREAEPYYVSSMAGLAQIPLRSAWAIATAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 LEDLFAG-RPYDMFDAALSDTVSRFPVDIQP--FMDMVEGMRMDLKKSRYKNFDELYLYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 YHVAGVVGLMMAQIMGV-----RDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLP
Narcissus pseudonarcissus (Daffodil).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Asparagales; Amaryllidaceae;
                                                                                                                                                                                                                                                                                                              Schledz M., Beyer P.; "Nucleotide sequence of a Narcissus pseudonarcissus cDNA for phytoene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phytoene.
--- PATHWAY: Carotenoid biosynthesis.
--- SUBGNIT: Monomer (By similarity).
---- SUBGRILUMAR LOCATION: Chloroplast.
---- SIMILARITY: Belongs to the phytoene/squalene synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate prephytoene diphosphate.
-:- CATALYTIC ACTIVITY: Prephytoene diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: Catalyzes the reaction from prephytoene diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prosite; Prod494; SQS_PSY; 1.
PROSITE; PSO1044; SQUALEN PHYTORN SYN 1; 1.
PROSITE; PSO1045; SQUALEN PHYTORN SYN 2; 1.
Multifunctional enzyme; Carotenoid biosynchesis;
Isoprene biosynthesis; Transferase; Chloroplast; Transit peptide.
TRANSIT [POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 LLYRQILDBIRANDYNNFTKRAYVSKVKRLAALPLAYGKSLLIPLSLRPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.4%; Score 328.5; DB 1; Length 27.9%; Pred. No. 7.8e-22; Live 58; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHYTOENE SYNTHASE.
8E76BA35312B73DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro, IPR002060; Squ/phyt_synthse.
Interpro, IPR008949; Terpenoid_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                       (In) Plant Gene Register PGR95-122
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84; Conservative
                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prephytoene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phytoene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Leaf
                                                                                                 LYCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 AKTPYLGIMIATPERRKAIWAIYVWCRRTDELVDGPN-----ASHITPAALDRWEDR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TROAYAGSOMHEPAFAAFOEVAMAH - DIAPAYAFDHLEGFAMDVRETRYLTLDDTLRYC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YHVAGVVGIAMAQIMGV.-RDNATLD----RACDLGLAFQLTNIARDIVDDAQVGRCYLP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESWLEEBGLIKANYAAPENRQALSRIAGRLVREABPYYVSSMAGLAQLPLRSAWAIATAK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                       Sukaryota, Viridiplantae; Srreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 YYVAGTVGIASVPIMGIAPESKATTESVYNAALALGIANQITNILKDVGEDARRGRVYLP
                                                                                                                                                                                                                                                                                                         Remer S., Hugueney P., Bouvier F., Camara B., Kuntz M.;
"Expression of the genes encoding the early carotenoid biosynthetic enzymes in Capsicum annuum."
Blochem. Blochem. Blochys. Res. Commun. 196:1414-1421 (1993).
-: FUNCTION: Catalyzes the reaction from prephytoene diphosphate to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.2%; Score 309.5; DB 1; Length 419;
28.2%; Pred. No. 3.8e-20;
iive 56; Mismatches 131; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Chloroplast. SIMILARITY: Belongs to the phytoene/squalene synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01044; SQUALEN PHYTOEN SYN 1; 1.
PROSITE; PS01045; SQUALEN PHYTOEN SYN 2; 1.
MAILTIGURCTIONAL enzyme; Carotenoid bioSynthesis;
Isoprene bioSynthesis; Transferase; Chloroplast; Transit peptide.
TRANSIT 1 141
CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  prephytoene diphosphate.
CATALYTIC ACTIVITY: Prephytoene diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 QVYRKIGVKVEQAGKQAWDHRQSTSTAEKLTLLTASGQAVTSRMKT 283
PSY_CAPAN STANDARD; PRT; 419 AA.
P37272;
01-OCT-1994 (Rel. 30, Created)
01-CCT-1994 (Rel. 30, Last sequence update)
01-CT-1994 (Rel. 41, Last annotation update)
Phytoene synthase, chloroplast precursor (EC 2.5.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 AA; 47126 MW; 9167953D6EA929B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHYTOENE SYNTHASE
                                                                                                                                                                                            lamiids; Solanales; Solanaceae; Capsicum
NCBI_TaxID=4072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X68017; CAA48155.1; -.
InterPro; IPR002060; Squ/phyt synthse.
InterPro; IPR008549; Terpenoid_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: Carotenoid biosynthesis.
                                                                                                                                                                                                                                                                            STRAIN=cv. Lamuyo;
MEDLINE=94071905; PubMed=8250898;
                                                                                                                                    Capsicum annuum (Bell pepper).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 28.2% ses 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00494; SQS PSY;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phytoene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YHVAGVVGLMMAQIMGV--RDNATLD----RACDLGLAFQLTNIARDIVDDAQVGRCYLF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 AKTFYLGTMLMTPDRRRAIWAIYVWCRRIDELVDGPN-----ASHITPQALDRWEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 SKSFATASTLFDAKTRRSVLALYAWCRHCDDVIDDQTLGFHADQPSSQMPBQRLQQLEMX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phytoene.
CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94064645; PubMed=8245008; Bartley G.E., Scolnik P.A.; CarbNa clonding, expression during development, and genome mapping of PSY2, a second tomato gene encoding phytoene synthase."; J. Biol. Chem. 268:25718-25721(1993).
                                                                                                                                                                                                                                      01-OCT-1994 (Rel. 30, Created)
1-OCT-1994 (Rel. 30, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Phytoene synthase 2, chloroplast precursor (EC 2.5.1.-) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the phytoene/squalene synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - FUNCTION: Catalyzes the reaction from prephytoene diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Prephytoene diphosphate = diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.0%; Score 307.5; DB 1; Length 310; 28.9%; Pred. No. 4e-20;
373 LLYRRILDEIEANDYNNFTKRAYVSKPKKLIALPIAYAKSLVPSTRT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <1 25 CHLOROPLAST (POTENTIAL).
26 310 PHYTOENE SYNTHASE 2.
310 AA, 35224 MW, 8EAF60FEID9F4CF5 CRC64,</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Mismatches 129;
                                                                                                                                                                    310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Chloroplast.
DEVELOPMENTAL STAGE: In mature leaves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A49558; A49558.
InterPro; IPR002060; Squ/phyt_synthse.
InterPro; IPR008949; Terpenoid_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carotenoid biosynthesis.
                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L23424; AAA34187.1; -.
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291 QEBLKLAGIT-----PEYIFKGKVTDKWRSFWKGQ-IKRARWFFDEAEKGVAELSSASR 343
174 INDLEDG-QPYDMYDAALADTVSTYPVDIQPFK--DMIDGMRMDIKKSRYQTFDBLYLYC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC P3721; O22375; O8LEB6;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DR Phytoene synthage, chiloroplast precursor (EC 2.5.1.-).
DR Phytoene synthage, chiloroplast precursor (EC 2.5.1.-).
DR PSY1 OR PSY OR AF5G1730 OR MRP11.8.
DS Arabidopsis thaliana (Mouse-ear cress).
C Bakaryota, Virialplantae, Streptophyta; Embryophyta; Tracheophyta;
C Spermatophyta; Magnoliophyta; endicocyledons; core eudicots; rosids;
C curosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YHVAGVVGLMMAQIMGV - - RDNATLD - - - - RACDLGLAFQLTNIARDIVDDAQVGRCYLP
                                                                                                                                                                                           177 ESWLEBEGLIKANYAAPE-----NRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAINSCY. COlumbia.
STRAINSCY. COlumbia.
MEDLINE-97471969; PubMeds-9330910;
Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
Miyajima N., Tabbata S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequenc
features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scolnik P.A., Bartley G.B.; "Nucleotide sequence of an Arabidopsis cDNA for phytoene synthase."; Plant Physiol. 104:1471-1472(1994).
                                                                                                                                                                                                                                                                                                                      230 WAIATAKQVYRKIGVKVBQAGKQAWDHRQSTSTAEKLTLLLTASGQAV 277
                                                                                                                                                                                                                                                                                                                                                               344 WPVWASILLYKQILDAIBANDYDNFTKRAYVGKAKKLVSLPLAYSRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Castrignano F., Giuliano G.;
"Sequence of the phytoene synthase gene of Arabidopsis.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
Feldmann K.A.;
"Full-length. CDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Columbia;
MEDLINE=94286755; PubMed=8016277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Res. 4:215-230(1997).
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          137 YYVAGTVGLMSVPIMGIAPESKATTESVYNAALALGIANQLTNILRDVGEDARRGRVYLP 196
                                                                       ESWLEEEGLTKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAK 236
                                                                                                                                     197 QDELAQAĞLSDEDIFAĞKVTDKWRIFWKKQIQRARKFFDEAEKGVTELSSASRWPVLASL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phytoene synthase, chloroplast precursor (BC 2.5.1.-).
Phytoene synthase, chloroplast precursor (BC 2.5.1.-).
Post.
Daucus carota (Carrot).
Bukaryota, Viridiplantae: Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Apiales, Apiaceae; Apioideae; Scandiceae; Daucinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.0%; Score 307.5; DB 1; Length 398;
ilarity 29.5%; Pred. No. 5.4e-20;
Conservative 57; Mismatches 113; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . FUNCTION: Catalyzes the reaction from prephytoene diphosphate to
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-!- CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBUNIT: Monomer (By similarity).
-i- SUBCELLULAR LOCATION: Chloroplast.
-i- SIMILARITY: Belongs to the phytoene/squalene synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 QVYRKIGVKVEQAGKQAWDHRQSTSTABKLTLLLTASGQAVTSRMKTYPPR 287
                                                                                                                                                                                                                                              prephytoene diphosphate.
CATALYTIC ACTIVITY: Prephytoene diphosphate = diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uno T., Sankawa U.;
"Daucus carota phytoene synthase.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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45199 MW, 1D1E043824730615 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                   398 AA
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InterPro; IPR002060; Squ/phyt synthse.
InterPro; IPR008949; Terpenoid_synth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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phytoene.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                    FUNCTION: Catalyzes the reaction from prephytoene diphosphate to
                                                                                                                                                                                                                                                                                                                      SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: Belongs to the phytoene/squalene synthetase family.
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., "Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 QVYRKIGVKVEQAGKQAWDHRQSTSTAEKLTLLITASGQAVTSRMKTYPPR 287
                                                                                                                                                                                                        prephytoene diphosphate.
CATALYTIC ACTIVITY: Prephytoene diphosphate +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 125812; AAA32836.1; --
EMBL; AP009544; AAB65697.1; --
EMBL; AP005234; BAB10510.1; --
EMBL; AP005235; AAM57277.1; --
EMBL; BT002084; AAM17427.1; --
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                                                                                                                                                                            CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate
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128 128 L
143 143 A
422 AA; 47486 WW;
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PRT;

PSY MAIZE STANDARD; P49085; 01-FEB-1996 (Rel. 33, Created)

ESULT 11 SY_MAIZE

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R PIR, 56843.

R AdizeDB; 66643.

R InterPro; IPR002060; Squ/phyt synthse.

DR InterPro; IPR008949; Terpenoid synth.

DR PROSITE; PS01044; SQUALEN PHYTOEN SYN 1; 1.

DR PROSITE; PS01045; SQUALEN PHYTOEN SYN 2; 1.

DR PROSITE; PS01045; SQUALEN PHYTOEN SYN 2; 1.

RW Hitfunctional enzyme; Carotemoid biosynthesis;

KW Isoprene biosynthesis; Transferase; Chloroplast; Transit peptide.

Thinosoprene biosynthesis; Transferase; Chloroplast; Transit peptide.

PHIGOREMS SYNTHASE.

410 PHYTOENE SYNTHASE.
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-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: Belongs to the phytoene/squalene synthetase family.
                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                  MEDIJNE=96304610; PubMed=8722797;
MEDIJNE=96304610; PubMed=8722797;
Buckner B., Sanmiguel P., Janick-Buckner D., Bennetzen J.L.;
The YI gene of maize codes for phytoene synthase.";
Genetics 143:479-488(1996).
-i- FUNCTION: Catalyzes the reaction from prephytoene diphosphate to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prephytoene diphosphate.
-!- CATALYTIC ACTIVITY: Prephytoene diphosphate +
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene synthase, chloroplast precursor (EC 2.5.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Carotenoid biosynthesis.
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                              Zea mays (Maize)
                                                                                                                                                                                                                                                                                    NCBI_TaxID=4577;
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                                                                                                                                                       Lycopersicon esculentum (Tomato).
Bukaryota, Vitidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;
Spermatosky, Solanales; Solanacees, Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Ailsa Craig; TISSUE-Leaf;
MEDLINE=2922971; PubMed=1623189;
Ray J., Moureau P., Bird C., Bird A., Grierson D., Maunders M.,
Ray J., Moureau P., Sind C., Schuch W.;
"Cloning and characterization of a gene involved in phytoene synthesis from comato.";
Plant Mol. Biol. 19:401-404(1992).
-!- FUNCTION: Catalyzes the reaction from prephytoene diphosphate to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate + prephytoene diphosphate.
-!- CATALYTIC ACTIVITY: Prephytoene diphosphate = diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roemer S., Hugueney P., Bouvier F., Camara B., Kuntz M.;
Expression of the genes encoding the early carotenoid biosynthetic
enzymes in Capsicum annuum. ";
Biochem. Biogbys. Res. Commun. 196:1414-1421(1993).
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDIINE=22184738; PubMed=1544888;
Bartley G.E., Viitanan P.V., Bacot K.O., Scolnik P.A.;
"A tomato gene expressed curing fruit ripening encodes an enzyme of the carotenoid biosynthesis pathway.";
J. Biol. Chem. 267:5036-5039(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- INDUCTION: By fruit ripening.
-!- SIMILARITY: Belongs to the phytoene/squalene synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phytoene.
-!- PATHWAR: Carotenoid biosynthesis.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- DEVELOPMENTAL STAGE: In seedlings and in late stages of fruit.
                                              01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene synthase 1, chloroplast precursor (BC 2.5.1.-) (Fruit ripening specific protein pTOM5).
PSYI OR PTOM5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=2 Craig;
MEDLINE=88096591; PubMed=3697097;
MEDLINE=88096591; Maunders M., Grierson D., Schuch W.;
"Sequence of proffs, a ripening related cDNA from tomato.";
Nucleic Acids Res. 15:10587-10587(1987).
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Marmande;
MEDLINE=94071905; PubMed=8250898;
                                    01-AUG-1988 (Rel. 08, Created)
01-OCT-1994 (Rel. 30, Last seq
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M84744, AAA34153.1, -.
EMBL, YOO521, CAA68575.1, -.
EMBL, XG0441, CAA42969.1, -.
EMBL, A21360, CAA01548.1, -.
  STANDARD;
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PSY1_LYCES
P08196;
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65 TRQAYAGSQMHEPAFAARQEVA-MAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLRYCY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                  242 YVAGTVGLMSVPIMGIAPESKATTESVYNAALALGIANQLTNILRDVGEDARRGRVYLPQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 SWIEEEGLIKANYAAPENRQALSRIAGRIVREAEPYYVSSMAGLAQLPIRSAWAIATAKQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                     STRAIN=74-OR33-1A, / FGSC 987;
MEDLINE=94216317; PubMed=8163509;
Schmidhauser T.J., Lauter F.-R., Schumacher M., Zhou W., Russo V.E.A.,
                                                                                                                                                                                                                                                                                                    5 SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPBQRLQQLEMK
                                                                                                                                                                                                                                                                                                                                                                                                                    124 HVAGVVGLAMAQIMGV--RDNATLD----RACDLGLAFQLTNIARDIVDDAQVGRCYLPE
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of al-2, the phytoene synthase gene of Neurospora crassa. Cloning, sequence analysis, and photoregulation.";
J. Biol. Chem. 269:12060-12066(1994).
I. PUNCTION: Catalyses the reaction from prephytoene diphosphate to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phytoene.
--- CATRIVICA ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate +
prephytoene diphosphate.
---- CATRIVITY: Prephytoene diphosphate = diphosphate +
                                                                                                                                                                                                                                           19.6%; Score 300.5; DB 1; Length 412; 29.0%; Pred. No. 2.4e-19; tive 51; Mismatches 135; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 VYRKIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 LYRKILDEIEANDYNNFTKRAYVSKSKKLIALPIAYAKSLVPPTKT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phytoene.
-!- PATHWAY: Carotenoid biosynthesis.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phycome synthase (EC 2.5.1.-) (Albino-2 protein)
PIR; A42102; A42102.
PIR; S2241; S2241; S2241; DINCEPRO; IRROUSG60; Squ/phyt synthse.
InterPro; IPR008949; Terpenoid_synth.
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                                                                                                                                                                                                                                                         Local Similarity 29.0
nes 83; Conservative
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P37295;
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CRTY SPIPL
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Matches
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                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL cutstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and prosper institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 SOFTFHOISDSTDLOYPIADDXDLENYAIYVAĞTVGELCIALİIYHCLPDMSDTOKRELE 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 -RACDLGLAFQLTNIARDIVDDAQVGRCYLPESWLEEEGELT-KANYAAPENRQALSRIAG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 SRSFYLANSLFSGRLRIDLILLYSFCRLADDLVDDAKSRREVLSWTAKLMHFLDLHYKDA 354
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Cucumis melo (Muskmelon).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Spermatophyta; Magnoliophyta; cuticotyledons; core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002060; Squ/phyt synthse.

InterPro; IPR002060; Squ/phyt synthse.

Ream; PP00494; SQS 58Y; 1.

REAM; PR00494; SQS 58Y; 1.

REAMSWEM 5 SQUALEN PHYTOEN SYN 1; 1.

RULtifunctional enzyme; Carotenoid biosynthesis; Transmembrane; Southier Southiers Proprent 6 26 POTENTIAL.

I TRANSWEM 76 96 POTENTIAL.

I TRANSWEM 118 138 POTENTIAL.

I TRANSWEM 168 188 POTENTIAL.
   SIMILARITY: Belongs to the phytoene/squalene synthetase family.
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene synthase, chloroplast precursor (BC 2.5.1.-) (XEL5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.3%; Score 297; DB 1; Length 602; 28.6%; Pred. No. 7.9e-19; Live 57; Mismatches 105; Indels
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146
168
230
602 AA;
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28-FEB-2003 (
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P49293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 TERYCYHVAGVVGLMMAQIMGV-----RDNATLDRACDLGLAFQL-TWIARDIVDDAQV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 GRCYLPESWLEBEGLIKANYAAPENRQALSRIAGRLVREAEPYYVSSWAGLAQLPLRSAW 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 LYLYCYYVAGTVGLMSVPVWGIAPESQASTESVYNAALALGIANQAPPNILRDVGEDARR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 GRIYLPODELAQAGLSDEDIRAGRVTDKWRNFWKNQIKRARMFFDEAEKGVLELNKASRW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELEULAR LOCATION: Chloroplast.
-!- SIMILARITY: Belongs to the phytoene/squalene synthetase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfan; PP00494; SQS PSY; 1.
PROSITE; PS01044; SQUALEN PHYTOEN SYN_1; 1.
PROSITE; PS01045; SQUALEN PHYTOEN SYN_2; 1.
Multifunctional enzyme; Carotenoid biosynthesis;
Isoprene biosynthesis; Transferase; Chloroplast; Transit peptide.
TRANSIT (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                                        prephytoene diphosphate.
-!- CATALYTIC ACTIVITY: Prephytoene diphosphate = diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 AIATAKOVYRKIGVKVEQAGKQAMDHRQSTSTAEKLTLLLTASGQAV 277
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STRAIN-CY Cantaloup Charentais; TISSUE-Pericarp;
MEDLINE-95284364; PubMed=7766896;
Karvouni Z., John I., Taylor J.E., Matson C.F., Turner A.J.,
Grierson D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125; Indels
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                                                                                                                                                                                                   Plant Mol. Biol. 27:1153-1162(1995).
-!- FUNCTION: Catalyzes the reaction from prephytoene
                                                                                                                                    "Isolation and characterisation of a melon cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.6%; Score 286; DB 1; 26.5%; Pred. No. 4.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHYTOENE SYNTHASE
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene synthase (EC 2.5.1.-).
CRTB OR PYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro, IPR002060; Squ/phyt synthse.
InterPro; IPR008949; Terpenoid_synth.
                                                                                                                                                                                                                                                                                                                                                                                                              phytoene.
PATHWAY: Carotenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 AA; 47392 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z37543; CAA85775.1; ..
                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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nes 76; Conserv
                                                                                                                                                                           phytoene synthase.
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Spirulina platensis. Bacteria; Cyanobacteria; Oscillatoriales; Spirulina. NCBI_TaxID=1156;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 YHVAGVVCIAMMAQIMGV-----RDNATL---DRACDIGLAFQLTNIARDIVDDAQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 RGRIYLPLDDLALFNYTEADLLNGKVDERWRELMRFQ---IQRARKFYTLAEEGIAALHP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 VGRCYLPESWLEEEGLIKA---NYAAPENROALSRIAGRIVREAEPYYVSSMAGLAQLPL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 SKSFATASTLFDAKTRRSVIALYAMCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=IAM M-135;
Kawata Y., Yano S., Kojima H.;
Kawata Y., Yano S., Kojima H.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the reaction from prephytoene diphosphate to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                         phytoene.
-!- CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate +
                                                                                                                                                                                                                                                                             phytoene.
-!- PATHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: Belongs to the phytoene/squalene synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 RSAWALATAKQVYRKIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQA 276
                                                                                                                                                                                                                prephytoene diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | | : | : | : | : | | : | DIRMPUWTALMLYRQILDEIERNEYDVFNQRAYVPTWKKNMCLFLAQLRA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
18.2%; Score 280; DB 1; Length 309;
Best Local Similarity 29.7%; Pred. No. 1.1e-17;
Matches 86; Conservative 44; Mismatches 128; Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB001284; BAA20384.1; -.
InterPro; IPR002060; Squ/ghyt synthse.
InterPro; IPR008949; Terpenoid_synth.
Prostra; Pr0044; SquAlen PHYTORN SYN 1; 1.
PROSTE; PS01044; SQUALEN PHYTORN SYN 1; 1.
PROSTE; PS01045; SQUALEN PHYTORN SYN 2; 1.
RANGITE; PS01045; SQUALEN PHYTORN SYN 2; 1.
SEQUENCE 309 AA; 35945 MM; C42A1C6431604C75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: February 29, 2004, 14:45:14 Job time : 6.98876 secs
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GenCore version 5.1.6
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protein - protein search, using sw model

February 29, 2004, 14:34:14; Search time 8.23902 Seconds (without alignments) 3455.835 Million cell updates/sec n on:

US-09-941-947A-34 1535 1 MAVGSKSFATASTLFDAKTR......VTSRMKTYPPRPAHLWQRPI 296 tle: rfect score: quence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 oring table:

283366 tal number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

arched:

nimum DB seq length: 0 ximum DB seq length: 2000000000

st-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* tabase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARIES

	Description	pyr	crtB protein - Erw	geranylgeranyl-dip	prephytoene pyroph	phytoene synthase	geranylgeranyl-dip	phytoene synthase	phytoene synthase					phytoene synthetas		phytoene synthase	d)	phytoene synthase												phytoene synthase
SUMMARIES	ei ei	S52587	E37802	B39273	T50895	849621	S04403	T50746	D75466	854135	A49558	S68307	A42102	832170	A53583	S22474	826668	T10702	AC2035	845360	A81118	520383	H81902	T36969	T35400	T46594	B70735	H84299	F69108	E84320
	80			7																										
	Length	296	296	309	344	355	339	355	325	423	310	410	412	336	602	412	422	425	310	337	290	307	290	331	312	319	302	322	299	322
	% Query Match	89.3	89.1	67.0	25.8	25.7	25.6		23.6					19.5		18.6	18.6	18.0	17.3	17.3	17.0	ė.	ő,	16.0	4.	귝.	4	14.0	ä	
	Score	1371	1368	1028	3.95.5	394	393.5	385	362	328.5	307.5	302.5	300.5	300	297	286	286	276.5		265.5	64	258	255.5	N	228.5	24	4	214.5	О	60
	ssult No.	-	C)	ო	4	ß	9	7	80	0	10	11	12	13	14	15	16	17.	18	o o	20	21	22	23	24	25	26	27	28	53

		squalene synthase	farnesyl-diphospha	farnesyl-diphospha		squalene desaturas	farnesyl-diphospha	farnesyl-diphospha		probable phytoene	phytoene synthase	phytoene synthase	crtM protein - Sta	farnesyl-diphospha
G90469 H81074	D81868	152090	A45998	138245	T45141	C90061	S52075	A84226	A45105	T35399	G69837	T51118	A55548	B48057
01 01	N	N	~	N	N	N	N	N	7	N	~	N	0	N
277	276	417	417	417	362	287	416	390	416	303	274	299	254	460
13.1	12.6	11.2	11.2	11.2	10.7	10.7	10.7	10.6	10.4	4.6	9.2	8.8	8.7	9.6
	īυ	1.5	1.5	1.5	165	54.5	53.5	163	59.5	14.5	10.5	135	134	32.5
201.5	193	17	17	17		Ä	Ä		Н	Ä	H			Н

# ALIGNMENTS

RESULT 1

S25587 Crypteric Crypteric Crypteric Crypteric Crypteric Crypteric Crypteric Crypteric Crypteric Article Article Article Article Article Article Article Article Article Article Article Crossid Article Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Crossid Cross	prephytoene pyrophosphate synthase - Erwinia herbicola CiSpecies: Erwinia herbicola CiSpecies: Erwinia herbicola CiSpecies: Erwinia herbicola CiSpecies: Erwinia herbicola CiSpecies: Erwinia herbicola CiSpecies: Erwinia herbicola CiSpecies: Erwinia herbicola CiSpecies: Erwinia herbicola CiSpecies: Erwinia Requence revision 01-Sep-1995 #text_change 02-Mar-2001 CiScession: S52887 Molifia, T.P., Lai, E.M., To, K.Y.; Chang, Y.S.; Liu, S.T. Molifia. Transcriptional activation of flanking sequences by Th1000 insertion. A; Reference number: S52883; MuID:95107237; PMID:7808390 A; Reference number: S52883; MuID:95107237; PMID:7808390 A; Reference number: S52883 A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule sequence was submitted to the EMBL Data Library, April 1992 C; Superfamily: Mycobacterium marinum phytoene synthase Cuery Match Best Local Similarity 88.5%; Pred. No. 78-116; Best Local Similarity 88.5%; Pred. No. 78-116; Matches 262: Conservative 12; Mismarches 22; Indels 0; Gaps 0;
A, Statu	ston: 35259; s. preliminary; nucleic acid sequence not shown; translation not shown
Best	), Gaps
March	DOVIDDOTLGFHADQPSSQMPEQRLQQ 60
<del>Q</del>	1 MAVGSKSFATASKLFDAKTRRSVLMLYSWCRHCDDV1DDQTG6FQTDQF6AG1FBGRADT 00
Š	61 LEMKTROAYAGSOMHEPAPAAROEVAMAHDIAPAYAPDHLEGFAMDVRETRYLTLDDTLR 120

0	0	0.0	20	20	80	80	240	240		
Best Local Simitatity 86.33; Fred. NO. /e.13; Matches 262; Conservative 12; Mismatches 22; Indels 0; Gaps	1 MANGSKSFATASTLFDAKTRRSVIMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ 60	MAVGSKSFATASKLFDAKTRRSVLMLYSWCRHCDDVIDDQTLGFQTDQPSLQTPEQRLMQ	61 LEMKTRQAYAGSQMHEDAPAARQEVAMAHDIAPAYAFDHLEGFAMDVRSTRYLTLDDTLR 120	61 LEMKTRQAYAGSQMHEPAPAPAPQEVAMAHDIAPAYAFDHLEGFAMDVREAEYIQLDDTER	121 YCYHVAGVVGLMMAQLMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPBSWL 180		181 EEEGITKANYAAPENRQALSRIAGRIVREAEPYYVSSMAGLAQLPLRSAMAIATAKQVYR 240		241 KIGVKVEQAGKQAWDHRQSTSTAEKLTLLIJASGQAVTSRMKTYPPRPAHLMQRPI 296	41 KIGVKVEQAGTEAWDHRQSTTTPEKLSLLLMASGQAITSRMRPHPPRFAHLWQRPI 296
E P Ca					H	⊣	H	н	Ò	73
Matches	Š	qq	è	qq	ò	q	λ	qq	Š	q

RESULT 2

E37802 crtB protein - Erwinia uredovora C;Space: Erwinia uredovora C;Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 02-Mar-2001 C;Accession: E37802 R;Misawa, N.; Nakagawa, M.; Kobayashi, K.; Yamano, S.; Izawa, Y.; Nakamura, K.; Harashim, J.; Bacteriol. 172, 6704-6712, 1990 A;Title: Elucidation of the Erwinia uredovora carotemoid biosynthetic pathway by functio

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241 KIGVKVEQAGKQAMDHROSTSTAEKLTLLETASGQAVTSRMKTYPPRPAHLWQRPI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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2, Species: Erwinia herbicola
2, Species: Erwinia herbicola
2, Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 02-Mar-2001
2, Accession: B39273; B33120
3, Accession: B39273; Alberti, M.; Hearst, J.E.
RyAmstrong, G.A.; Alberti, M.; Hearst, J.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 9975-9979, 1990
A; Title: Conserved enzymes mediate the early reactions of carotenoid biosynthesis in non A; Reference number: A39273; MUID:91088634; PMID:2263648
                                                                      .;Wolecule type: DNA .
.Residues: 1-296 «MI» .
.Cross-references: GB:D90087; NID:g216681; PIDN:BAA14128.1; PID:d1014831; PID:g216686 ;Superfamily: Mycobacterium marinum phytoene synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geranylgeranyl-diphosphate geranylgeranyltransferase (BC 2.5.1.32) - Erwinia herbicola
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YCYHVAGVVGLAMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAHAGRCYLPASWL 180
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                                                                                                                                                                                                                                                                                                                                                                                                     61 LEWKTRQAYAGSQMHEPAFPAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YCYHVAGVVGLAMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 LRTLTLAAFEGAEMODPAFAAFQEVALTHGITPRMALDHLDGFAMDVAQTRYVTFEDTLR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YCYHVAGVVGIAMAQIMGVRDNATLDRACDIGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BEEGLIKANYAAPENRQALSRIAGRIVREAEPYYVSSMAGLAQUPLRSAWAIATAKQVYR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                    1 MAVGSKSFATASKLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFQARQPBQRPBQRLMQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPBQRLQQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 MANGSKSFATAAKLFDPATRRSVLMLYTWCRHCDDVIDDQTHGFASBAAABEEATQRLAR 73
                                                                                                                                                                                                                                                                                                 1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 XIGVKVEQAGQQAWDQRQSTTTPEKLTLILAASGQALTSRMRAHPPRPAHLWQRP1 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 KIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPPRPAHLWQRPI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                 89.1%; Score 1368; DB 2; Length 296; 88.9%; Pred. No. 1.3e-115; tive 11; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.0%; Score 1028; DB 2; Length 309;
64.9%; Pred. No. 6.2e-85;
tive 36; Mismatches 68; Indels
Reference number: A37802; MUID:91072214; PMID:2254247; Accession: B37802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CrtB
C;Superfamily: Mycobacterium marinum phytoene synthase
C;Keywords: transferase.
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Best Local Similarity 64.9%
Matches 192; Conservative
                                                                                                                                                                                                 Query Match
Best Local Similarity 88.9%
Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-309 <ARM>
                                                   Status: preliminary
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R.Jeng, H.B.; Cogdell, R.J.; Takaichi, S.; Hunter, C.N. submitted to the EMBL Data Library, November 1994
A.Desoription: The complete DNA sequence, specific TNS insertion map and gene assignment A.Reference number: 849619
A.Reference number: 849619
A.Reference number: 849619
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-355 cLANA
A.Residues: 1-355 cLANA
A.Cross-references: EMBL:X82458; NID:g575405; PID:g575408
                                                                                                                                                                                                                                                                                                                                       C, Accession: T50895
R; Magashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.
Submitted to the EMBL Data Library, November 1999
A; Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynth A; Reference number: Z25270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 YGARVAGTVGAAMALIMGVRSPQALARACELGVAMQFTNIARDVGEDARNGRLYLPREML 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDFTLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 IRTRIDAVYAGTPAPIAADRALASTVHRYGVPRVILIDALIEGFILWDADGRRYDTIADVEA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 EEEGL-TKANYAAPENRQALSRIAGRLVREABPYYVSSMAGLAQLPLRSAWAIATAKQVY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 VEAGLDVDAWLONPVHCPEVAQTVRKLLRAADELYERSEHGIAALPROCRPAIRAARLVY 246
                                                                                                                                                                                                                       prephytoene pyrophosphate synthase [imported] - Rubrivivax gelatinosus
C;Species: Rubrivivax gelatinosus
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phytoene synthase - Rhodobacter sphaeroides
C.Species: Rhodobacter sphaeroides
C.Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDGTLGFHADQPSSQMPBORLQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.8%; Score 395.5; DB 2; Length 344; 36.2%; Pred. No. 7.3e-28; tive 32; Mismatches 140; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.7%; Score 394; DB 2; Length 355; Best Local Similarity 36.6%; Pred. No. 1e-27; Matches 105; Conservative 32; Mismatches 128; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Superfamily: Mycobacterium marinum phytoene synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DMA
A, Residues: 1.-14 CMA
A, Cross-references: EMBL: ABO34704; PIDN: BAA94048.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Experimental source: strain IL144
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J.D.; Dodson, R.J.; T.; Zalewski, C.; Ma
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A.Experimental source: strain R1
Nucleic Acids Res. 28, 862-867, 2000
A,Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides:
A,Reference number: 225222; MUID:20115911; PMID:10648776
A,Accession: T50746
A,Accession: T50746
A,Besidues: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-355 < CHO>
A,Residues: 1-355 < CHO>
A,Residues: 1-355 < CHO>
A,Residues: 1-355 choses: EMBL:AF195122; PIDN:AAF24290.1
A,Residues: 1-365 chores: EMBL:AF195122; PIDN:AAF24290.1
A,Gross-references: EMBL:AF195122; PIDN:AAF24290.1
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Cispecies: Delinococcus radiodurans (Structus All)
Cipate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Mar-2001
Cipate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Mar-2001
Cipacession: D75466
Symble, 0.; Siben, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.C.; Fraser, C.M.
Soince 286, 1571-1577, 1999
A; Saith, H.O.; Venter, J.C.; Fraser, C.M.
A; Science 286, 1571-1577, 1999
A; A; Saith, B; Sibenson Sequence of the radioresistant bacterium Deinococcus radiodurans in A; Reference number: A75250; MUID:20036896; PMID:10567266
A; A; Accession: D76466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 YLPRDWMBEEGLPVEBFLARPVVDDRIRAVTHRQLRAADRLYLRSBAGVCGLPLACRPGI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 KRRAVLSLRDRLDLVYGGRPRNAPADRAFAAVVEBFBMPRALPBALLBGLAWDAVGRSYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 TLDDTLRYCYHVAGVVGLAMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 GSYSFHAASRILPERVRAPSLALYAFCRVADDAVDE------AVNDGQREEDAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLPESWLEEEGLTKANY-AAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAI
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Pred. No. 7.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phytoene synthase - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                 A;Gene: crtB
C;Superfamily: Mycobacterium marinum phytoene synthase
C;Reywords: carotenoid biosynthesis; transferase
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C,Superfamily: Mycobacterium marinum phytoene synthase
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.1%; Score 385; DB 2; I Best Local Similarity 35.9%; Pred. No. 6.8e-27; Matches 103; Conservative 33; Mismatches 129;
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al Similarity 37.5%;
103; Conservative 37
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A;Molecule type: DNA
A;Residues: 1-325 <WHI>
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Alternate names: phytoene pyrophosphate synthase
Species: Rhodobacter capsulatus
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Accession: S04403
Armstrong, G.A.; Alberti, M.; Leach, F.; Hearst, J.B.
1. Gen. Genet. 216, 254-268, 1989
Title: Nucleotide sequence, organization, and nature of the protein products of the Reference number: S04401; MUID:89313663; PMID:2747617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 RYCYHVAGVVGLAMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 LEEEGL-TKANYAAPENRQALSRIAGREVREAEPYYVSSMAGLAQLPLRSAWAIATAKQV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIRQAYAGSQMHEP---AFAA-FQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLILDDTL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLEDIYAGRPRNAPSDRAFAAVVBEPEMPRELPBAL----LBGFAWDAEGRWYHTLSDVQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244
                                                                                                                                                                       114 ILDDTLRYCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRC 173
                                                                                                                                                                                                                                                                            126 SFSGVLDYSARVAAAVGAMMCVLMRVRDPDVLARACDLGLAMQLTNIARDVGTDARSGRI 185
                                                                                                                                                                                                                                                                                                                                                          174 YLPESWIEBEGLTKANY-AAPENROALSRIAGRIVREAEPYYVSSMAGIAQLPIRSAWAI 232
                                                                                                                                                                                                                                                                                                                                                                                                                245
                                                                                                                                   64 KTRQ------AYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                     4 GSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDGTLGFHADQPSSQMPEQRLQQLEM 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hytoene synthase (BC 2.5.1.-) [imported] - Rhodobacter sphaeroides Species: Rhodobacter sphaeroides | Species: Rhodobacter sphaeroides | Species: L-Unl-2000 #seguence_revision 21-Jul-2000 #text_change 02-Mar-2001 | Accession: T50746 | Schoudhary, M.; Kaplan, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GSXSFATASTLPDAXTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEM
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: EMBL:X52291; NID:g45996; PIDN:CAA36534.1; PID:g45999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 25.6%; Score 393.5; DB 2; Length 339; Best Local Similarity 35.6%; Pred. No. 1.1e-27; Matches 103; Conservative 44; Mismatches 125; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 YRKIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRWKTYPPR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 ATAKOVYRKIGVKVEQAGKQAWDHROSTSTAEKLTLLLTASGQAVTS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene: crtB
Superfamily: Mycobacterium marinum phytoene synthase
Keywords: carotenoid biosynthesis; transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-339 <ARM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: DNA
Residues: 1-339 <A
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130 AKTFYLGTMLMTBERRRAIWALYVWCRRTDBLVDGPNANY-----ITPTALDRWBKR 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 ESWLEBEGLIKANYAAPENROALSRIAGRLVREAEPYYVSSWAGLAQLPLRSAWALATAK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U32636; NID:g1098664; PIDN:AAB60314.1; PID:g1098665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phytoene synthase - maize
C;Species: Zea mays (maize)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 QDELAQAĞLSDEDIFAĞKVTDKWRIFWKKQIQRARKFFDEABKĞVTELSSASRWPVLASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDGTLGFHADQPSSQMPEQRLQQLEMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRQAYAGSQMHBPAFAAFQEVAMAH - DIAPAYAFDHLEGFAMDVRETRYLTLDDTLRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYVAGTVGLMSVPVMGIATESKATTESVYSAALALGIANQLTNILRDVGEDARRGRIYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSWLEEEGLIKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAK
                                                                                                                                                                                                                                                                                                                                28 AKTFYLGTMIMTPDRRRAIWAIYVWCRRTDELVDGPN-----ASHITPQALDRWEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YHVAGVVGLMMAQIMGV--RDNATLD----RACDLGLAFQLTNIARDIVDDAQVGRCYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YHVAGVVGLMMAQIMGV--RDNATLD----RACDLGLAFQLTNIARDIVDDAQVGRCYLP
                                                                                                                                                                                                                                                                       5 SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK
                                                                                                                                                                                                                                                                                                                                                                                                                65 TRQAYAGSQMHEPAFAAFQEVAMAH--DIAPAYAFDHI.BGFAMDVRETRYI.TLDDTLRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 QVYRKIGVKVEQAGKQAWDHRQSTSTABKLTLLLTASGQAVTSRMKTYPPR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S68307
R;Buckner, B.; San Miguel, P.; Janick-Buckner, D.; Bennetzen, J.L.
R;Buckner, B.; 479-488, 1996
A;Title: The yl gene of maize codes for phytoene synthase.
A;Reference number: S68307; MUID:96304610; PMID:8722797
A;Accession: S68307
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                                                                                                                          Length 310;
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                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 136/1; 153/1; 210/3; 289/2; 353/3
C;Superfamily: Mycobacterium marinum phytoene synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.7%; Score 302.5; DB 2; larity 28.1%; Pred. No. 2.2e-19; Conservative 53; Mismatches 130;
           C;Superfamily: Mycobacterium marinum phytoene synthase
C;Keywords: plastid
                                                                                                                             20.0%; Score 307.5; DB 2; 28.9%; Pred. No. 5.5e-20; iive 53; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: mRNA was also sequenced
                                                                                                                                                                                                      84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Status: preliminary
A Molecule type: DNA
A;Residues: 1-410 <BUC>
                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
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                                                                                                                                     Query Match
Best Local
A; Gene: PSY2
                                                                                                                                                                           Best Loc
Matches
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Matches
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C.Species: Lycoperai.con esculentum (tomato)
C.Species: Lycoperai.con esculentum (tomato)
C.Accession: A49559
R.Bartley, G.E.; Scolnik, P.A.
T. Biol. Chen. 268, 25718-25721, 1993
A.Title: CDNA cloning, expression during development, and genome mapping of PSY2, A;Reference number: A49558; MUID:94064645; PMID:8245008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ņ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YHVAGVVQLMMAQIMGV-----RDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESWLEEEGLTKANYAAPENROALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDBLAEAGLSDEDVFTGKVTDKWRSPMKRQIKRARTFFEQAEKGVTELSQASRWPVWASL 368
                                                                                                                                                                                                                             220 YGLSRAALERWGQGEPLSPAYRALMTHIGG-IARE---WYAAGRAGIPQLDGRGPLAVIT 275
                                      124 HVAGVVGLMMAQIMGVRDN-ATLDRACDIGLAFQLTNIARDIVDDAQVGRCYLPESWLBE 182
                                                                            160 RVAGVVGFRVAPISGYRGGAATLNDALQLGQAMQLTNILRDVGEDLFRGRVYLPQSLLDE 219
                                                                                                                                                                               ----NYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIAŢ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ohytoene synthase (EC 2.5.1.-) - Narcissus pseudonarcissus
?;Species: Narcissus pseudonarcissus
?;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \(\frac{1}{2}\)Accession: S54135
\(\frac{1}{2}\)Affinologile type: \(\triangle \triangle                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4, Residues: 1-310 < BAR>
4, Cross.references: GB:L23424; NID:g437019; PIDN:AAA34187.1; PID:g437020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyschedr, M.; Lintig, J.; Albabili, S.; Kleinig, H.; Beyer, submitted to the EMBL Data Library, April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.4%; Score 328.5; DB 2; Best Local Similarity 27.9%; Pred. No. 1.1e-21; Matches 81; Conservative 58; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    v;Gene: PSY
?;Superfamily: Mycobacterium marinum phytoene synthase
                                                                                                                                                                                                                                                                                                                                                                                         276 AARAYEGILDDLERAGYDNFGRRAYVSGRRKLLML 310
                                                                                                                                                                                                                                                                                                                        235 AKQVYRKIGVKVEQAGKQAWDHRQSTSTAEKLFLL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Keywords: transferase
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C;Accession: A53583
R;Schmidhauser, T.J.; Lauter, F.R.; Schumacher, M.; Zhou, W.; Russo, V.E.A.; Yanofsky, C
Biol. Chem. 269, 12060-12066, 1994
A;Title: Characterization of al-2, the phytoene synthase gene of Neurospora crassa. Clon
A;Reference number: A53583; MUID:94216317; PMID:8163509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 geranylgeranyl-diphosphate geranylgeranyltransferase (BC 2.5.1.32) - Neurospora crassa
C,Species: Neurospora crassa
C,Date: 07-0ct-1994 #sequence_revision 07-0ct-1994 #text_change 17-Mar-1999
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                                                                                                                                                                                                                                                                                 204 DLERGRYYLPAEKLAAFGLS------EDDLRRGQVGARWRSFWRFQVERSRAYARAAA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLAQLP-LRSAWAIATAKQVYRKIGVKVEQAGKQAWDHROSTSTAEKLTLLLTASGQAVT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 GVRYLTGFGSORMVRLMGAIÝADILRDIRARDYDVFSARAHVTTRRKLAL---ASAAMV- 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 SRSFYLANSLFSGRERIDLILLYSFCRLADDLVDDAKSRREVLSWTAKLNHFLDLHYKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 PSSQMPEQRLQQLEMKTRQAYAGSQMHEPAFAAFQEVAM--AHDIAPAYAFDHLEGFAMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 -RACDIGLAFQITNIARDIVDDAQVGRCYLPESWLEEEGLT-KANYAAPENRQALSRIAG
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                                                                                                25 AKSFFFASYLLFGLRRRAAFALYAFCRRLDDWVDGDDAASAADALPVRLARRARQRVAELY
                                                                                                                                                   LOOLEMKTRO-----AYAGSOMHEP----AFAAFOEVAMAHDIAPAYAF-DHLEGFAMD
                                                                                                                                                                                                      85 LEMPELASRELGPPADRVKGSBAATPWDARBFAAL-EHTVRHFRIFEQPFQDLISGMEMD
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                                                  SKSPATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHAD------OPSSQMPEQR
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  46; Gaps
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Mismatches 134; Indels
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C;Genetics:
A:Introns: 7/2; 316/2
C;Keywords: transferase; transmembrane protein
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28.6%; Pred
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Best Local Similarity 28.6
Matches 88; Conservative
     Conservative
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A; Residues: 1-602 <SCH>
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     98;
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     Matches
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Species: Myxococcus xanthus
Species: Myxococcus xanthus
Accession: 6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 02-Mar-2001
Accession: S31170; S67951
Botella, J.; Murillo, F.; Ruiz-vazquez, R.
Dmitted to the EMBL Data Library, March 1993
Dmitted to the EMBL Data Library, March 1993
Reference number: S32168
Accession: S32170
                                                                                                                                                   Accession: A42102
Bartley, G.E.; Vlitanen, P.V.; Bacot, K.O.; Scolnik, P.A.
Biol. Chem. 267, 5036-5039, 1992
Iitle: A Lomato gene expressed during fruit ripening encodes an enzyme of the Reference number: A42102; MUID:92184738; PMID:1544888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 HVAGVVGLMMAQIMGV--RDNATLD----RACDLGLAPQLTNIARDIVDDAQVGRCYLPE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 LEDVENGRPFOMLDGALSDTVSNFPVDIQPPR--OMIEGARMDLRKSRYKNFDELYLYCY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 YVAGTVGLMSVPIMGIAPESKATTESVYNAALAIGIANQITNIIRDVGEDÄRRGRVYLPQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 SWLEEEGLTKANYAAPENROALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                             ytoene synthase (EC 2.5.1.-) peripheral plastid membrane - tomato
Species: Lycopersicon esculentum (tomato)
Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA Residues: 1-336 <BOT>
Residues: 1-336 <BOT>
Cross_references EMBL:Z21955, NID:g577589; PIDN:CAA79957.1; PID:g288222
Experimental source: scrain DX1050
Botella, J.A.: Murillo, F.J.; Ruiz-Vazquez, R.
T. J. Biochem. 233, 2334-248, 1995
Title: A cluster of structural and regulatory genes for light-induced can Reference number: 567950; MUID:96061955; PMID:7588751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQFLGFHADQPSSQMPEQRLQQLEMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 TRCAYAGSQMHEPAFAAFQEVA-MAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLRYCY
                                                                                                                                                                                                                                                                                                                                 Molecule type: mRNA
Residues: 1-412 <BAR>
Cross-references: GB:M84744; NID:g170415; PIDN:AAA34153.1; PID:g170416
Mote: sequence extracted from NCBI backbone (NCBIN:87066, NCBIP:87067)
Superfamily: Mycobacterium marinum phytoene synthase
Keywords: chloroplast; transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.6%; Score 300.5; DB 2; Length 412; 29.0%; Pred. No. 3.4e-19; ive 51; Mismatches 135; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 VYRKIGVKVEQAGKQAWDHRQSTSTAEKLILLLTASGQAVTSRMKT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 LYRKILDEIEANDYNNFTKRAYVSKSKKLIALPIAYAKSLVPPTKT 407
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Pred. No. 2.9e-19;
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Residues: 151-175;185-213 <BOW>
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Matches 83; Conserv
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                                                                                                                                                                                                                                                                                      Accession: A42102
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106 406 146 466 204 254

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Scatus: not compared with conceptual translation
| Molecule type: mRNA |
| Molecule type: mRNA |
| Molecule type: mRNA |
| Cross-references: GB: Y00521; NID: g19340; PIDN: CAA68575.1; PID: g19341 |
| Fray, R.G.; Grierson, D |
| Int. Mol. Biol. 22, 899-602, 1993 |
| Title: Identification and genetic analysis of normal and mutant phytoene synthase gene |
| Reference number: S35154; MUID: 93344508; FMID: 8343597 |
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hytoene synthase (EC 2.5.1.-) - tomato
;Alternate names: ripening protein 5
;Species: Lycopersicon esculentum (tomato)
;Species: Lycopersicon esculentum (tomato)
;Date: 19-Mar-1997 #sequence revision 18-Jul-1997 #text change 02-Mar-2001
;Accession: 522474; S06221; S35155; S35154; S21981; S24367; S24968
;Ray, J.; Moureau, P.; Bird, C.; Bird, A.; Grierson, D.; Maunders, M.; Truesdale, M.; Flant Mol. Biol. 19, 401-404, 1992
lant Mol. Biol. 19, 401-404, 1992
;Ritle: Cloning and characterization of a gene involved in phytoene synthesis from toma ;Reference number: S22474; MuID:92322971; PMID:1623189
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Residues: 1-107, 'VECLESDPLQTERTGVSLPGQRVGGSRGAT','RWPGGPGGRRRGADGIQCCCIGPLIFC' <FRA2>
Cross-references: EMBL:X67143; NID:g19398; PIDN:CAA47624.1; PID:g19399
Experimental source: mutant r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: DNA
Residues: 1-412 <RAY>
(Cross-references: RMBL:X60441; GB:S39572; NID:g19248; FIDN:CRA42969.1; PID:g19249;
(Cross-references: RMBL:X60441; GB:S39572; NID:g19248; FIDN:CRA42969.1; PID:g19249;
Note: the authors did not translate the codon for residue 155
Ray, J.; Bird, C.; Maunders, M.; Grierson, D.; Schuch, W.
oleic, Acids Res. 15, 10587, 1987
(Fille: Sequence of pTOMS, a ripening related cDNA from tomato.
Reference number: S06321; MuID:88096591; PMID:3697097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 SWLEEEGLIKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | | : : | | : : : | 302 DELAÇAGLSDEDIFAGRYTDKWRIFWKKQIHRARKFFDEAEKGVTELSSASRFFWWASLV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 AKTFNLGTMLMTPERRRAIWAIYVWCRRTDELVDGPN------ASYITPAALDRWENR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEWK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
Residues: 1-387,'NMLKDFFSNFKGSKRGSNATTILVGLAPCE','TYIAIDDRGFIGITF' <FRA1>
Cross-references: BMED:X67144; NID:g19346; PIDN:CAA47625.1; PID:g19347
Experimental source: mutant rY
Accession: S35154
Status: translation not shown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.6%; Score 286; DB 2; Length 412
29.7%; Pred. No. 6.9e-18;
tive 46; Mismatches 119; Indels
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Superfamily: Mycobacterium marinum phytoene synthase
Keywords: chloroplast; transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 LYRKILDEIE----ANDYNNFTKRA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 VYRKIGVKVEQAGKQAWDHRQSTSTA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: translation not shown
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Best Local Similarity 29.7%
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: Psyl
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Search completed: February 29, 2004, 14:52:54 Job time : 10.239 secs

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Sequence 34, Appl
Sequence 10, Appl
Sequence 3, Appli
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Sequence 133, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 130, Appli
Sequence 131, Appli
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                                                                                                         February 29, 2004, 14:51:24; Search time 19.6527 Seconds (without alignments) 3180.293 Million cell updates/sec
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1 MAVGSKSFATASTLFDAKTR......VTSRMKTYPPRPAHLWQRPI 296
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1: \cgn2_6/ptodata/2/pubpaa/PCT_PUBCOMB.pep:*

2: \cgn2_6/ptodata/2/pubpaa/PCT_PMF PUB.pep:*

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11: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

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(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                    - protein search, using sw model
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US-10-438- US-10-438- US-09-220- US-09-220- US-09-220- US-09-220- US-09-220- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-358- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338- US-10-338-	US-10-429-949- US-10-369-493- US-10-369-493- US-10-028-854- US-10-024-130A US-10-038-854- US-10-156-761- US-10-149-759-
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0 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	W W W 4 4 4 4 4 C 8 9 0 1 1 1 1 1 1 2 1 2 1

# ALIGNMENTS

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APPLICANT: Erzostowicz, Patricia C.
APPLICANT: Cheng, Qiong
APPLICANT: Cheng, Qiong
APPLICANT: Dicosimo, Denna J.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Picateggio, Steve
APPLICANT: Picateggio, Steve
APPLICANT: Pouviere, Pierre E.
TITLE OF INVENTION: CAROTRENCID PRODUCTION FROM A SINGLE CARBON SOURCE
FILE REFERENCE: CL1903 US NA
CURRENT APPLICATION NUMBER: US/09/941,947A
CURRENT FILING DATE: 2000-09-01
PRIOR PLING DATE: 2000-09-01
PRIOR PLING DATE: 2000-09-01
PRIOR PLING DATE: 2000-09-01
NUMBER OF SRQ ID NOS: 60
SOFTWARE: MICLOSOFT OFFICE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAVGSKSPATASTLPDAKTRRSVIALYAWCRHCDDVIDDQTLGFHADQPSSCMPEQRLCQ
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                           , Sequence 34, Application US/09941947A; Publication No. US20030003528A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Pantoea stewartii
US-09-941-947A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 296; Conservative
US-09-941-947A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 34
LENGIH: 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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9 9 61 LEMKTRQAYAGSQMHEPAFAAFQBVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR 120

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FERMENTATIVE CAROTENOID PRODUCTION
TITLE OF INVENTION: FERMENTATIVE CANDERS OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-547-267-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                               USA
                                                                                                                                                                                   07110
                                                                                                                 CITY: Nut
STATE: N.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-920-923-3
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                                                                                                121 YCYHVAGVVGLMAAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
                                                                                                                                                                                          181 EEEGLIKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQVYR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAXDVRETRYLTLDDTLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEEGLIKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQVYR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 EEEGLIKANYAAPENRQALSRIAGRIVREAEPYYVSSMAGLAQLPIRSAWALATAKQVYR 240
  YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPBSWL 180
                                                                                                                                                               EEEGLIKANYAAPENROALSRIAGRIVREAEPYYVSSMAGLAQLPLRSAWAIATAKQVYR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLARQLTNIARDIVDDAQVGRCYLPBSNL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEMKTROAYAGSOMHEPAFAAFOEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ
                                                                                                                                                                                                                                                         241 KIGVKVEQAGKQAMDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPPRPAHLWQRPI 296
                                                                                                                                                                                                                                                                                    KIGVKVEQAGKQAMDHROSTSTAEKLTLLLTASGQAVTSRMKTYPPRPAHLWQRPI 296
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/10218118
Publication No. US20030148319A1
GENERAL INFORMATION:
APPLICANT: Brostowicz, Patricia
APPLICANT: Brostowicz, Patricia
APPLICANT: Picataggio, Stephen
APPLICANT: Cheng, Qiong
TITLE OF INVENTYON: Genes Encoding Carotenoid Compounds
FILE REPERENCE: CL1876 US NA
CURRENT PILING DATE: 1020-08-13
PRIOR APPLICATION NUMBER: 60/312,646
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 14
SOPTWARE: Microsoft Office 97
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Pantoea stewartii
S-10-218-118-10
                                                                                                                                                                                                                                                                                                                                                                                            5-10-218-118-10
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S-09-547-267-3
Sequence 3, Application US/09547267
Partent No. US20020147371A1
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter

Tessier, Michel van Loon, Adolphus

APPLICANT: Pasamontes, Luis APPLICANT: Tessier, Michel

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70 LRADTLAA----LHEDGPMSPPFAALRQVARRHDPPDLWPMDLIBGFAMDVADRBYRSL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 PESWLEBEGLIKANYAAPENRQALSRIAGRLVREAEPYYVSSWAGLAQLPLRSAWAIATA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 KQVYRKIGVKVEQAGKQAWDHRQSTSTAEKCILLITASGQAVTSRMKTYPPRPAHLMQRP 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LEMKTROAYAGSOMHE-----PAFAAFOEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTL
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Publication No. US20030022273A1
GENERAL INFORMATION:
APPLICANT: Pagantee, Luis
APPLICANT: Pagantev, Yuri
ITIE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFRENCE: Improved Fermentive Carotenoid
CURRENT APPLICATION NUMBER: US/09/920,923
CURRENT FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

44.7%; Score 686.5; DB 9; Length 3
Best Local Similarity 48.7%; Pred. No. 7.8e-67;
Matches 146; Conservative 35; Mismatches 104; Indels
                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/547,267 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: POKras, Bruce A.
REGISTRATION NUMBER: 32,748
REPRERCY/POCKET NUMBER: RAN 6002/170
TELECOMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
                                                                                                                               COMPUTER READABLE FORM ABDION TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
: 340 Kingsland Street
Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 DDVLEYSYHVAGVVGVMMARVMGVQDDAVLDRACDLGLGREFQLTNIARDVIDDAAIGRCYL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 PESWLEEEGLIKANYAAPENRQALSRIAGRLVREABPYYVSSMAGLAQLPLRSAWAIATA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 PADMLAEAG---ATVEGPVPSDALYSVIIRILIDAAEPYYASARQGLPHLPPRCAMSIAAA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LEMKTRQAYAGSQMHE-----PAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 DDTLRYCYHVAGVVGLAMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 KQVYRKIGVKVEQAGKQAWDHRQSTSTAEKLITLLTASGQAVTSRMKTYPPRPAHL#QRP 295
                                                                                                                                                                                                                                                                                        1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ 60
                                                                                                                                                                                                                                                                                                                             12 IAQGSQSFAQAAKIMPPGIREDTVMLYAWCRHADDVIDGQVMGSAPEAGGD--PQARLGA 69
                                                                                                                                                                                                     44.7%; Score 686.5; DB 10; Length 303; 48.7%; Pred. No. 7.8e-67; tive 35; Mismatches 104; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: MacDougall, John R
TTLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/038,854
PRIOR APPLICATION DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PACENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 133, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
                                                                                                                       TYPE: PRT ORGANISM: Flavobacterium sp. R1534-09-920-923-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Casman, Stacie J
Boldog, Ferenc
Burgess, Catherine E
Edinger, Shlomit R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patturajan, Meera
Gusev, Vladimir Y
Gangolli, Bsha A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-12-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guo, Xiaojia S
Shenoy, Suresh G
Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vernet, Corine
Eisen, Andrew J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karen
                                                                                                                                                                                                                         Best Local Similarity 48,7
Matches 146, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gunther, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ellerman,
                                                                            SEQ ID NO 3
LENGTH: 303
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 AGRIVREAEPYTVSSMAGIAQIPIRSAWAIATAKQVYRKIGVKVEQAGKQAWDHRQSTST 262
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PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR PLILING DATE: 2001-01-02
PRIOR PLILING DATE: 2001-01-04
PRIOR PLILING DATE: 2001-01-02-02
PRIOR PLILING DATE: 2001-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 SKSPATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.9%; Score 336.5; DB 9; Best Local Similarity 30.3%; Pred. No. 4.7e-28; Matches 88; Conservative 52; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09847081B Patent No. US20020128464A1 GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85; Conservative
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; ORGANISM: Homo sapiens
US-10-038-854-133
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Best Local Similarity
Matches 85; Conserv
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APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 QDELAQAGLFDDDIFAGKVTDKWRSFWKKQIQRAKKFFDEAEBGVTQLSSASRWPVWASL 358
                                   : : | : | | : | | : | | : | | 327 QDELAQAGLSDED1FAGRVIDKWRNFWKKQIQRAKKFPDESEKGVIELDSASRWPVLTAL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 TRQAYAGSQMHBPAFAAFQEVAMAH--DIAPAYAFDHLEGFAMDVRETRYLTLDDTLRYC 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 YHVAGVVGLAMAQIMGVRDN-----ATLDRACDIGLAFQLTNIARDIVDDAQVGRCYLP 176
                                                                                                          123 YHVAGVVGLMMAQIMGV--RDNATLD----RACDLGLAFQLTNIAROIVDDAQVGRCYLP 176
                                                                                                                                                                                                                     177 ESWLEBEGLTKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAMAIATAK 236
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65 TRQAYAGSQMHEPAFAAFQEVAMAH--DIAPAYAFDHLEGFAMDVRETRYLTLDDTLRYC 122
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Sequence 4, Application US/09847081B
Patent No. US2020128464A1
GENERAL INFORMATION:
APPLICANT: BAYER AG
TITLE OF INVENTION: DNA encoding the tobacco phytoene synthase
FILE REFERENCE: Le A 34 34 356
FULE REFERENCE: Le A 34 34 356
FULE REFERENCE: 2001-05-02
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                                                                                      387 LYRKILDEIEANDYNNFTRRAYVSKPKTLITPIAYAKSLVPPNATSSP 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.2%; Score 310.5; DB 9; Length 410; 28.2%; Pred. No. 3.1e-25; Live 56; Mismatches 131; Indels 19;
                                                                                                                                                                                                                                                                                                                                  237 QVYRKIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPP 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: 135, 139
COTHER INFORMATION: Xaa is unknown or other
S-09-847-0818-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Nicotiana tabacum
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Matches 81, Conservative
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Sequence 130, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li,
APPLICANT: Wolenc, Adam R

S-10-038-854-130

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123 YHVAGVVGLAMAQIMGVRDN----ATLDRACDLGLAPQLTNIARDIVDDAQVGRCYLP 176
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TITLE OF INVENTIOR: Processins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Processins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Processins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: 60/259,928
PRIOR PAPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR PILING DATE: 2001-01-03
PRIOR PLING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-03
PRIOR PAPLICATION NUMBER: 60/259,814
PRIOR PILING DATE: 2001-02-03
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR PLING DATE: 2001-03-03
PRIOR PLING DATE: 2001-03-03
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PRIOR PLING DATE: 2001-04-14
PRIOR PLING DATE: 2001-04-15
PRIOR PLING DATE: 2001-04-15
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR PLING DATE: 2001-04-15
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Bisen, Addrew U
Liu, Xiaohong
Malyankar, Urial M
Shinkets, Richard A
Tcherney, Vellzar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
Petturajan, Meera
Gusev, Vladimir Y
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ORGANISM: Staphylococcus aureus
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Boldog, Ferenc
Burgess, Catherine B
Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
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Millet, Isabelle
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Gangolli, Esha A
Guo, Xiaojia S
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Rastelli, Luca
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Matches 80; Conserva
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65 TROAYAGSOMHEPAFAAFQBVAMAH--DIAPAYAFDHIEGFAMDVRETRYLTLDDTLRYC 122
                                                                                                                                                                                                                                                                           123 YHVAGVVGLAMAQIMGV--RDNATLD----RACDIGLAFQLTNIARDIVDDAQVGRCYLP 176
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                                                                                                                                                                              130 AKTFYLGTMLATBERRRAIWALYVWCRRTDELVDGPNANY-----ITPTALDRWEKR 181
                                                                                                                                                                                                                                                                                                                                                                            177 ESWLEEEGLTKANYAAPENROALSRIAGRLVREAEPYYVSSMAGIAQLPLRSAWAIATAK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 QDELAQAGLSDEDIFKGVVTNRWRNFWKRQIKRARMFFERAERGVNELSQASRWPVWASL 358
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                                                                                                                          5 SKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK 64
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US-09-371-307-76

US-09-371-307-76

Sequence 76, Application US/09371307A

Patent No. US20020053095A1

GENERAL INFORMATION:

APPLICANT: Hock, Gregory R.

APPLICANT: Filer, Kenneth J.

APPLICANT: Elich, Tedd D.

APPLICANT: Loguesch, Rugene W.

APPLICANT: Rao, Sudabathula

APPLICANT: Rao, Sudabathula

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APPLICANT: Rao, Sudabathula

APPLICANT: Rao, Sudabathula

APPLICANT: PRINTING NOBI: 10

CURRENT PILING DATE: 10

SUGAPTARE: PLENTENT PILING

SUGAPTARE: PLENTENT VET. 2.0

SUGAPTARE: PLENTENT VET. 2.0
                 19.7%; Score 302.5; DB 16; Length 410; 28.1%; Pred. No. 2.4e-24; artive 53; Mismatches 130; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
19.6%; Score 300.5; DB 9; Length 412;
Best Local Similarity 29.0%; Pred. No. 4e-24;
Matches 83; Conservative 51; Mismatches 135; Indels 17;
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Query Match
Best Local Similarity 28.2.,
19; Conservative
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RESULT 13
US-10-156-761-8563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 AKTENLGTMIMTPERRRAIWAIYVWCRRTDELVDGPN-----ASYITPAALDRWENR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 TRQAYAGSQMHEPAPRARQEVA-MAHDIAPAYAFDHLEGFRAMDVRETRYLTLDDTLRYCY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 LEDVENGREPDMLDGALSDTVSNPPVDIQPPR--DMIEGMRVDLRKSRYKORDBLYLYCY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 SWLEEBGLTKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQ 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S SKSFATASTLFDAKTRRSVLMLYAMCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK 64
                                                                                                                                                                                                                         APPLICANT: Brownillow:
APPLICANT: Brown Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Filshore, Ganesh M.
APPLICANT: Rilshore, Ganesh M.
APPLICANT: Rilshore, Ganesh M.
APPLICANT: Roguech, Eugene W.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Beginson, Scott R.
APPLICANT: Beginson, Scott R.
TITLE OF INVENTIONS: Methods for Controlling Gibberellin Levels FILE REPERENCE: 11699.0216.DVUS01 (MOBT:216--1)
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT APPLICATION NUMBER: 2003-03-27
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.2
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362 LYRKILDEIEANDYNNFTKRAYVSKSKKLIALPIAYAKSLUPPTKT 407
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Best Local Similarity 29.0%; Pred. No. 4e-24;
Matches 83; Conservative 51; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 318, Application US/10259194A Publication No. US20040010815A1 GENERAL INFORMATION:
                                                                                                                                                         Sequence 76, Application US/10401321
Publication No. US20030233679A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Lycopersicon esculentum S-10-401-321-76
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JS-10-259-194A-318
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237 LÝCYÝVÁGTVGLÁTVEVÁGTREPOSKASTESVYNAALALGIANOLTNILRDVGEERR-GRI 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 AKTFYLETQLMTPERRKAVWAIXGMDLVWCRRTDELVDGPN-----SSYITPKALDR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LEWKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAF-DHLEGFAMDVRETRYLTLDDTL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 RYCYHVAGVVGIMMAQIMGVRDN-----ATLDRACDIGLAFQLTNIARDIVDDAQVGRC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 YLPLDELAEAGLTEEDIFRGKVTDKWRKFWKGGILR-ARLFFDEAEKGVAHLDSASRWFV 354
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TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 ATAKQVYRKIGVKVEQAGKQAWDHRQSTSTABKLTLLLTASGQAVTS 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: X region
LOCATION: (58)..(58)
OTHER INPORVATION: Xaa = any naturally occuring amino acid
US-10-259-194A-318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 27.2%; Pred. No. 7.7e-21;
Matches 78; Conservative 60; Mismatches 126; Indels
                                       FILE REFERENCE: 70029-NP
CURRENT PELING NUMBER: US/10/259,194A
CURRENT FILING NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR PELICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
SPIOR FILING DATE: 2002-04-04
SPIOR FILING DATE: 2002-04-04
SPIOR PRIOR FILING DATE: 2002-04-04
SPIOR NUMBER OF SEQ ID NOS: 662
SEQ ID NO 318
LENGTH: 402
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APPLICANT: ISHIKAMA, JUN
APPLICANT: ISHIKAMA, JUN
APPLICANT: ISHIKAMA, JUN
APPLICANT: HORLKAWA, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-30
SRQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-8563
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                      61 LEMKTRQAYAGSQWHEPAFAAFQGVAMAHDIAPAYAFDHLEGFAMDVRSTRYLTLDDTLR 120
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                                                                                                                                           6 KSPATASTLFDAKTRRSVLMLYAWCRHCDDVID--DQTLGFHADQPSSQMPBQR----LQQ 60
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                                                                         90;
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15.1%; Score 232; DB 14; Length 342; 27.6%; Pred. No. 1.1e-16; tive 40; Mismatches 136; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9192, Application US/10156761
Publication No. USZ0030119018A1
Publication No. USZ0030119018A1
APPLICANT: OMURA, SATOSHI
APPLICANT: TREDA, HARUO
APPLICANT: SHIRAW, JUN
APPLICANT: HERRAW, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HARIKAWA, HIROSHI
APPLICANT: HARIKAWA, HIROSHI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2010-05-30
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TYPE: PRT
ORGANISM: Streptomyces avermitilis
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                              Local Similarity 27.6 ses 90; Conservative
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 RSAWALATAKOVYRKIGVKVEQAGKQAWDHROSTSTABKUTL----LLTASGQAVTSRMK 282
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179 WLEEEGLTKANYAAPENRQALSRIAGRL---VRBAEPYYVSSMAGIAQLPLRSAWAIATA 235
                               204 DLAKFGCS-AGFDRPIPPEG-SDFAGLVHFEVRRARALFAEGYRLLPMLDRRSGACVAAM 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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TITLE OF INVENTION: Genes Involved in Isoprenoid Compound Production
FILE REPRENCE: CL.1788
CURRENT APPLICATION US/10/128,713A
CURRENT FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 314;
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13.9%; Score 213; DB 14; Length 31:
Best Local Similarity 27.7%; Pred. No. 1.1e-14;
Matches 83; Conservative 46; Mismatches 143; Indels
                                                                                         236 KOVYRKIGVKVEQAGKQAWDHRQSTSTAEK 265
                                                                                                                         completed: February 29, 2004, 15:28:05
ne : 22.6527 secs
                                                                                                                                                                                                                                           ; Sequence 16, Application US/10128713A; Publication No. US20030170847A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Rhodococcus erythropolis
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US-10-128-713A-16
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us-09-941-947a-34.rai

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STATE: NY

COUNTRY: USA

ZIP: 10023

ZOUNTRY: USA

ZIP: 10023

COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720Kb storage COMPUTER: EMADBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720Kb storage COMPUTER: IBP CCOMPATIBLE
OPREATING SYSTEM PC-DOS/MS-DOS
SOFTWARE: N/A : 1991023
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 107/783,705A
FILING DATE: 1991023
FILING DATE: 21-APR-1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 19-RR-1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 19-RR-1990
APPLICATION NUMBER: 33,778
FELECOMMUNICATION INFORMATION:
MAGE: SCHWENCH, Jane 13.
FELECOMMUNICATION INFORMATION:
TELEPHONE: 212-246-5959
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

TELEPHONE: 212-708-1935
TELEPHONE: Z12-708-1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/07783705A
Patent No. 5429939
PAPLICANT: Misawa, No. 5429939iniko
APPLICANT: Kobayashi, Kazuo
APPLICANT: Yamano, Shigeyuki
TITLE OF INVENTION: DNA SEQUENCES USEFUL FOR THE TITLE OF INVENTION: DNA SEQUENCES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
US-09-091-725-19
US-08-31-981-6
US-09-820-004-2
US-09-820-004-6
US-09-820-004-6
US-09-820-004-6
US-09-820-004-6
US-09-821-981-7
US-08-31-981-9
US-08-351-981-9
US-08-351-981-8
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US-08-351-981-8
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US-08-310-693-2
US-08-310-693-2
US-08-310-693-2
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                                    RESULT 1
US-07-783-705A-5
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        8800H88489668444444
                                                                                                                                                                                                                                                             February 29, 2004, 14:35:44; Search time 8.99489 Seconds (without alignments) 1698.885 Million cell updates/sec
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Sequence 3, p
Sequence 3, p
Sequence 3, p
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1535
1 MAVGSKSFATASTLFDAKTR......VTSRMKTYPPRPAHLWQRPI 296
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Sequence 2,
Sequence 6,
Sequence 6,
Sequence 6,
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-691-270A-4
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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rfect score:
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121 YCYHVAGVVGLAMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
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64.9%; Pred. No. 2.7e-105;
iive 36; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hauptmann, Randal
APPLICANT: Bschenfeldt, William H
APPLICANT: English, Jami
APPLICANT: Brinkaus, Friedhelm L
TITLE OF INVENTION: Enhanced Carotenoid Acci
TITLE OF INVENTION: In Storage Organs of Ger
TITLE OF INVENTION: Regineered Plants
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Amoco Corporation, law Dept
STREET: 55 Shuman Boulevard, Suite 600
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563-8437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.24 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13937A. FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application PC/TUS9513937A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Galloway, Norval B
TELECOMUNICATION INFORMATION
TELEPHONE: 7087172447
TELEFAX: 7087172430
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ATTORNEY/AGENT INFORMATION:
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amino acid
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Matches 192; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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                                                                                             1 MAVGSKSFATASKLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFQARQFALQTPSQRLMQ
                                                                     1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ
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64.9%; Pred. No. 2.7e-105;
ive 36; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bachenen, Randal
APPLICANT: Bschenfeldt, William H
APPLICANT: Brinthaus, Rildiam H
APPLICANT: Brinthaus, Priedhelm L
APPLICANT: Brinthaus, Priedhelm L
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APPLICANT: Brinthaus, Priedhelm L
APPLICANT: Brinthaus, Brinthaus of Genetically
TITLE OF INVENTION: Brinthaus Organically
TITLE OF INVENTION: Brinthaus Plants
CORRESSES: Amoco Corporation, Law Dept
STREET: SS Shuman Boulevard, Suite 600
CITY: Naperville
                           22; Indels
al Similarity 88.9%; Pred. No. 5.9e-143; 263; Conservative 11; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC_DOS/MS-DOS
SOPTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,004A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: GALLOWAY, NO. 5618988val B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08331004A
Patent No. 5618988
GENERAL INFORMATION:
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STATE: NECESTATES
COUNTRY: USA
ZIP: 60563-843
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: Patentin Release #1.
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TELEFAX: 7087172430
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 309 amino acids
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S-08-331-004A-2
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Best Local Similarity
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                                                                                                                                                                                        181 EEEGLIKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWALATAKQVYR
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181 EBEGLTKANYAAPENRQALSKIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQVYR 240
                                   74 IRTITLAAFEGAEMQDPAFAAFQEVALTHGITPRMALDHIDGFAMDVAQTRYVTFEDTLR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 MANGSKSFATAAKLFDPATRRSVLMLYTWCRHCDDVIDDQTHGFASEAAAEEEATQRLAR 73
                                                                                                 241 KIGVKVEQAGKQAMDHRQSTSTARKLTLLLTASGQAVTSRMKTYPPRPAHLWQRPI 296
                                                                                                                           1 MAVGSKSFATASTLFDAKTRRSVLALYAWCRHCDDVIDDQTLGFHADQPSSQAPBQRLQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedelm L
APPLICANT: Brinkhaus, Friedelm L
APPLICANT: Brinkhausi, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yeager, James G
APPLICANT: Yen, Huei-Che B
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/096,043
FILING DATE: 22-JUL-1993
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,568
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: GABLOWAY, NO. 5530189VAI B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                Sequence 6, Application US/08096043
Patent No. 5530189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 3128567180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-096-043-6
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STATE: IL
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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US-08-096-043-6
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                                              181 EEEGITKANYAAPENRQALSRIAGRIVREAEPYYVSSMAGLAQLPLRSAWAIATAKQVYR 240
134 YCTHVAGVVGLMMARVMGVRDERVLDRACDLGLAFQLTNIARDIIDDAAIDRCYLPAEWL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 LRILILAAFEGAEWQDPAFAAFQEVALTHGITPRMALDHIDGFAMDVAQTRYVTFEDTLR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LEMKTRQAYAGSQMHBPARAARQEVAMAHDIAPAYARDHLEGFAMDVRETRYLTLDDTLR 120
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                                                                                            194 QDAGLTPENYAARENRAALARVAERLIDAAEPYYISSQAGLHDLPPRCAWALATARSVYR
                                                                                                                                                                           241 KIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPPRAHLWQRPI 296
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                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Minharji, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yanger, James G
APPLICANT: Yen, Huei-Che B
ITTLE OF INVENTION: Beta-Carotene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 200 E Randolph St Clivago STREET: Licensing Dept STREET: Licensing Dept STREET: Licensing Dept STREET: Licensing Dept STREE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60680-0703
ZIP: 60680-0703
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 31-UUL-1993
CLASSIFFCRATION: 435
PRIOR APPLICATION UMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
WHEN COMPANY AND ATTORNEY ARE STORED ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Galloway, No. 5530188val B
TELECOMOUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
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amino acid
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-08-095-726-6
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241 KIGVKVEQAGKQAWDHRQSTSTABKLTLLTASGQAVTSRMKTYPPRPAHLWQRPI 296
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Best Local Similarity 63.99
Matches 189; Conservative
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                                                                                                                       RESULT 7
US-08-096-623A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 BEEGLIKANYAAPENRQALSRIAGRLVREAEPYYVSSWAGLAQLPLRSAWAIATAKQVYR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ 60
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                                                   241 KIGVKVEQAGKQAWDHRQSTSTAEKLTLLIFASGQAVTSRMKTYPPRPAHLWQRPI 296
                                                                                  Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70; Indels
                                                                                                                                                                                                                                                                                                            APPLICANT: Muchaer, Friedhelm L.
APPLICANT: Muchaer, Friedhelm L.
APPLICANT: Muchaerj, Indrani
APPLICANT: Profitt, John H.
APPLICANT: Profitt, James G.
APPLICANT: Yen, Huei-Che B.
TITLE OF INVENTION: Phytoene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 43
CORRESPENDENCE ADDRESS:
ADDRESSE: Amoco Corp., Patents and Licensing Dept
STREET: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.0%; Score 997.5; DB 1; 63.9%; Pred. No. 6.3e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUNTRY: USA

ZIP: 60680-0703

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,577
FILING DATE: 19-UUL-1993
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/093,F77
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Galloway, No. 5545816val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
                                                                                                                                                                                                                                                                                            Ausich, Rodney L
Brinkhaus, Friedhelm L
Mukharji, Indrani
Proffitt, John H
                                                                                                                                                                                             3.08-093-577-6
Sequence 6, Application US/08093577
Patent No. 5545816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 308 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.9%
Matches 189; Conservative
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S-08-093-577-6
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APPLICANT: Ausich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: C
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US-08-096-623A-6

Sequence 6, Application US/08096623A

Patent No. 5684238

GENERAL INCOMATION:

APPLICANT: Micharly, Indiani
APPLICANT: Micharly, Indiani
APPLICANT: Proffitt, John H.

APPLICANT: Yen, Huel-Che

APPLICANT: Yen, Huel-Che

APPLICANT: Yen, Huel-Che

APPLICANT: Yen, Huel-Che

APPLICANT: Yen, Huel-Che

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APPLICANT: Yen, Huel-Che

APPLICANT: Yen,
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Length 308;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRALING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSCIPLOATION DATA:
APPLICATION NAMER: US 07/805,061
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NAMERE: US 07/662,921
FILING DATE: 28-FEB-1991
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION NUMBER: US 07/562,551
FILING DATE: 18-MAY-1990
PRIOR APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-MAY-1990
PRIOR APPLICATION NUMBER: US 07/487,613
FILING DATE: 18-MAY-1990
PRIOR APPLICATION NUMBER: US 07/487,613
FILING DATE: US-MAR-1990
ATTONEY/AGENT INFORMATION:
AMADEL OF THE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE O
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es 70;
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63.9%; Pred. No. 6.3e
:ive 36; Mismatches
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REGISTRATION NUMBER: 29,381
REFREENCE/DOCKET NUMBER: AMO-006.1
TELECOMMUNICATION INFORMATION:
TELEPROME: (312) 655-1500
INFORMATION FOR SEQ ID NO: 6:
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70 LRADTLAA-----LHEDGPMSPPFAALRQVARRHDFPDLWPMDLIEGFAMDVADKBYRSL 124
70 LRADTLAA-----LHEDGPMSPPFAALRQVARRHDFPDLWPWDLIEGFAWDVADREYRSL 124
                                                                                    PESWLEEEGLTKANYAAPENROALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATA 235
                                                                                                                                                                             185 PADWLAEAG---ATVEGPVPSDALYSVIIRLIDAAEPYYASARQGLPHLPPRCAWSIAAA 241
                                                                                                                                                                                                                          236 KQVYRKIGVKVEQAGKQAWDHRQSTSTABKLTLLLTASGQAVTSRMKTYPPRPAHLWQRP 295
                                                                                                                                                                                                                                                    61 LEMKTROAYAGSOMHE----PAFAAPOEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTL 115
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                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09298718
Patent No. 6124113
CENERAL INFORMATION
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pessmentes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDER: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.7%; Score 686.5; DB 3;
48.7%; Pred. No. 1.6e-67;
tive 35; Mismatches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSFTWARE: Patentin Dalace
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POKEAS, BRUCE A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6
TELECOMUNICATION INFORMATION:
TELEPHONE: (201) 235-2363
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 340 Kingsland Street CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 amino acida
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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US-09-298-718-3
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                                               121 YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
                                                                                                                                                                                   EEEGLTKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQVYR 240
                       61 LEWKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR 120
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                                                                                                                             1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ
                                                                                                                                                                                                                                                                                           KIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPPRPAHLWQRPI 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Pesier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
FILING DATE: US/08/660,645A
FILING DATE: 0.7-UNN 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9510888.9
FILING DATE: 09-UNA-1995
ATTORNEY/ACENT INFORMATION:
NAME: POKTAS Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2363
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08660645A
Patent No. 6087152
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 amino acids
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Best Local Similarity 48.7
Matches 146; Conservative
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LENGTH: 303 amino acid
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MEDIUM TYPE: Floppy
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ZIP: 07110
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; Sequence 3, Application US/09547267
; Patent No. 6613543
; Patent No. 6613543
; APPLICANT: Rohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
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APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: AUSA
CORRESPONDENCE ADDRESS:
ADDRESSES: 340 Kingsland Street
CITY: Nutley
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.7%; Score 686.5; DB 3;
48.7%; Pred. No. 1.6e-67;
tive 35; Mismatches 104;
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Best Local Similarity 48.75
Matches 146; Conservative
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                                                              176 PESWLEEBGGITKANYAAPENRQALSRIAGRIVREAEPYYVSSMAGLAQLPLRSAWAIATA 235
                                                                                                                                                     236 KQVYRKIGVKVEQAGKQAMDHRQSTSTAEKLILLLTASGQAVTSRMKTYPPRPAHLWQRP 295
                                                                                                                                                                                                                                            116 DDTLRYCYHVAGVVGLAMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYL 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, luis
APPLICANT: Pasamontes, luis
APPLICANT: Tessler, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
ACKRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PR PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/546,969
FILING DATE:
CLASSIFICATION NUMBER: US/09/546,969
FILING DATE:
APPLICATION NUMBER: 08/660,645
FILING DATE:
APPLICATION NUMBER: 32,746
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION 1215-5801
TELEFAK: (201) 235-2363
INFORMATION POR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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44.7%; Score 686.5; DB

Best Local Similarity 48.7%; Pred. No. 1.6e-67

Matches 146; Conservative 35; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: UJ
COUNTRY: USA
ZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09546969
Patent No. 6207409
GENERAL INFORMATION:
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STRANDEDNESS: sin
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116 DDTLRYCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYL 175
                                                                                                  236 KOVYRKIGVKVBOAGKOAWDHROSTSTAEKLTLLLTASGOAVTSRMKTYPPRPAHLWORP 295
                                                                                                                             242 LRIYRAIGTRIRQGGPEAYRQRISTSKAAKIGILARGGLDAAASKLRGGEISRDGLWTRP 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LEMKTROAYAGSOMHE----PAFAAROEVAMAHDIAPAYARDHLEGFAMDVRETRYLTL
176 PESWLEEEGLIKANYAAPENROALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATA
                                                                                                                                                                                                                                                                     Sequence 3, Application US/08980832B
Patent No. 6291204
GERNERAL INFORMATION:
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
TITLE OF INVENTION: Improved Fermentive Carotenoid
CURRENT APPLICATION WUMBER: US/08/980,832B
CURRENT PILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
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LENGTH: 489 amino acids TYPE: amino acid
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MOLECULE TYPE: protein
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US-07-783-705A-4
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Patent No. 568428
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Priedhelm L.
APPLICANT: Brinkhaus, Priedhelm L.
APPLICANT: Wukharji, Indrani
APPLICANT: Wen, Huei-Che B.
TITHE OF INVENTION: Biosynthesis of Zeaxanthin and
TITHE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
62 ALSALFTLAGRRWEDYVRLLPVKPFYRLCWESGKTLDYANDSFELEAQITQFNPRDVRGY 121
                                                                                                 184 DPKLVEIINYFIKYVGSSPYDAPALMNLLPYIQYHYGIMYVKGGWYGMAQAMEKLAVELG 243
                                                                                                                                                                                                                                                                          236 GEIELMARVEELVVADNRVSQVRLADGRIFDTDAVASNADVVNTYKKLLGTIPVGQKRAA 295
                                                                                                                                                                                                                                                                                                                                     301 KWORFEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAP 360
                                                                                                                                                                                                                                                                                                                                                                  CKTDPAQAPAGCELIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTDLRQHIVT 420
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                                                                                                                                                                                                176 DEHLRQAFSFHSLLVGGNPFTTSSIYTLIHALEREWGVWPPBGGTGALVNGMVKLFTDLG 235
                                                                                                                                                                                                                                             244 VEIKLDAEVSEIQKODGRACAVKTANGDVLPADIVVSNMEVIPAMEKLLRS-PASBLK-- 300
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COMPUTER: PLODPY disk
MEDIUM TYPE: PLODPY disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: DetentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSENIA APPLICATION DATA:
APPLICATION NUMBER: US 07/805,061
FILING DATE: 22-UUL-1993
CLLSSIFICATION NUMBER: US 07/805,061
FILING DATE: 28-FEB-1991
PRIOR APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION NUMBER: US 07/662,921
FILING DATE: 03-AUG-1990
PRIOR APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
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120 S. Riverside Plaza, 22nd Floor
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STREET: 120 S.
CITY: Chicago
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ZIP: 60606
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67 IFEALFTGAGKNWADYVQIQKVEPHWRNFFEDGSVIDLCEDABTQRRELDKLGFGTYAQF 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 VEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNNEVIPAMEKLLRS-PASELK-- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 CKTDPAQAPAGCELIKILPHIDPDKILTAEDYSALRERVIVKGERMGLTDLKQHIVT 420
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Patent No. 5429939
GENERAL INCRMATION:
APPLICANT: Misawa, No. 5429939ihiko
APPLICANT: Kobayashi, Kazuo
APPLICANT: Nakamura, Katsumi
APPLICANT: Yamano, Shigeyuki
TITLE OF INVENTION: DNA SEQUENCES USEFUL FOR THE
TITLE OF INVENTION: STATHESIS OF CAROTENDIDS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 702.5; DB 1;
; Pred. No. 1.9e-63;
96; Mismatches 212;
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATE:
PRIOR APPLICATION DATE:
FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAMB: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
REPERENCE/DOCKET NUMBER: AMO-006.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 655-1500
INFORMATION FOR SEQ. 1D NO: 8:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 32.9%;
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485 GQLVRDKIVADL 496 : :: || 480 AKATAGIMLEDL 491

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32.7%; Pred. No. 3.3e-60;
tive 89; Mismatches 230; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, 720Kb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/783,705A
FILING DATE: 19911023
CLASSIPTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-103078
FILING DATE: 21-ARP.1989
APPLICATION NUMBER: UP 2-53225
FILING DATE: 05-WAR.1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 19-APR.1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 11-APR.1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Schwadron, Janet I.
REGISTRATION UNMERS: 33,778
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-708-1935
                              ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGIH: 492 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 492 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                        10023
                                                                                                                                                         STATE: N
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70 ALFTGAGKNMADTVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTVAQFQRF 129
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Best Local Similarity 31.2%; Pred. No. 1.1e-56;
Matches 155; Conservative 90; Mismatches 233; Indels 18; Gaps
                                                             GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Peasannte, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
ITTLE OF INVENTION: FERMENTATIVE CAROFENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/660,645A FILIG DATE: 07-JUN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,748
REPERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95108988.9
FILING DATE: 09-UUN-1995
ATTORNEY/AGENT INFORMATION;
NAME: POKES, BLUCG A.
                                                                                                                                                                                                                                                               SEE: Hoffmann-La Roche Inc.: 340 Kingsland Street
Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
CMMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                     Sequence 5, Application US/08660645A Patent No. 6087152
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INPORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
TYPE: amino acid
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US-08-660-645A-5
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250 AEVSEIOKODGRACAVKLANGDVLPADIVVSNMEVIPAMEKLL-----RSPASELKKKWO 303
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70 ALFTGACKAMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQFQRF 129
                                         65 BLWALSGQPMERDVTLLPVSPFYRLTWADGRSFEYVNDDDBLIROVASFNPADVDGYRRF 124
                                                                                         130 IDYSKNICTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDGGVRRFISDPKLVB 189
                                                                                                                             125 HDYABEVYRE---GYLKLGTTPFLKLGQMLNAAPALMKLQAYRSVHSMVARFIQDPHLRQ 181
                                                                                                                                                                                190 ILNYFIKYVGSSPYDAPALMNILPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVEIRLD 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
ITILE OF INVENTION: PERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Hoffmann-La Roche Inc.
STRRET: 340 Kingsland Street
CITY: Nutley
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
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Patent No. 6207409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hobmann, Hans-Peter
APPLICANT: Pasamontes, Luis
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REGISTRATION NUMBER: 33,748
REGISTRATION NUMBER: RA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 VTLSGQLVRDKIVADL 496
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476 VVGSAKATAQVMLSDL 491
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TELEPAX: (201) 235-2363
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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COUNTRY: U
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                                                                                                                                                                           416 SRIFSPADPSTELSAHHGSAFSVEPILTQSAWFREHNRDRAIPNFYIVGAGTHPGAGIPG 475
         242 ARVTRIDTEGDRATGVT-LLDGRQLRADTVASNGDVMHSYRDLLGHTRRGRTKAAILNR-Q 300
                                                     304 RFEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKT 363
                                                                               421 BEYWTPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSBLSNLYFVGGSVNPGGGMPM 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Passamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NÜMBER OF SEGUENCES: 47
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenter Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION TOWNER: US/05/298,718
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ATTORNEY/AGENT INFORMATION:
NAME: POKIES, BILGE A.
REGISTRATION NUMBER: 32,748
REFREENCR/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09298718
Patent No. 6124113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
STATE: NJ
STATE: NA
STATE: 05A
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INFORMATION FOR SEQ 1D NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
TYPE: amino acid
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Best Local Similarity 31.2
Matches 155; Conservative
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STRANDEDNESS:
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S-09-298-718-5
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                AEVSEIQKQDGRACAVXLANGDVLPADIVVSNMEVIPAMEKLL-----RSPASELXKONQ 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPAQAPAGCEIIKILPHIPHL---DPDKILTAEDYSALRERVLVKLERMGLTDLRQHIVT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPSLAPEGMSTHYVLAPVPHIGRADVDWEAEAPGYA---ERIFEELERRAIPDLRKHLTV 415
                                                                                                                                                                                                                                                  |: :|: | : | : :| | : :| | : :| | ELWALSGQPMERDVTLLPVSPFYRLTWADGRSFSFYNDDDELIRQVASFNPADVDGYRRF 124
                                                                                                                                                                                                                                                                                              LDYSKOLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDGGVRRFISDFKLVE 189
                                                                                                                                                                                                                                                                                                                                                                  190 ILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGWYGMAQAMEKLAVELGVEIRLD 249
                                                                                                                                                                                                                              70 ALFIGACKAMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQFQRF 129
                                                                                                                                                                                                                                                                                                                                HDYAEEVYRE---GYLKIGITPFLKIGOMLNAAPALMRLQAYRSVHSMVARFIQDPHLRQ 181
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US-08-980-832-4
Sequence 4, Application US/08980832B
Patent No. 6291204
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
TITLE OF INVENTION: Improved Fermentative Carotenoid
FILE REPERBNCE: Improved Fermentiative Carotenoid
CURRENT APPLICATION UNBER: US/08/980,832B
CURRENT FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
                                                                                              Length 494;
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31.2%; Pred. No. 1.1e-56;
tive 90; Mismatches 233; Indels
                                                                                                              Best Local Similarity 31.2%; Pred. No. 1.1e-56;
Matches 155; Conservative 90; Mismatches 233; Indels
                                                                                              24.5%; Score 637; DB 3; 31.2%; Pred. No. 1.1e-56;
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Best Local Similarity 31.2%
Matches 155; Conservative
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amino acid
EDNESS: single
                              TOPOLOGY: linear
MOLECULE TYPE: protein
     STRANDEDNESS: SIL
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; ORGANISM: F]
US-08-980-832-4
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US-09-546-969-5
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101 RW--SMSLFVLHFGLSKRPENLAHHSVIFGERYKGLVNEIFNGPRLPDDFSMYLHSPGVF 358
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                                                                                                                                                                                                                                                                                                                                                                 ABVSEIQKODGRACAVKLANGDVLPADIVVSNWEVIPAMEKLL-----RSPASELKKWQ 303
                                         130 LDYSKNLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFISDPKLVE 189
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125 HDYABEVYRE---GYLKLGTFPFLKLGQMINAAPALMRLQAYRSVHSWVARFIQDPHLRQ 181
                                                                                                                                                                                                                    190 ILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVEIRLD 249
ALFIGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETORRELDKLGPGTYAQFQRF 129
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APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: PERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/547,26
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APPLICATION NUMBER: 08/660,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09547267
Patent No. 6613543
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
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TELEFAX: (201) 235-2263
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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TITLE OF INVENTION: Impr
TITLE OF INVENTION: and
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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                                                                                                                                                   Query Match 24.5%; Score 637; DB 4; Length 494; Best Local Similarity 31.2%; Pred. No. 1.1e-56; Matches 155; Conservative 90; Mismatches 233; Indels 18;
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Patent No. 6677134
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Vari
TITLE OF INVENTION: Fermentative Carotemoid Production
FILE REFERENCE: 15464 US (C38435/125944)
CURRENT APPLICATION NUMBER: US/09/920,923B
PRIOR APPLICATION NUMBER: US/09/920,923B
PRIOR PILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE Patentin version 3.1
SEQ ID NO 4
LENGTH: 494
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      494 amino acids
                           TYPE: amino acid
STRANDEDNESS: single
                                                                 TOPCLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                          190 ILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGWYGMAQAMEKLAVBLGVEIRLD
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                                                           70 ALFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQFQRP
                                                                                       65 ELWALSGQPMERDVTLLPVSPFYRLTWADGRSFEYVNDDDELIRQVASFNPADVDGYRRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25 (BPO)
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APPLICATION NUMBER: BP 95203620.0
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: BP 96200943.7
FILING DATE: 11-APR-1996
ATTORNEY AGENT INFORMATION:
NAME: E. VICCOT DODANUE
REGISTRATION NUMBER: 35,492
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America CIP: 2006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-00S/MS-DOS SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA: FILING DATE: 23-DEC-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Morrison & Foerster llp
STREET: 2000 Pennsylvania Avenue,
CITY: Mashington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/09091725 Patent No. 6329141 GENERAL INFORMATION:
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
S-09-091-725-17
Query Match
23.8%; Score 618.5; DB 4; Length 582;
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	10;	64	67	123
	Gaps	PSILTM	PSILLL	-GPGTY
582;	33;	PTFDLG	YRFDOG	RELDK
23.8%; Score 618.5; DB 4; Length 582;	Indels	LNIMTKD	CSLIERDO	CEDAETOR
DB 4;	229;	CNDKVGGK	ONDYSGGR	SDGSVIDE
618.5;	smatches	FSVOLIE	POVTVFE	PHWRNPF
Score	, red.	ISLATAG	ARLAKEG	VOTOKVE
23.8%;	z8./\$; ive 14	GGLSAA	GGIATA	KNMADY
-	Best Local Similarity 28.7%; Frun. No. 1.15-54; Matches 148; Conservative 106; Mismatches 229; Indels 33; Gaps 10;	5 DNORVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTM 64	8 DXPTAIIVGCGIGGIATAARLAKBGFQVTVFEKNDYSGGRCSLIERDGFRFDQGFSLLLL 67	65 PHTERALFWRAGKNMADYVOLOKVBPHWRNFFBDGSVIDLCEDAETORRELDKL-GPGTY 123
	48; C	5 DNOR	B DKPT	5 5415
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RESULT 1
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Phytoene
                                                                                   ; Search time 58.7617 Seconds (without alignments) 2389.754 Million cell updates/sec
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                                                                                                                                                                              1 MNSNDNQRVIVIGAGLGGLS.........APMVTLSGQLVRDKIVADLQ 497
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Aae22314 |
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Abm72613 S
Ada14542 S
Aar07466 B
Aaw82257 Q
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                 otal number of hits satisfying chosen parameters:
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AAW87889	AAN99099	AAY26333	AAR64269	ABP97465	AAW00871 .	AAW69532	AAW22499	AAE22309	ABG61588	AAU80332	ADA14534	AAW77702	AAR95697	ABU32531	ABB49224	AA015521	AA015518	AAB76640	AAB76641
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## ALIGNMENTS

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Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; diapophytoene dehydrogenase; CrtN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon
                                                                                                                                                                                               Methylomonas 16a sp. diapophytoene dehydrogenase (CrtN2) enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koffas M, Miller ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dicosimo DJ,
Rouviere PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 37; Page 131-133; 156pp; English.
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                          AAE22310 standard; protein; 497 AA
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Odom JM, Picataggio SK,
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N-PSDB; AAD35508.
                                                                                                                                                                                                                                                                                                                                                       Methylomonas sp.
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                                                                                                                          07-AUG-2003
25-JUL-2002
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                                                                          AAE22310;
AAE2231
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The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule contoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by

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using microorganism having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Methylomonas 16a sp. diapophycome dehydrogenase (CrkR) enzyme used in the invention. (Updated on 07-AUG-2003 to correct OS field.)
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Sequence 497 AA;

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High growth methanotrophic bacterial strain polypeptide #39. Ā ABG61589 standard; protein; 497 (revised)
(first entry) 07-AUG-2003 27-AUG-2002 8XXX55X8X888888XXXX

High growth methanotrophic bacterial strain; Cl carbon substrate; enzyme; methane; methanol; Embden-Meyerhof carbon flux pathway; 16s RNA; pyrophosphate dependent phosphofrutokinase; nitrogen-containing compound; ammonia; nitrate; nitrite; nitrogen; pigment; oxygen; landfill; methane-containing environment; waste water treatment system; isoprenoid; nitrous oxide; terpenoid; animal feed; carotemoid; exopolysaccharide.

WO200220728-A2

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The invention relates to a high growth methanotrophic bacterial strain, which grows on a CI carbon substrate e.g. methane and methanol, and comprises a functional Embden-Meyerhof carbon flux pathway comprising a comprises a functional Embden-Meyerhof carbon flux pathway comprising a gene coding a pyrophosphate dependent phosphofrutokinase enzyme or a 16s CRNA. The bacterial strain is useful for the production of single cell protein and for the biotransformation of a nitrogen-containing compound, e.g. ammonia, nitrate, nitrite or nitrogen. It is also useful for the production of a feed product comprising a protein, carbohydrates and a pigment and for reducing oxygen demand, for removing nitrates and contrintes in methane-containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are contribly agent for the conversion of nitrate or nitrite to nitrous coile with methane or methanol as a carbon source. It is also used in the cord with methane or methanol as a carbon source. It is also used in the cord writing animal feeds), in production of terpenoid and carotenoid of generating animal feeds), in production of terpenoid and carotenoid compounds, useful as pigments and as monomers in polymeric materials and cin production of expolysaccharides at high levels. Sequences ABG61551-CR ABG61590 represent high growth methanotrophic bacterial strain proteins of the invention.
                                                                                                                                                                                                                                                                                                                        New high growth methanotrophic bacterial strain, useful for producing single cell proteins, grows on a Cl carbon substrate, and comprises a functional gene encoding in Embden-Meyerhof carbon pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 153-154; 157pp; English.
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                                                                                                                                                            (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                01-SEP-2000; 2000US-0229858P.
                                                                  28-AUG-2001; 2001WO-US026827.
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N-PSDB; ABK83268.
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                                                             PISDPKLVEILNYPIKYVGSSPYDAPALMNILPYIQYHYGLWYVKGGMYGMAQAMBKLAV
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 Length 497;
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Query Match 100.0%; Score 2598; DB 5; Best Local Similarity 100.0%; Pred. No. 1.5e-241; Matches 497; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                             241 ELGVEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSPASELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding carotenoid biosynthesis enzymes, useful for preparing functionalized carotenoids, e.g. pigments and antioxidants, also encoded polypeptides.
                                          61 ILTMPHIFEALFTGAGRUMADYVQIQKVBFHRRNFFEDGSVIDLCEDAETQRRELDKLGP
                                                                                                                                                                                      181 FISDPKLVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEKLAV
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                      61 ILTMPHIFEALFTGAGKNWADYVQIQKVEPHWRNFFBDGSVIDLCEDAETQRRELDKLGP
                                                                                                    121 GTYAQPQRFLDYSKALCTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 VILSGOLVRDKIVADLO 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-697524/66.
N-PSDB; ADA14537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methylomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA14538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA14538
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                                                                                                                                        용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new nucleic acid molecule encoding an isoprenoid biosynthetic enzyme isolated from Methylomonas 16a. The invention is useful for obtaining a nucleic acid molecule encoding an isoprenoid compound biosynthetic enzyme, and for the microbial production of isoprenoid compounds. The molecules of the invention are also useful for requlating isoprenoid biosynthesis in an organism and for production recombinant organisms for producing various isoprenoid compounds. The nucleic acid is also useful for feed additive, for the production of keratenoids and their derivatives, isoprenoid intermediates, and as pure products useful as pigments, flavours and fragrances. The present amino acid sequence represents the Methylomonas 16a open reading frame 9 (ORPS) cerro? ((crth copyz) copy 2 of diapophytoene dehydrogenase enzyme) protein of the invention, as described above
CKTDPAQAPAGCEIIXILPHIPHIDPDKLLTABDYSALRERVLVKJERMGLTDLRQHIVT 420
                                                                480
                                                                                       421 EEYMTPLDIQAKYYSNQSSIYGVVADRPKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPM 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid molecule encoding a isoprenoid biosynthetic enzyme, isolated from Methylomonas 16a, useful for the production of isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSNDNQRVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPS
                                                                  EEYWTPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNSNDNQRVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isoprenoid biosynthetic enzyme; isoprenoid compound; feed additive; keratenoid; pigment; flavour; fragrance; open reading frame 9; ORP9; crtN2; crtN copy2; diapophytoene dehydrogenase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 100.0%; Score 2598; DB 5; Length 497; al Similarity 100.0%; Pred. No. 1.5e-241; 497; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Odom JM, Picataggio SK;
                                                                                                                                                                                                                                                                                                                                                                                                                          Methylomonas 16a ORF9 crtN2 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DUPO ) DU PONT DE NEMOURS & CO B I.
                                                                                                                                                                                                                                                                                                  AAU80333 standard; protein; 497 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheng Q, Koffas M, Norton KC, Oc
Rouviere PE, Schenzle A, Tomb J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 81-82; 84pp; English.
                                                                                                                                                 481 VILSGOLVRDKIVADLO 497
                                                                                                                                                                                  481 VTLSGQLVRDKIVADLQ 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-2000; 2000US-0229907P.
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                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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N-PSDB; ABK50089.
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Best Local Similarity
Matches 497; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 497 AA;
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Staphylococcus aureus

WO2003068917-A2

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The present invention describes nucleic acid sequences encoding carotenoid biosynthetic enzymes (CBES). Also described: (1) a CBE polypeptides; (2) a chimeric gene (CG) containing a CBE linked to regularory sequences; (3) host cell transformed with CG; (4) obtaining a nucleic acid that encodes a CBE; (5) products of method (4); (6) producing an omega-aldehyde-functionalised carotenoid (X); (7) producing an omega-carboxy-functionalised carotenoid (Y); (8) producing an omega-carboxy-functionalised carotenoid (Y); (8) producing Carotenoids (2); and (9) regulating carotenoid (Y); (8) producing Carotenoids (BES can be used for microbial production of aldehyde-or carboxy-functionalised carotenoids and are potentially useful as pigments and and C30 carotenoids, and are potentially useful as pigments and cartox carboxy-functionalised carotenoids antioxidants, e.g. as feed additives. The present sequence represents a used in the exemplification of the present invention.
              SSSSSSSSSSSSSS
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Sequence 497 AA;

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CKTDFAQAPACCEIIKILPHIPHLDFDKLLTAEDVSALRERVLVKLERAGLTDLRQHIVT 420
                                                                                                                                            61 ILTMPHIFEALFTGAGKNMADYVQIQKVEPHWRNFFEBGSVIDLCEDAETQRRELDKIGF 120
                                                                                                                                                                             GTYAQFQRFLDYSKNLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSWDQGVRR 180
                                                                                                                                                                                                                                                                                                                      CKTDPAQAPAGCELIKILPHIPHLDPDKLLTAEDYSALRERVLVKGLERMGLTDLRQHIVT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REYWTPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPM 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ILTMPHIFEALFTGAG: GAMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGP 120
                                                                                                                                                                                                          121 GTYAQFQRFLDYSKNLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRR 180
                                                                                                                                                                                                                                         PISDPKLVEILNYFIKYVGSSPYDAPALMNILPYIQYHYGLWYVKGGMYGMAQAMEKLAV 240
                                                                                                                                                                                                                                                                                                     ELGVEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSPASELK 300
                                                                                                                                                                                                                                                                                                                                                               KMORFEPSCSGLVIJHLGVDRLYPQLAHHNPFYSDHPREHFDAVFKSHRLSDDPTIYLVAP 360
                                                                                     9
                                                         1 MNSNDNQRVIVIGAGLGGLSAAISLATAGPSVQLIEKNDKVGGKLNIMTKDGFTFDLGPS 60
                                                                          181 FISDPKLVEILNYFIKYVGSSPYDAPALMNIJPYIQYHYGLWYVKGGMYGMAQAMEKLAV
                              Gaps
                            ö
DB 6; Length 497;
                              Indels
Score 2598; DB 6;
Pred. No. 1.5e-241;
O; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VILSGQLVRDKIVADLQ 497
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100.0%;
              Best Local Similarity 100.
Matches 497; Conservative
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Query Match
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carotenoid biosynthetic enzyme; CBB; omega-aldehyde-functionalised carotenoid; omega-arboxy-functionalised carotenoid; C30 carotenoid; carboxy-functionalised carotenoid; C30 carotenoid biosynthesis; antioxidant; microbial; pigment; feed additive; CrtN2.
                                                                                                            Staphylococcus aureus CrtN2 protein SEQ ID NO:14
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                          ADA14544 standard; protein; 497
                                                                                  06-NOV-2003
                                                       ADA14544;
             ላይልገ 4544
RESULT
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The present invention describes mucleic acid sequences encoding carotenoid biosynthetic enzymes (CBES). Also described: [1] a CBE polypeptides; [2] a chimeric gene (CG) containing a CBE linked to polypeptides; [3] host cell transformed with CG; [4] obtaining a cequiatory sequences; [3] host cell transformed with CG; [4] obtaining a mucleic acid that encodes a CBE; [5] products of method (A); [6] producing an omega-aldehyde-functionalised carotenoid (X); [7] producing carotenoids (Z); and (9) regulating carotenoid (Y); [8] producing CG carotenoids (Z); and (9) regulating carotenoid biosynthesis in an organism. CBE sequences have antioxidant activity. CBEs can be used for microbial production of aldehyde- or carboxy-functionalised carotenoids and CGO carotenoids, and are potentially useful as pigments and crivity cas sefect additives. The present sequence represents a CTLNZ CBE protein isolated from Staphylococcus aureus, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHIVIGGGLGGISAAIRWAQSGYSVSLYEQNNHIGGKVNRHESDGFGFDLGPSILTMPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 IPEKLFEYSKKQMSDYVTIKRLPHQWRSFFPDGTTIDLYBGIKETGQHNALLSKQDIBBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 ORFIDYSKNLCTETBAGYFAKGIDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFISDPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 LVEILNYFIKYVGSSPYDAPALMALLPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 RLDAEVSBIOKODGRACAVKLANGDVLPADIVVSNMEVIPAMBKLLRSPASBLKKMQR-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 ORVIVIGACLGGLSAAISLATAGFSVOLIEKNDKVGGKLNIMTKDGFTFDIGPSILTMPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I PEAL FIGACKAMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQF
                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding carotenoid biosynthesis enzymes, useful for preparing functionalized carotenoids, e.g. pigments and antioxidants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.6%; Score 1289; DB 6; Length 497; S1.9%; Pred. No. 3.7e-115; ive 85; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 19; Page 114-117; 125pp; English.
                                                                                                                                                                                              Ξ.
                                                                                                                                                                                                DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                         11-FEB-2003; 2003WO-US004150
                                                                                                                                                            11-FEB-2002; 2002US-0355939P
                                                                                                                                                                                                                                                                                                                                                   preparing functionalized c
also encoded polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 254; Conservative
                                                                                                                                                                                                                                    Norton KC,
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                                                                                                                                                                                                                                                                                           N-PSDB; ADA14543
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                                                                                   21-AUG-2003
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                                                                                                                                                                                                                                      Cheng Q,
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186 182

99 62 425 421

303 BPASSGYVWHLGVACQYPQLAHHNFFFTENAYLAYQQVFHEKVLPDDPTIYLVNTDH

366 AQAPAGCEIIKILPHIPHLDPDKLLTAEDYSALRERVLVKLBRMGLTDLRQHIVTBEYWT 

EPSCSGLVLHLGVDRLYPQLAHENFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKTDP

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Wall D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLDIQAKYYSNQGSIYGVVADRFKOLGFKAPQRSSELSNLYFVGGSVNPGGGMPMVTLSG 485
                 PEDIEKNYRSNRGAIYGVVADKKKNKGFKFPKESQYFENLYFVGGSVNPGGGMPMYTLSG 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORFLDYSKNLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFISDPK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein, useful as a vaccine for treating or infection, specifically an infection caused ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QRVIVIGAGIGGISAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHILLINGGGLGGISAAIRWAQSGYSVSLYEQNWHIGGKVNRHESDGFGFDLGPSILTWPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I FEALFTGAGKNMADYVQIOKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                             Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel genes and encoded proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.6%; Score 1289; DB 6; Length 5
51.9%; Pred. No. 3.8e-115;
iive 85; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 3712; 49pp; English
                                                                                                                                                                                                                                                Staphylococcus aureus protein #1856.
                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                          enzymatic assay; antibiotic target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scarselli
                                                                                                                                                            ABM72616 standard; protein; 500
                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2002; 2002WO-IB002637
                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-2001; 2001GB-00007661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Staphylococcus aureus preventing Staphylococcal S. aureus, e.g. sepsis.
                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity 51.9
254; Conservative
                                                                                  COVADKINA 490
                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masignani V, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003-120786/11.
                                                         QLVRDKIVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 500 AA;
                                                                                                                                                                                                                                                                                                                                                   WO200294868-A2
                                                                                                                                                                                                                  20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-2002.
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Matches
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365
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                                                                                                                                                                                                                                                                                                                                                                      PIDIQAKYYSNQGSIYGVVADRPKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPMYTLSG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         essential gene; cell proliferation; drug design
                                                                                                                                                                                                                          EPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKTDP
                                                                                                                                        246 HTGARVDNIKTYQRRVTGVRLDTGEFVKADYIISNMEVIPTYKYLIHLDTQRLNKLEREF
                                                                                                                                                                                                                                                                                                                                        366 AQAPAGCEIIKILPHIPHIDPDXLLTAEDYSALRERVLVKLERMGLTDLRQHIVTBEYWT
                                                                                                          247 RLDAEVSBIOKODGRACAVKLANGDVLPADIVVSNMEVIPAMEKLIRSPASBLKKMOR-F
                              LVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #1558.
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU16031 standard; protein; 497 AA
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-03072851.
06-MAR-2002; 2002US-0362699P.
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Carr G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEVRDKIVA 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQVADKINA 493
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Trawick JD,
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N-PSDB; ACA19901.
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proliteration, 17) reductiving a compound using a biological pathway required for proliferation, or that inhibits callular proliferation. (8) identifying a gene required for callular proliferation or the biological pathway in which a proliferation required for callular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity, (11) a culture comprising strains in which the gene or product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational dascovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryoric essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of ftp.wipo.int/pub/published_pct_sequences

Sequence 497 AA;

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IFEALFTGAGRAMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQF 126
                                                                         7 QRVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPH 66
                                                                                                         62
                                                                                              I PEKL FEYSKKOMSDYVTIKRLPHQWRSFFPDGTTIDLYEGIKETGQHNAILSKQDIEEL
                                       Gaps
                                       7
                                   Indels
49.5%; Score 1287; DB 6;
51.9%; Pred. No. 5.8e-115;
live 84; Mismatches 149;
   Query Match
Best Local Similarity 51.9%
Matches 254; Conservative
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QRFLDYSKNLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFISDPK 186 187 LVEILNYFIKYVGSSPYDAPALMNILPYIQYHYGLMYVKGGMYGMAQAMEKLAVELGVEI 127 g ò

> 吕 ઠે 셤 ઠે B

306 EPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKTDP

> В 8 g

QLVRDKIVA 494

ABU43877 standard; protein; 502 AA. ABU43877 ABU43877 ID ABU4 XX AC ABU4

RESULT 8

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Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                           Zyskind JW;
Xu HH;
                                                                                                                           Ohlsen KL,
Forsyth RA,
               Protein encoded by Prokaryotic essential gene #29404
                                                                                                                           Haselbeck R,
Yamamoto R,
                                                                                                                            Malone C,
Carr GJ,
                                                                                2001US-00815242.
2001US-00948993.
2001US-0342923P.
2002US-00072851.
                                                                     21-MAR-2002; 2002WO-US009107
                                                                                                      2002US-0362699P
                                     Staphylococcus haemolyticus
                                                                                                                 (BLIT-) ELITRA PHARM INC.
                                                                                                                            Zamudio C,
Trawick JD,
                                                                                                                                            WPI; 2003-029926/02
                                                                                                                                                 N-PSDB; ACA47747
                                                WO200277183-A2.
                                                                                      06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                21-MAR-2001;
                                                                                                      06-MAR-2002;
     19-JUN-2003
                                                          03-0CT-2002
                                                                                                                            Wang
Wall
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or screening

New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

The invention relates to an isolated nucleic acid comprising any one of the invention relates to an isolated nucleic acid comprising any one of the soll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid.

(2) a lost cell containing the the nucleic acid antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation, (8) identifying a gene preduct for cellular proliferation or the biological pathway in which a proliferation required gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) namifacturing an antiploid; (10) profiling a much contains an activity of the proliferation of an organism acts; (9) namifacturing an antiploid; (10) profiling a much contains an acts of the proliferation of an organism acts; (9) namifacturing an antiploid; (10) profiling a much contains and acts of the proliferation of an organism acts; (9) namifacturing an antiploid; (10) profiling a much contains and acts of the proliferation of an organism acts and acts of the proliferation of an organism acts and acts of the proliferation of an organism acts are accompanied to the proliferation of an organism acts and acts of the proliferation of an organism acts and acts of the proliferation of an organism acts and acts of the proliferation of an organism acts and acts of the proliferation of an organism acts and acts of the proliferation of an organism acts and acts of the proliferation of an organism acts and acts of the proliferation of an or compound's activity; (11) activities comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate micleules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Claim 25; SEQ ID NO 71801; 1766pp; English. ftp.wipo.int/pub/published_pct_sequences n electronic

ä Gaps 7 Indels 49.3%; Score 1280; DB 6; 52.1%; Pred. No. 2.8e-114; iive 80; Mismatches 152; Conservative Local Similarity es 255; Conserv Query Match Best Loca Matches

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P 426
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                                                              127 QRFLDYSKNLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFISDPK 186
                                                                                                          LVEILNYFIKYVGSSPYDAPALMNILPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVEI 246
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                                                                                                                                                                                           RLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNWEVIPAMEKLIRSPASBLKKMQR-F 305
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                                                                                                                                                                                                                                                       366 AQAPAGCEIIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTDLRQHIVTEBYWT 425
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                         63
QRVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPH
           184 LRDMLGYFIXYVGSSSYDAPAVLTLIHMOYEOGLWYVKGGIHKLAOALBOLAIBEGVAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 AA
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23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-0207777P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-025855P.
25-DEC-2000; 2000US-025855P.
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N-PSDB; AAS52059.
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Yamamoto RT,
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is a also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify antibodies capable of binding to the express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The proteins can be used to screen compounds in rational drug discovery programmes. The used to screen compounds in rational drug discovery programmes. The proteins can be used to screen compounds in rational proliferation in a wide variety of organisms. The present sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Wide at the propertices.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 QRVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPH
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New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                  Example 3; SEQ ID NO 5696; 511pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 205; Conservative
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ID ABM7
XX AC ABM7
XX DT 20-N
XX XX
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Antibacterial, fungicide, insecticide, polymorphism, genetic analysis, detection; food, gene expression; plant; animal; microorganism; toxin, antibiotic, biopesticide; virulence factor; disease model; plague;
                                                                                                                               Glaser P,
                                                                                07-FEB-2002; 2002WO-IB003040.
                                                                                            07-FEB-2001; 2001FR-00001659.
                                                                                                                 RECH
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 32.1%
Matches 158; Conservative
                                       Photorhabdus luminescens
                                                                                                                               Taourit S,
                                                                                                          (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT
                                                                                                                                                   WPI; 2003-148459/14.
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                       Sequence 494 AA;
                                                    WO200294867-AZ.
                         whooping cough.
                                                                                                                                       Búchrieser C;
                                                                  28-NOV-2002
                                                                                                                               Duchaud E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       128
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                  The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the geneme of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorphisms encoded by the genes are used for detection/identification of polymorphisms; for gene analysis and for a detection/identification. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, requires, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. cembraction of the proteins, particularly toxins and antibacterials useful as insectioides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens containing the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 FEALFTGAGKNMADYVQIQKVEPHWRNPPEDGSVIDLCEDAETQRRELDKLGPGTYAQFQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFLDYSKALCTETEAGYPAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFISDPKL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 IEELFTQAGKRMADYVDLLPVHPFYRLCWESGKMFDYDNDQQHLEAQIHTFNPRDVNGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFLDYSREAFNE---GYLKLGTVPFLSFROMLSAAPQLIRLHAWRSVYSQVARFIKDESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 VEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVEIR
                                                                                                                                                                                                                                                      Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 RVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPHI
                                                                                                                                                    Danchin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.4%; Score 713; DB 6; Length 494; 32.1%; Pred. No. 1.6e-59; tive 97; Mismatches 231; Indels
                                                                                                                                                    Kunst F,
                                                                                                                                                    Frangeul L,
                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 3220; 1205pp; French
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There are a total of six relevant genes in a 7900 bp region that cause B. coli cells to produce GGPP and the carotenoids phytoene through caxoanthin digliucoside, which is the final prod. identified in the carotenoid pathway contd. in plasmid paRG376 (contg. a ca. 13 kb chromosomal DNA fragenet isolated by Perry et al., J. Bacteriol., 168:607 (1986). The genes for geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene deranylgeranyl pyrophosphate (GGPP) synthase, phytoene devanthin glycosylase are represented in AAQ13716, AAQ13718, AAQ13719, AAQ13722, AAQ13724 and AAQ13726 are respectively. Recombinant expression plasmids can be used to produce large ants. of the enzymes and hence large ants. of the carotenoids which they synthesise. Carotenoids are pigments with a variety of applications.
                                                                                         364
                                                                                                                                                                                   PAGAPAGCELIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTDLROHIVTEEYW 424
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LDABVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLL-RSPA--SELKKMQR 304
                             300 KRMSNSLFVLYFGLNHEHTYQLAHHTVCFGPRYKELIEDIFYHDRLSEDFSLYLHAPSVTD
                                                                                                                                                                                                                 PSLAPRGCASYYVLAPVPHLGTANLNWDIEGFRLRDRIFAYLBKYYWPGLLKQLVVHRIF
                                                                                                                                                                                                                                                                                                           305 FEPSCSGLVLHLGVDRLYPQLAHENPPYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKTD
                                                                                                                                                                                                                                                                             TPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPMVTLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGPP; carotenoid; phytoene; zeaxanthin; lycopene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR13985 standard; protein; 489 AA.
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90US-00525551.
90US-00562674.
91US-00662921.
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25-MAR-2003
26-NOV-1991
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18-MAY-1990;
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(STAD ) AMOCO CORP

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                                                                                                                                                                                                                                                                                                                                                                                       DPKLVEIINYFIXYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEKLAVELG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKIDDAQAPAGCBIIKILPHIDPDKLLITAEDYSALRERVLVKLERMGLTDLRQHIVT 420
                                                                                                                                                                                                                                                                         67 IFEALFTGAGKAMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQF 126
                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                            ORFLDYSKALCTETEAGYFAKG---LDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFIS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEYWTPLDIOAKYYSNOGSIY-----GVVADRFKNLGFKAPORSSELSNLYFVGGSV 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRIFTRQTSRHAWIAILGSLFIEPPSLTQGLFA------ANATRHSNLYLVAAGT 464
                                                                                                                                                                                         99
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                                                                                                                                                                                                                  62 ALEALFTLAGRRMEDYVALLPVKPFYRLCMESGKTLDYANDSFELBAQITQFNPRDVEGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KWORFEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPT1YLVAP
                                                                                                                                                                                       7 ORVIVIGAGIGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPH
                                                                                                                                                 Gaps
                                                                                                                                               31;
                                                                                                         489;
                                                                                                    Query Match 27.1%; Score 703.5; DB 2; Length Best Local Similarity 32.9%; Pred. No. 1.3e-58; Matches 166; Conservative 96; Mismatches 212; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (E. vulneris - ATCC 39368)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|| |:| | ; | | ; | | ; | | 465 HPGAGIPGVVGLAESTASLMIEDLQ 489
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(first entry)
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                                                                Sequence 489 AA;
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25-MAR-2003
26-NOV-1991
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18-MAY-1990;
03-AUG-1990;
28-FEB-1991;
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There are a total of six relevant genes in a 7900 bp region that cause E. coli cells to produce GGPP and the carotenoids phytoene through zeaxanthin diglucoside, which is the final prod. identified in the carotenoid pathway confd. in plasmid pARG376 (cong. a ca. 13 Kb chromosomal DNA fragment isolated by Perry et al., J. Bacteriol., 168:607 (1986). The genes for geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene dehydrogenase-4H, lycopene cyclase, beta-carotene hydroxylase, and zeaxanthin glycosylase are represented in AAG13718, AAG13719, AAG13722, AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and AAG13724 and
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                                                                                                                                                                                      Biosynthesis of carotenoid(s) in genetically engineered hosts encoding enzymes from Erwinia herbicola.
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                                            Yarger
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27.1%; Score 703.5; DB 2; Length 4
Best Local Similarity 32.9%; Pred. No. 1.3e-58;
Matches 166; Conservative 96; Mismatches 212; Indels
                                            Proffitt JH,
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                                            Mukharji I,
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N-PSDB; AAQ13719.
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                                            Ausich RL,
Yen HC;
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Increasing prodn. of total carotenoid(s) in a higher plant - by transforming with vector encoding chloroplast transit peptide operably linked to the Erwinia herbicola lycopene cyclase structural gene. GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene; phytoene dehydrogenase-4H; carotenoid; C40; zeaxanthin; diglucoside; pigment; food colourant; chloroplast transit peptide; increase yield; tobacco ribulose bis-phosphate carboxylase-oxygenase. Brinkhaus FL, Proffitt J, Mukharji I, Yarger J; Phytoene dehydrogenase-4H encoded on pARC146D. Example 12; Col 97-100; 99pp; English Ą 489 90US-00487613. 90US-0052551. 90US-00562674. 91US-00662921. 91US-00785566. 93US-00095726 AAW01123 standard, protein; (first entry) (revised) (revised) WPI; 1996-308823/31. N-PSDB; AAT40793. Pantoea agglomerans (STAD ) AMOCO CORP. Sequence 489 AA; 03-AUG-1990; 28-FEB-1991; 30-OCT-1991; 16-OCT-2003 25-MAR-2003 11-DEC-1996 21-JUL-1993; 02-MAR-1990, 18-MAY-1990, US5530188-A 25-JUN-1996 RL; AAW01123; Yen HB, Ausich R 

The present sequence is that of a recombinant Erwinia herbicola phytoene dehydrogenase-4H (from pARC146D) which produces lycopene biosynthetically from phytoene through four sequential dehydrogenations coher cardinal phytoene through four sequential dehydrogenations. Other caranylgeranyl pyrophosphate (AAW01119), phytoene synthase (W01121) and lycopene cyclase (AAW01125). Manipulation of, in partic., lycopene (AAW01125), by in frame linkage to the chloroplast transit peptide (AAW01124) of the tobacco ribulose bis-phosphate carboxylase-cyclase gene can lead to increased production of total carotenoids in the chloroplast of transformed plants as compared to native, nontransformed plants of the same type. Beta-carotene is an effective and apparently harmless food colourant and is also in the pathway for biological synthesis of further C40 carotenoids such as zeaxanthin and zeaxanthin diglucoside. (Updated on 25-MAR-2003 to correct PP field.)

œ Query Match 27.1%; Score 703.5; DB 2; Length 489; Best Local Similarity 32.9%; Pred. No. 1.3e-58; Matches 166; Conservative 96; Mismatches 212; Indels 31; Gaps

61 7 QRVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKINIMTKDGFTFDLGPSILIMPH

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67 IFEALFTGAGKOMMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQF 126 121 ALEALFTLAGRRMEDYVRLIPVKPFYRLCWESGKTLDYANDSFELEAQITQFNPRDVEGY

420 415 244 VEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRS-PASELK-- 300 360 355 236 GEIELMARVEELVVADNRVSGVRLADGRIFDTDAVASNADVVNTYKKLLGTIPVGQKRAA 295 421 BEYWTPLDIQAKYYSNOGSIY-----GVVADRFKNLGFKAPQRSSBLSNLYFVGGSV 472 464 E. herbicola, geranylgeranyl pyrophosphate synthase, pARC376, GGPP synthase; biosynthesis, carotenoid; lycopene; farnesyl pyrophosphate; phytoene; FPP; isopentyl pyrophosphate; IPP; tail to tail dimerisation; phytoene synthase; phytoene dehydrogenase-4H; food colourant; herbicide; norflurazon. 296 RLERKSMSNSLFVLYFGLNQPHSQLAHHTICFGPRYRELIDEIFTGSALADDFSLYLHSP KMORFEPSCSGLVLHLGVDRLYPOLAHENFFYSDHPREHFDAVFKSHRLSDDPTIYLVAP ORFLDYSMILCTETRAGYFAKG---LDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFIS DEHLRQAFSFHSILVGGNPFTTSSIXTLIHALERBWGVWFPEGGTGALVNGWVKLFTDEG 361 CKTDPAQAPAGCELIKILPHIDPDKLLTAEDYSALRERVLVKLERMGLTDLRQHIVT DPKLVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEKLAVBLG - used for DNA encoding Brwinia herbicola phytoene debydrogenase-4H - used prodm. of lycopene, and to produce transgenic plants resistant norflurazon. Phytoene dehydrogenase-4H encoded by DNA derived from pARC146D. Yarger Proffitt J, Mukharji I, 497 489 473 NPGGGMPMVTLSGQLVRDKIVADLQ AAW00174 standard; protein; 489 AA 90US-00487613. 90US-00525551. 90US-00562674. 91US-00662921. 91US-00785568. 93US-00096043. (first entry) Brinkhaus FL, (revised)
(revised) WPI; 1996-308824/31 Pantoea agglomerans (STAD ) AMOCO CORP N-PSDB; AAT37095 18-MAY-1990; 03-AUG-1990; 28-FEB-1991; 22-JUL-1993; 02-MAR-1990; 30-0CT-1991; Yen HB, b. 16-OCT-2003 25-MAR-2003 17-0CT-1996 US5530189-A 25-JUN-1996 AAW00174; 301 184 176 127 RESULT 14 AAW00174 요 셤 Š 셤 음 유 셤 à 엄 à 8 Š à

Example 4; Fig 15; 87pp; English.

Brwinia herbicola phytoene dehydrogenase-4H.

This sequence represents Erwinia herbicola phytoene dehydrogenase encoded by DNA from the plasmid pARC146D. Phytoene dehydrogenase is an enzyme which is involved in the biosynthesis of carotenoids, esp. lycopene, from the ubiquitous precursor, farmesyl pyrophosphate. In B. harbicola, phytoene has been found to be formed biosynthetically in a two-step process. The initial step is the condensation of farmesyl pyrophosphate (FPP) and isopentyl pyrophosphate of form GGPP. This reaction is catalysed by GGPP synthase. This first step is immediately followed by a tail to tail dimerisation of GGPP, catalysed by the enzyme phytoene synthase, to form phytoene dehydrogenase-4H. The genes encoding catalytic action of phytoene dehydrogenase-4H. The genes encoding a host call for the commercial production of lycopene which is used as a food colourant. Plants transformed with the phytoene dehydrogenase-4H coding sequence are protected from the herbicide norflurazon. (Updated on 25-WAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise

Sequence 489 AA;

295 360 420 126 243 244 VEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLIRS-PASELK-- 300 355 464 QRFLDYSKNLCTETEAGYFAKG---LDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFIS 183 EEYWTPLDIQAKYYSNQGSIY-----GVVADRFKNLGFKAPORSSELSNLYFVGGSV 472 99 61 236 GEIELNARVEELVVADNRVSQVRLADGRIFDTDAVASNADVVNTYKKLLGTIFVGQKRAA 2 EKTVVIGAGFGGLALAIRLQAAGIPTVLLEQRDKPGGRAYVWHDQGFTFDAGFTVIDPT YMORFEPSCSGLVLHLGVDRLYPQLAHINFFYSDHPREHFDAVFKSHRLSDDPTIYLVAP RIERKSMSNSLFVLYFGLNQPHSQLAHHTICFGPRYRELIDBIFTGSALADDFSLYLHSP QRVIVIGAGLGGLSAAISLATAGFSVQLIBKNDKVGGKLNIMTKDGFTFDLGPSILTMPH 67 IPEALFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETORRELDKGPGTYAQF ALEALFTLAGRRMEDYVRLLPVXZPFYRLCWESGKTLDYANDSFELEAQITQFNPRDVEGY 184 DPKLVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEKLAVRLG CKTDPAQAPAGCELIKILPHIDPDKLLTAEDYSALRERVLVKLERMGLTDLRQHIVT 356 CVTDPSLAPPPCASFYVLAPVPHLGNAPLDWAQEGPKLRDRIFDYLEERYMPGLRSQLVT Gaps 31, 27.1%; Score 703.5; DB 2; Length 489; 32.9%; Pred. No. 1.3e-58; ive 96; Mismatches 212; Indels 31 : :| : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 473 NPGGGMPMVTLSGQLVRDKIVADLQ 497 al Similarity 32.9% 166; Conservative 301 296 1 361 62 127 421 Query Match Local Best Loca Matches

AAW32475 standard; protein; 489 (revised)
(revised)
(first entry) 17-0CT-2003 25-MAR-2003 15-JAN-1998 AAW32475; ESULT 15

KMORFEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAP 360

301

244 VBIRLDAEVSEIQKODGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRS-PASELK--

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A novel DNA molecule has been isolated which encodes an Erwinia herbicola lycopene cyclase enzyme that converts lycopene to beta- carotene. The DNA molecule comprises at least 1125 bp and is present in the plasmids pARC1510; pARC1510 and pARC1520. The present sequence represents the amino acid sequence corresponding to the structural gene for phytoene fehygrogenase-4H. The new DNA molecule can be used to produce the recombinant enzyme and transgenic organisms, e.g. yeasts or plants, increased beta-carotene levels. Beta- carotene is used as a colourant in margarine and butter and as an intermediate for vitamin A, and may prevent cancer. (Updated on 25-MAR-2003 to correct PP field.) (Updated on 17-OCT-2003 to standardise OS field) J Brwinia herbicola lycopene cyclase - for producing enzyme, and transgenic organisms with increased beta-carotene 126 121 QRFLDYSKOLCTETEAGYFAKG---LDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFIS 183 243 Geranylgeranyl pyrophosphate synthase; Erwinia herbicola; GGPP; lycopene cyclase; recombinant enzyme; transgenic organism; beta-carotene; yeast; plant; vitamin A; cancer. 99 61 7 QRVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPH 2 EXTVVIGAGEGGLALAIRLOAAGIPFVLLEGRDKPGGRAYWHDQGFTFDAGFTVITDPT 67 IPEALFTGAGKNMADYVQIQKVEPHWRNPFEDGSVIDLCEDAETORRELDKLGPGTYAQF 62 ALEALFTLAGRRABDYVRLIPVKPFYRLCWESGKTLDYANDSPELBAQITQFNPRDVEGY 184 DPKLVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMBKLAVELG 31; 27.1%; Score 703.5; DB 2; Length 489; 32.9%; Pred. No. 1.3e-58; ive 96; Mismatches 212; Indels 31. Yen Ausich RL, Yarger J, Disclosure, Fig 15, 102pp, English. 90US-00487613. 90US-00525551. 90US-00562674. 91US-00662921. 95US-00473512. 93US-00095726 Proffitt J, 166; Conservative DNA encoding Erwinia WPI; 1997-414592/38. Pantoea agglomerans CORP. Similarity N-PSDB; AAT91546 Sequence 489 AA; (STAD ) AMOCO Mukharji I, | Brinkhaus FL; 21-JUL-1993; 07-JUN-1995; USS656472-A. 03-AUG-1990; recombinant 02-MAR-1990, L8-MAY-1990, L2-AUG-1997 28-FEB-1991 127 122 Query Match Local Best Loca Matches d Š g 셤 ò ð  $\delta$ ద

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   DGYEQFMEQERKRFNALYPCITRDYSSLKSFLSLDLIKALPWLAFPKSVFNVLGQYFNQE 180
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PRODOM: PD139017; PHYLD dehydro; 1.
Hypothetical protein; Complete proteome,
SEQUENCE 490 AA; 55998 MM; 922937F84COBC3F8 CRC64;
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InterPro; IPR000759; Adrndx reductase.
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                                                                                                                                          65 VLDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVYSDRENWRAELORVFDEGTDGYE
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein lin0999.
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InterPro; IPR000759; Adrndx reductase.
InterPro; IPR008151; Phytn_dehydro.
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X MEDLINE=99061957; PubMed=9843979;

X Xiong J., Incue K., Bauer C.E.;

Tracking molecular evolution of photosynthesis by characterization of a major photosynthesis gene cluster from Heliobacillus mobilis.";

Proc. Natl. Accad. Sci. U.S.A. 95:14851-14856(1998).

E EMBL; AFC80002; AAC84034-1; -..

R GO; GO:0016491; Foxidoreductase activity; IEA.

R GO; GO:0016491; Foxidoreductase activity; IEA.

R GO; GO:0016491; Pesidoreductase.

R GO; GO:001818; Pielectron transport; IEA.

R InterPro; IPR002937; Amino _xidase.

R InterPro; IPR00295; AAby NAD BS.

R InterPro; IPR001851; Phyfn_dehydro.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
101-OCT-2003 (TrEMBLrel. 25, Last annotation update)
101apophytoene dehydrogenase CrtN.
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                                        Hypothetical protein; Complete proteome.
SEQUENCE 488 AA; 55685 MW; P60D539D3C1D49EB CRC64;
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ProDom; PD139017; Phytn_dehydro; 1
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                                                                                                                                                                                 517;
                                                                                                                                                                           Query Match 32.6%; Score 883.5; DB 2; Length Best Local Similarity 35.2%; Pred. No. 4.9e-59; Matches 174; Conservative 117; Mismatches 194; Indels
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01-UTN-2003 (TrEMBirel. 24, Last sequence update)
01-UTN-2003 (TrEMBirel. 24, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
Squalene synthase (EC 1.3.-).
CRTM OR LP 3262.
Lactobacillus plantarum.
Bacteria, Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus pism.
InterPro; IPR001100; Pyr_redox.
Pfam; PP01593; Amino oxidase; 1.
PRINTS; PR00419; ADXEDTASE.
PRINTS; PR00411; PRNEDEDTASE.
ProDom; PD139017; Phytn dehydro; 1.
SEQUENCE 517 AA; 58340 MW; BB933977999C4587 CRC64;
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STRAIN=NCIMB 8826 / WCFS1;
MEDLINB=22480296; PubMed=12566566;
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L----VCGKLVSEQ 495
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                                                                                                                              KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFLLMKG
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MEDGINE=2195285; PubMed=11759840;

KADEINE=2195285; PubMed=11759840;

KADEINE=2195285; PubMed=11759840;

KADEINE=2195285; PubMed=11759840;

KADEINE=2195285; PubMed=11759840;

MATABRA T., KADEINE M., MATSHUROTO M., MATSHURO A., MURAKI A.,

KISHIGA Y., KOADERA M., MATSHUROTO M., TARAZAWA M., Yamada M.,

YASHAZAKI N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

YASHO M., Tabata S.,

"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";

EMBL; AP003600; BAB78339.1; -.
                                                                                                       æ
                                                                              Query Match

29.8%; Score 808; DB 16; Length 498;
Best Local Similarity 34.4%; Pred. No. 2.8e-53;
Matches 168; Conservative 109; Mismatches 204; Indels
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Plasmid pCC7120alpha.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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Last annotation update)
                                                         C12B1FF421DEB31B
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000759; Adrndx_reductase.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00419; ADXRDTASE.
SEQUENCE 498 AA; 56453 MW; C12B1FF421DEB31B
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2003 (TrEMBLrel. 24,
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PIR; S43124; S43324.

GO; GO:0006118; P:electron transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Gaps
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01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.UN-2003 (TrEMBLrel. 24, Last annotation update)
26ta-carotene desaturase.
Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostoca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
29.3%; Score 794.5; DB 16; Length
Best Local Similarity 35.4%; Pred. No. 3e-52;
Matches 177; Conservative 102; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56658 MW; BC4072FACE5E016B
PIR; AG2509; AG2509.

GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000759; Adrndx reductase.
InterPro; IPR00151; Phytn_dehydro.
PRINTS; PR00419; ADXBDTASE.
ProDom; PD139017; Phytn_dehydro; 1.
Plasmid; Complete proteome.
SEQUENCE 499 AA; 56558 MW; BC4072FACESB016;
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MEDLINE=94154256; PubMed=8111038;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                          122 FDRWYSEHIRKYELGYKPYLAGPARSIFGYLRPDDLMKELSFRFW----BNLYQHFWRFF 177
                                                                                                                                                                                                                                                                                                                                                                                                                             298 ENLKOREYSCSTFMLYLGLDKIY-DLPHHTIVFAKDYTTNIRNI----FDNKTLTD-DFS 351
                                                                                                                                                                                                 64 GVLDEMFELCERRSEDYLEFLPLSPMYRL-LYDDRDIFVYSDRENMRAELORVFDEGTDG 122
                                                                                                                                                                                                                                                        123 YEQEWEQERKRFNALY-PCITRDYSSLKSFLSL-DLIKAL---PWLAFPKSVFNNLGQYF 177
                                                                                                                                                                                                                           HLYKELFERAGLNFADYVQLKRLEPYTRLKFWDGTQLDITSDLQSFKTQLATLRSDLPLA 121
                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                               178 NOEKWRLAFCFOSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAEN
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                                                                                                                                                                     2 SKKVAIVGAGPGGLATAIRLAGLGYQVEIFEAAERVGGRWRGFEVDSYAFDTGPTILQLP
                                                                                                                                        4 TKHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHABIGGRNRPINMNGFTFDTGPFFLLMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A. STAIN / JCM 11309;
STRAIN=HTEB31 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus ineyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                Gaps
                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBL_TaxID=182710;
                                                                                    DB 2; Length 499;
                                                                                 Query Match 28.9%; Score 783.5; DB 2; Length Best Local Similarity 35.0%; Pred. No. 2.1e-51; Matches 175; Conservative 103; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phytoene dehydrogenase (phytone desaturase) (BC 1.3.-).
InterPro; IPR000759; Adrndx reductase.
InterPro; IPR08151; Phytn Gehydro.
PRINTS; PR00419; ADXEDTASE.
PRINTS; PR00419; Phytn dehydro; 1.
SEQUENCE 499 AA; 56743 MW; ACICP06F745B4D34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP004601; BAC14417.1; -. GO: 0016491; F: oxidoreductase activity; IEA. GO; GO:0006119; F: oxidoreductase activity; IEA. GO; 00:0006119; P: electron transport; IEA. InterPro; IPR00759; Adradx reductase. InterPro; IPR002937; Amino_oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     511 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 TSMEKLFLELGGTIHYNSPVEKVIIEKKKATGIKLEN-LEINADYVVCNADFPYSMKNLI 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 DEIDEFKGIKDEVISETYMTPLDFESKFNAYNGACFGLRPTLSGSNHLRPQSKAKNCENL 468
                                                                                                                                                                                                                                                                                                                                                                                                                                        288 KPGVLK-KYTPENLKQREYSCSTFMLYLGLDKIYDLƏH--HTIVFAKDYTTNIRNIFDNK 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 GARLGLSDIRAHIECEKIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELANC 462
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Beja O., Suzuki M.T., Heidelberg J.P., Nelson W.C., Preston C.M.,
Hamada T., Eisen J.A., Fraser C.M., DeLong B.F.;
"Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
Nature 415:630-633(2002).
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                                                                                                                                                                                                                                                                              5 KHIIIVGAGBGGLCAGMLLSQRGFKVSIFDKHABIGGRNRPINMMGFTFDTGPTFLLMKG
                                                                                                                                                                                                                                                                                                                    65 VLDEMPELCERRSEDYLEFLPLSPMYRLLY----DDRDIFVYSDRENMRAELORVFDEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DGYEQEMEQERKRENALYPCITRDYSSLKSFLSLDLIKALPWLAR-PKSVFNNL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 AAMAQVIAENGGEIHLMSEIESLIIENGAAKGVKLQHGAELRGDEVIINADFAHAMTHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITDDFSFYVQNASASDDSLAPAGKSALYVLVPMPN-NDSGLDW-QAHCQNVREQVLDTL
                                                                                                                                                                Ouery Match 27.3%; Score 739.5; DB 16; Length 511; Best Local Similarity 32.6%; Pred. No. 5e-48; Matches 167; Conservative 110; Mismatches 198; Indels 37;
InterPro; IPR000205; NAD BS.
Pfaz; PF01593; Amino oxidase; 1.
PRINTS; PR00419; ADXEDTASB.
Oxidoreductase; Complete proteome.
SEQUENCE 511 AA; 58463 MW; 8E70FD9F71D406AB CRC64;
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Last annotation update)
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NCBI_TaxID=153809;
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EMBL; AE008921; AAM48646.1; -.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:000958; P:biosynthesis; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro: IPR002397; Amino oxidase.
InterPro: IPR008150; Bac_phytoene_dh.
InterPro: IPR008150; Bac_phytoene_dh.
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(TrEMBLrel. 22, L
(TrEMBLrel. 25, L
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SEQUENCE FROM N.A.
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01-OCT-2003
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24 ;

Length 513;

CRC64

63 83 126

EMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVYS - DRENMRAELORVFDEGTDGYBOP

68

127 MEQERKRENALYPÇITRDYSSL--KSFLSL-DLIKALP-----WLAFPKSVFNNLGQY

8 IIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFLLMKGVLD  177 FNQEKMELAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAE 193 LKHPKIRIAMSLQSLIIGGNPFSVTSNYALVNALERQWGVHWAMGGTGBLIRGLVDVFBG

176

296 312 355

356 NASASDDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHI 

297 PENLKQREYSCSTFMLYLGLDKIY-DLPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQ

NGCRIHLINSKIESLIIENGAAKGVKLOHGAELRGDEVIINADFAHAMTHLVKPGVLKKYT

ECEKIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELANCYLVGGGTHPGSGL 475

432 RVSFCITPLDFQHRLLSYKGAGFGLEPLILQSAYFRPHNRSEDVKVLFMVGASTHPGAGV

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491

415 431

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Ouery Match
26.8%; Score 726; DB 2; Length 51
Best Local Similarity 32.6%; Pred. No. 5.4e-47;
Matches 159; Conservative 97; Mismatches 208; Indels
InterPro; IPR008150; Bac_phytoene_dh.
InterPro; IPR002051; NDB BS.
InterPro; IPR00151; Phytn dehydro.
Pfam; PP01593; Amino_oxidase; 1.
ProDom; PD139017; Phytn dehydro; 1.
PR0517; Phytn dehydro; 1.
PR0517; Phytn StyroRnE DH; 1.
SEQUENCE 513 AA; 57074 MW; 9C46447BB02F6B2D
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LKDSQXRYIIGYBGMVAEPMIRLWETLKVLPTFAMIRA-----DRSIYGLAARRVKDER
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-DUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT--2003 (TrEMBLrel. 25, Last annotation update)
Phytoene dehydrogenase.
CRTI.
Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
Rhodocyclus kubitytyax.
NTBL-TaxID=28068;
                                                                                                                      26;
                                                                                           Length 514;
                                                                                           Query Match 26.9%; Score 729; DB 2; Lengtn 51
Best Local Similarity 32.2%; Pred. No. 3.2e-47;
Matches 160; Conservative 101; Mismatches 210; Indels
    InterPro; IPR008151; Phytn. dehydro.
Pfam; PF01593; Amino oxidase; 1.
Probom; PD139017; Phytn. dehydro; 1.
PROSITE; PS00982; PHYTOENE DH; 1.
SEQUENCE 514 AA; 56824 WW; D5177500CAB56773 CRC64;
                                                                                        26.9%; Score 729; DB 2; 32.2%; Pred. No. 3.2e-47;
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Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
Bacteria, Proteobacteria; Betaproteobacteria; Burkholderiales;
Comamonadecee; Rubrivivax.
NCBI_TaxID=28068;
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PGVIMSAK 499
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SEQUENCE FROM N.A.
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Positive

Ouchane S., Steunou A.-S., Astier C.,
"Photosynthesis Gene Regulation in Rubrivivax gelatinosus:
Transcription Pactor PpsR is Involved in both Negative and
Control.";

FROM N.A.

[1] SEQUENCE PRO STRAIN=S1;

Control.";
submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
Submittal XY234385; AA093135.1; -.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR002937; Amino_oxidase.

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STRAIN=1144;

MEDLINE=20031519; PubMed=10563807;

MEDLINE=20031519; PubMed=10563807;

MEDLINE=20031519; PubMed=10563807;

MEDLINE=20031519; PubMed=10563807;

Parct P., Vermeglio A.;

"Dark aerobic growth conditions induce the synthesis of a high midpoint protential cytochrome c8 in the photosynthetic bacterium T whorivivax gelatinosus.";

EMBL; AB054704; BA54963.1;

EMBL; AB054704; BA54963.1;

CO; GO:0016491; F:oxidoreductase activity; IEA.

R O; GO:000581; P:biosynthesis; IEA.

R O; GO:000581; P:biosynthesis; IEA.

R O; GO:000581; P:biosynthesis; IEA.

R InterPro; IPR008150; Manino oxidase.

InterPro; IPR008150; Manino oxidase.

R InterPro; IPR008151; Phytnidehydro.

P Fam; PF01593; Amino oxidase; 1.

P ProDom; PD139017; Phytnidehydro.

R PROSITE; PS00982; PHYTOREE FII.

P PROSITE; PS00982; PHYTOREE FII.

R SEQUENCE 511 AA; 56818 WW; 9E64897196033903 CRC64;
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             Nagashima K.V., Matsuura K., Ohyama S., Shimada K.; "Primary structure and transcription of genes encoding B870 and photosynthetic reaction center apoproteins from Rubrivivax
                                                                                                                                                                (In) Garab G. (eds.);
Photosynthesis:
mechanisms and effects (Proceedings of the 11th international or
on photosynthesis), pp.4:2889-2892, Kluwer Academic Publishers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                    gelatinosus.";
J. Biol. Chem. 269:2477-2484(1994).
(1) Biol. Chem. 269:2477-2484(1994).
SEQUENCE FROM N.A.
STRAIN=IL144;
Igarashi N., Shimada K., Matsuura K., Magashima K.V.;
"Photosynthetic gene cluster in purple bacterium, Rubrivivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 511;
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MEDLINE=94132007; PubMed=8300574;
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Garab G. (eds.);
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SEQUENCE FROM N.A.
                                                                                                                                                        gelatinosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oracyrnizobium sp. ORS278.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=114615;
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EMBL; AF218415; AAF78201.1; -. GO; GO:0016491; Froxidoreductase activity; IEA.

GO; GO:00016491; Froxidoreductase activity; IEA.

GO; GO:0000518; F: biosynthesis; IEA.

GO; GO:0006118; P: biosynthesis; IEA.

InterPro; IPR008150; Paino oxidase.

InterPro; IPR008150; Phyfn dehydro.

Pfam; PF0153; Amino_oxidase; 1.

ProDom; PP019917; Amino_oxidase; 1.

ProDom; PP019917; Phyfn dehydro.

PROSITE; PS01982; PHYTOENE DH; 1.

PROSITE; PS01982; PHYTOENE DH; 1.

SEQUENCE 506 AA; 56223 WW; 435F949E6FDBEED3 CRC64;
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26.7%; Score 723; DB 2; Length 50
Best Local Similarity 31.5%; Pred. No. 9e-47;
Matches 158; Conservative 107; Mismatches 224; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                             412 RAHIBCEKIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELANCYLVGGGTHP 471
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                                                                                                                  294 KYTPENLKQREYSCSTFMLYLGLDXIYD-LPHHTIVFAKDYTTNIRNIFDNKTLTDDFSF
                                                                                                                                                                                                                                 353 YVQNASASDDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQVLDTLGARLGLSDI
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Byphomicrobiaceae; Xanthobacter.
Hyphomicrobiaceae; Xanthobacter.
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(TremBLrel. 19, Last sequence update)
(TremBLrel. 24, Last annotation update)
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361 HAPSVTDPSLAPQGCSTYYVLSPVPHLAAAPIDWSVBGPRYRDRILDYLRARI-LPGLKS 419
                                                                                                                        420 DLATCRIFTPQDENTELNAHLGSAPSLBPILIQSAYFRAHNADDKIKGLYLVGAGTHPGA 479
                                                                                       HIECEKIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELANCYLVGGGTHPGS 473
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TO K.Y., Lai E.M., Lee L.Y., Lin T.P., flung C.H., Chen C.L.,
To K.Y., Lai E.M., Lee L.Y., Lin T.P., flung C.H., Chen C.L.,
Thang Y.S., Liu S.T.;
"Analysis of the gene cluster encoding carotenoid biosynthesis in
Erwinia herbicola Ehol3.";
Microbiology 140:331-339(1994).
EWHL; M90698, AAA21263.1;
PIR; SS2586; SS2586.
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Enterobacteriaceae; Pantoea.
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GO: GO:0009058; P:biosynthesis; IEA.
GO: GO:0009058; P:biosynthesis; IEA.
GO: GO:000918; P:biosynthesis; IEA.
InterPro: IPR00293; Amino_oxidase.
InterPro: IPR008150; Bac_phytoene_dn.
InterPro: IPR008151; Phytn dehydro.
Pfam; PF01593; Amino_oxidase; 1.
ProDom; PD139017; Phytn dehydro; 1.
PROSTIE; PS00982: PHYTORE DH; 1.
SEQUENCE 492 AA; 55010 WW; 2D6551A2A32D0635 CRC64;
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MEDLINE=93371414; PubMed=8395826;
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01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
Phytoene dehydrogenase.
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Best Local Similarity
Matches 158; Conserv
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                                                                   353 YVQNASASDDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQVLDTIGARLGLSDI 411
                                                                                                                                                         RAHIECEKII TPOTWETDEHVYKGATFSLSHKFSOMLYWRPHNRFBELANCYLVGGGTHP
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                                                       QREYSCSTEMLYLGLDKIYD-LPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQNASAS 360
                                                                                 KTRHSMSLEVIYFGARRIWDHLQHHTVLFGPRYRGLVDBIFKGPNLPDDFSLYIHAPIVT 366
                                                                                                                                             DDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIECER 419
                                                                                                                                                                  IITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELANCYLVGGGTHPGSGLPTIY 479
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             RLISPVDRIVVEGORATAVKLKSGETLPFDLVASNADVVHTYRHLLRGAARGRSEGARLA 306
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T 01-Max-20...
T 01-Max-20...
T 01-OCT-2003 (TrEMBLrel. 25, Las. ...
E Phytoene desaturase.
C CTT-2003 (TremBlrel. 25, Las. ...
S Partoes stewartii.
S Partoes stewartii.
C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
C Enterobacteriaceae; Pantoea.
X NCBI_TaxID=66269;
X ...
Y A. ...
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deSouza M.L., Kollmann S.R., Schroeder W.A.;
carotenoid Blosynthesis (WO 02/079395 A2).";
submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY166713, AAN85599.1; -.
GO, GO:0009058; P:biosynthesis; IRA.
GO, GO:0009058; P:biosynthesis; IRA.
GO, GO:000518; P:electron transport; IRA.
InterPro; IRR008150; Bac phytoene_dh.
Rem; PRO1593; Amino_oxidase.
InterPro; IRR008150; Bac phytoene_dh.
REM; PRO1593; Amino_oxidase.
REM; PROSITE; PS00982; PHYTOENE_DH; I.
SEQUENCE 492 AA; 54836 MW; RJOCD224547A5FBA CRC64;
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25.9%; Score 703.5; DB 2; Length 4
Best Local Similarity 31.7%; Pred. No. 2.7e-45;
Matches 158; Conservative 105; Mismatches 210; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLMKGVLDEMFELCERRSEDYLEPLPLSPMYRL-LYDDRDIFVYSDRENMRAELQRVFDE 118
                                                                                                                                                                                                      119 GTDGYEQFMEQERKRFNALYP---CITRDYSSLKSFLSLDLIKALPWLAFP-----KS 168
                                                                                                                                                                                                                                                                                                                                                                                127 QASALRQWMƏDGREXYGIAYQKFICTSAD------NLGYYAPWRLAPTLRFKPWQT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 VFNNLGQYFNQEKMRLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 AMAQVIAENGGEIHLNSEIESLIIENGAAKGVKLOHGAELRGDEVIINADFAHAMTHLV- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 ---KPGVLKKYTPENLKQREYSCSTFMLYLGLDKIY-DLPHHTIVFAKDYTTNIRNIFDN 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :::| || || :| || || 355 RHVDLEDPPFYVCNPGVTDPSGAPAGHSTLYVLVPTPNTGRPVDWVKTEQALRERIPAML 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GARIGESDIRAHIECEKIITPQTWETDEHVYKGATPSLSHKFSQMLYWRPHNRFEELANC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415 - 3KVGLKGVREHIRBERYFTAETWRDDFNVFRGAVFNLSHTWLQLGPLRPKVKNRDIBGL 473
                                             | SVEHVIVVGAGPGGLSAAINLAGQGFRVTVVEXDAVPGGRWKGLTLGASGEYAVDTGPSI 66
8
NTXHIIIVGAGPGGLCAGMLLSQRGFKVSIFDXHAEIGGRNRPINMNG---FTFDTGPTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 KTL-TDDFSFYVQNASASDDSLAPAGKSAL,YVLVPMPNNDSGLDWQAHCQNVREQVLDTL
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A cluster of structural and regulatory genes for light-induced carotemogenesis in Myzococcus xanthus.";

Bur. J. Blochem. 233:238-248(1995).
-!- FUNCTION: This enzyme converts phytoene into zeta-carotene via intermediary of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11' positions of phytoene.
-!- COFACTOR: FAD (Probable).
-!- COFACTOR: FAD (Probable).
-!- COFACTOR: FAD (Probable).
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
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Cystobacterinae; Myxococcaceae; Myxococcus.
NCBI TaxID=34;
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1-0c7-1996 (Rel. 34, Last sequence update)
28 FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14,99.-) (Phytoene desaturase)
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MEDLINE=96061955; PubMed=7588751;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 EQFWEQERKRF-NALYPCITRDYSSLKSFLSLDLIKALPWLAPPKSVFNULGQYFNQBKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 LNSEIESLIIENGAAKGVKLQHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTPENLKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 REYSCSTEMLYLGLDKIY-DLPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQNASASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 DSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIBCE-KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 ITPQTWETDEHVYKGATPSLSHKFSQMLYWRPHNRFEELANCYLVGGGTHPGSGLPTIYB
                                                                                                                                                                                                                                                                                                                                            5 KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHARIGGRNRPINMNGFTFDTGPTFLLMKG
                                                                                                                                                                                                                                                                                                                                                                                                                        65 VLDEMFELCERRSEDYLEFLPLSPMYRLLYDDR-DIPVYSDRENMRAELORVFDEGTDGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 RLAFCFOSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAENGGEIH
                                                                                                                                                                                                                                                                                                        Gaps
R PIR; 532169; S32169.
R InterPro; IRR000759; Adrndx reductase.
R InterPro; IRR0012937; Amino_oxidase.
R InterPro; IRR001205; Bac_phytcone_dh.
R InterPro; IRR001816; Phytn_dehydro.
R R InterPro; IRR001816; Phytn_dehydro.
R PRINTS; PR00419; ADXRDTASE;
R PRODOM; PD139017; Phytn dehydro; I.
R PROSITE; PS00982; PHYTOENE_DH; I.
W Carotenoid biosynchesis; Oxidoreductase; FAD; Flavoprotein; NAD.
III 444
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01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
                                                                                                                                                                                                                                                                   Length 517;
                                                                                                                                                                                                                                                               Query Match
29.3%; Score 794; DB 1; Length 51
Best Local Similarity 35.8%; Pred. No. 4.7e-52;
Matches 177; Conservative 106; Mismatches 201; Indels
                                                                                                                                                                                                                             CECDD74AB9F9F8CB CRC64;
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STRAIN=SB1003 / St Louis, and BEC404;
MEDLINE=89313663; PubMed=2747617;
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                                                                                                                                                                                                                               517 AA; 57783 MW;
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483 SARLVTERLMTWAH 496
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P17054;
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CRTI_RHOCA
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307 KKRWSMGLFVWYFGTKGTAKYMKDVGHTVVVVGPRYKEHVQDIFIKGELAEDMSLYVHRP 366

302 QREYSCSTFMLYLGLD---KIY-DLPHHTIVPAKDYTTNIRNIFDNKTLTDDFSFYVQNA 357

243

301

RLAPCFOSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAENGGEIH 242

187 RFALSFHPLFIGGDPFHVTSMYILVSQLEKKFGVHYAIGGVQAIADAMAKVITDQGGEMR INSELESLII-ENGAAKGVKLQHGAELRGDEVIINADPAHAMTHLVKPGVLKKYTPENLK 116 BCEKIITPQTWEIDEHVYKGAIFSLSHKFSQMLYWRPHNRFEELANCYLVGGGTHPGSGL

SASDDSLAPAGKSALYVLVPMPN--NDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-9036827; PubMed-2144293;
Bartley G.E., Schmidhauser T.J., Yanofsky C., Scolnik P.A.;
Bartley G.E., Schmidhauser T.J., Yanofsky C., Scolnik P.A.;
Carotenoid desaturases from Rhochacter cappulatus and Neurospora crassa are structurally and functionally conserved and contain domains homologous to flavoprotein disulfide oxidoreductases.";
J. Biol. Chem. 265:16624-(1990).
I. FUNCTION: This enzyme converts phytoene into zeta-carotene via the intermediary of phytofluene by the symmetrical introduction of two double bonds at the C-11 and C-11' positions of phytoene.
I. COPACTOR: PAD (Probable).
I. PATHWAY: Carotenoid and chlorophyll biosynthesis.
I. SIMILARITY: Belongs to the phytoene dehydrogenase family.
Armstrong G.A., Alberti M., Leach F., Hearst J.E.;
"Nucleotide sequence, organization, and nature of the protein
products of the carotenoid biosynthesis gene cluster of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IRR00315; Adrndx reductase.
InterPro; IRR00317; Amino Oxidase.
InterPro; IRR00315; Bac_Dhytoene_dh.
InterPro; IRR00151; Bac_Dhytoene_dh.
InterPro; IRR00151; Phytn_dehydro.
InterPro; IRR00415; Phytn_dehydro.
Pfam; PRO1991; Amino oxidase; 1.
PRONTS; PRO0419; ADXRDTASE.
PROSTIE; PS00982; PHYTORNE DH; 1.
PROSTIE; PS00982; PHYTORNE DH; 1.
Photosynthesis; Chlorophyll biosynthesis; Oxidoreductase; PAD; Photosynthesis; Carotenoid biosynthesis; Oxidoreductase; PAD; Plavoprotein; NAD.
12 45 Photosynthesis; Chorophyll Phythosis; PAD; Padry (PADENTIAL).
                                                                                                                                                                                           SECTENCE FROM N.A.
MEDLINE-89327279; PubMed=2546948;
MEDLINE-89327279; Scolnik P.A.;
"Carotenoid biosynthesis in photosynthetic bacteria. Genetic characterization of the Rhodobacter capsulatus Crtl protein.";
J. Biol. Chem. 264:13109-13113(1989).
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J. Biol. Chem. 264:18260-18260(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [4]
SIMILARITY TO CAROTENOID DESATURASES.
                                                                                                     capsulatus.";
Mol. Gen. Genet. 216:254-268(1989)
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EMBL; X52291; CAA36533.1; ...
EMBL; Z11165; CAA77540.1; ...
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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Nucleic Acids Res. 28:862-867(2000).
-!- FUNCTION: This enzyme converts phytoene into zeta-carotene via intermediary of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11' positions of phytoene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=AFCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
STRAIN=AFCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
STRAIN=AFCC 17023 / DAMEG=8021167;
Lang H.P., Cogdell R.J., Gardiner A.T., Hunter C.N.;
Lang H.P., Cogdell R.J., Gardiner A.T., Hunter C.N.;
"Barly steps in carotenoid biosynthesis: sequences and
transcriptional analysis of the crtl and crtB genes of Rhodobacter
sphaeroides and overexpression and reactivation of crtl in
Bscherichia coli and R. sphaeroides.";
J. Bacteriol. 176:3859-3869(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE-20115911; Pubmed=10648776;
Choudhary M., Kaplan S.;
"DNA sequence analysis of the photosynthesis region of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ARCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE=95238278; PubMed=7721699;
Lang H.P., Cogddil R.J., Takaichi S., Hunter C.N.;
"Complete DNA sequence, specific ThS insertion map, and gene assignment of the carotenoid biosynthesis pathway of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- PATEWAY: Carotenoid biosynthesis.
-i- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                             P54980; OSRFD0; STANDALD, FALL, SIE AR. P54980; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSRFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0; OSSFD0
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Bacteriol. 177:2064-2073(1995).
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476 PTIYESARISAKLI 489
                                                                           PSVIGSGELVAQMI 499
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1063;
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126 131

67 71

Gaps

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8 IIVGAGPGGLCAGMILSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFLLMKGVLD 12 VVIGAGLGGLAAAMRLGAKGYKVTVVDRLDRPGGRGSSITKGGHRFDLGPTIVTVPDRLR 68 EMFELCERRSEDYLBFLPLSPMYRLLYDDRDIF-VYSDRENMRAELQRVFDBGTDGYEQF MEGERKRENALYPCITRDYSSLKSFLSL-DLIKALP---WLAFPKSVFNNLGQYFNQEKM 182

127

| | : | | : : | | : : | : : | : : | SEWADCGRDFDKDVSLVPMEPFYTIDFPDGEKYTAYGDDAKVKABVARISPGDVEGFRHF

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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 DLWKICGRDFDADVELKPIDPPYEVRWPDGSHFTVROSTEAMKAEVARLSPGDVAGYEKF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 MEQBRKRFNALYPCITRDYSSLKSFLSL-DLIKALP---WLAFPKSVFNNLGQYFNQEKM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLAFCFOSKYLGMSPWECPALPTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAENGGEIH 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSELESLIIENGAAKGVKLQHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTPENLKQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 MNTEVDEILVEKGTATGVRLASGEVLRAGLVVSNADAGHTYMRLIRNHPRRRWTDAHVKS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REYSCSTFMLYLGLDKIY----DLPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQNAS 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 RRWSMGLFVWYFGTKGTKGMWPDVGHHTIVNAPRYKGLVEDIFLKGKGAKDMSLYIHRPS 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 ASDDSLAPAGKSALYVLVPMPN--NDSGLDWQAHCQNVREQVLDTL-----GARLGLS 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 ITDPTVAPEGDDTFYALSPVPHLXQAQPVDWQAVAEPYRESVLEVLEQSMPGIGERIGPS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410 DIRAHIECEKIITPQTWETDEHVYK-GATFSLSHKFSQMLYWRPHNRFEELANCYLVGGG 468
                                                                                                                                                                                                                                                                                                                                                                                                  8 IIVGAGPGGLCAGMLLSQRGFKVSIFDKHABIGGRNRPINWNGFTFDTGPTFLLMKGVLD 67
                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                                                                                 Length 518;
                                                                                                                                                                                                                                                                                                                                                27.2%; Score 737; DB 1; Length 51. 33.5%; Pred. No. 8.9e-48; ive 97; Mismatches 207; Indels
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47
74 174
292
395
5724 MW; 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 EQFMEQERKRENALYPCITRDYSSLKS--FLSL-DLIKALP-----WLAFPKSVFNNL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHABIGGRNRPINMNGFTFDTGPTFLLMKG 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 VLDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-SDRENMRAELQRVFDEGTDGY
                                                                                                                                                                                                                                             Armstrong G.A., Alberti M., Hearst J.E.;

"Conserved enzymes mediate the early reactions of carotenoid

"Conserved enzymes mediate the early reactions of carotenoid

biosynthesis in nonphotosynthetic and photosynthetic prokaryotes.";

Proc. Natl. Acad. Sci. U.S.A. 8:9975-9979(1990)

-!- FUNCTION: This enzyme converts phytoene into lycopene via the
intermediaries of phytofluene, zetta-carotene and neurosporene by
the introduction of four double bonds.
-!- COPACTOR: FAD (Probable).
-!- FATHMAY: Carotenoid biosynthesis.
-!- PATHMAY: Carotenoid biosynthesis.
                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
NCBL_TaxID=549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD. NP BIND 5 38 FAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
01-AUG-1991 (Rel. 19, Created)
1-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99..) (Phytoene desaturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
26.0%; Score 704.5; DB 1; Length
Best Local Similarity 31.7%; Pred. No. 2.3e-45;
Matches 158; Conservative 102; Mismatches 213; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8EDC5DB1562083F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pir, A39273; A33120. Anino oxidase. interPro; PRR008150; Bac phyroene dh. interPro; IPR008151; Phytn. dehydro. IPR01891; Amino oxidase. i. Probom; PD139017; Phytn. dehydro. PROSITE; Pytn. dehydro; PROSITE; PROSITE; PROSITE; PHYTOENE DH; 1.
                                                                                                                                                                                                                             MEDLINE=91088634; PubMed=2263648;
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EMBL; M87280; AAA64981.1; -.
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                              Erwinia herbicola.
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62 AIEELFALAGKQLKEYVELLPVTPFYRLCWESGKVFNYDNDQTRLEAQIQQFNPRDVEGY 121
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                                                        |: : : | | | | | | : : | | | | : : | | | : : | | | : : | 351 YLHSPCVTDPSLAPPGRAPUDWAQEGPKLRDRIFDYLEERY-MPGL 409
                                                                                                                                                                                                                                             YVQNASASDDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQVLDTLGARLGLSDI 411
                                                                                                                                                                                          412 RAHIECEKIITPOTWETDEHVYKGATFSLSHKFSOMLYWRPHNRFEELANCYLVGGGTHP 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ጵ
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carotenoid biosynthesis; Oxidoreductase; PAD; Flavoprotein; NAD. NP_BIND (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: Carotenoid biosynthesis. SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.8%; Score 700.5; DB 1; Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
02-PEB-2003 (Rel. 41, Last annotation update)
Phyroene dehydrogenase (EC 1.14.99.-) (Phyroene desaturase)
CRII.
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"Elucidation of the Erwinia uredovora carotenoid biosynthe by functional analysis of gene products are according to a contract of the contract of gene products and programmed to the contract of gene products of gene products of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the co
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InterPro; PR002937; Amino oxidase.
InterPro; IPR002937; Amino oxidase.
InterPro; IPR008150; Bac_phyroene_dh
InterPro; IPR008151; Phytn_dehydro.
Pfam; PF012937; Amino oxidase; 1.
ProDom; PD139017; Phytn_dehydro; 1.
PROSITE; PS00982; PHYTOENE_DH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                    GSGLPTIYESARISAKLI 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 GAGIPGVVASAKATASLM 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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124 EQFWEQERKRFNALYPCITRDYSSLK----SFLSL-DLIKALPWLA---FPKSVFNNLGQ 175
                                173 YIEDEHLRQARSFHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVQGMIKLFQ 232
                                                                                                                                                                                                       236 ENGGEIHLNSEIESLIIENGAAKGVKLQHGAELRGDEVIINADFAHAMTHLVK--PGVLK 293
                                                                                                                                                                                                                                              233 DIGGEVVLNARVSHMETTGNKIEAVHLEDGRRFITQAVASNADVVHTYRDLISQHPAAVK 292
                                                                                                                                                                                                                                                                                                             294 KYTPENLKQREYSCSTFMLYLGLDKIYD-LPHHTIVFAKDYTTNIRNIFDNKTLTDDFSF 352
                                                                                                                                                                                                                                                                                                                                           C--SNKLQTKRMSNSLFVLYFGLNHHHDQLAHHTVCFGPRYRELIDEIFNHDGLAEDFSL 350
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                                                                                                  YFNQEKMRLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIA
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Ruiz Hidalgo M.J.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This enayme converts phytoene into zeta-carotene via tintermediary of phytofluene by the symmetrical introduction of intermediary  Parotenoid biosynthesis.
-!- SAMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Pungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
Phycomyces.
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Phytoene dehydrogenase (EC 1.14.99..) (Phytoene desaturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
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InterPro; IPR00237; Amino oxidase.
InterPro; IPR008150; Bac_phytoene_dh.
InterPro; IPR008151; Bytn_dehydro.
InterPro; IPR008151; Phytn_dehydro.
Ipfam; PP01593; Amino.oxidase; 1.
ProDom; PD139017; Phytn_dehydro.
PROSITE; PS00982; PHYTOENE_DH; 1.
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49 61 65 VLDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-SDRENWRABLQRVFDEGTDGY 123

5 KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMWGFFFDTGPTFLLMKG

Best Local Similarity 31.5%; Pred. No. 4.6e-45; Matches 157; Conservative 103; Mismatches 213; Indels

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PATHWAY: Carotenoid biosynthesis.
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P48537;
01-FEB-1996 (Rel. 33, Created)
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595 AA;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                       119 PÖGFLRFLDFMKÉSHTHYEGGVEMAÍKQNFETIWKLIRLÓYVPÁLFRLHIFDFVYSRAAK 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                            EN-GGEIHLNSEIBSLIIENGAAK--GVKLQHGAELRGDEVIINADFAHAMTHLVKFGVL 292
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STRAIN=74-OR23-1A / FGSC 987;
STRAIN=74-OR23-1A / FGSC 987;
Schmidhauser T.G., Lauter F.-R., Russo V.E.A., Yanofsky C.;
"Cloning, sequence, and photoregulation of al-1, a carotenoid
biosynthetic gene of Neurospora crassa.";
Mol. Cell. Biol. 10:5064-5770(1990).
-!- FUNCTION: This enzyme converts phytoene into zeta-carotene via the intermediary of phytofluene by the symmetrical introduction of two double bonds at the C-11 and C-11' positions of phytoene.
                                                                                                                                                                  1 MANTXHIIIVGAGPGGLCAGMLLSQRGFXVSIFDKHARIGGRNRPINMNGFTFDTGPTFL
                                                                                                                                                                                                 1 MAPPKHVIIIGAGAGGTATAARLARBGIKVTVVEKNNFGGGRCSLINHNGHRFDQGPSLY
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LTNFIDILVEHEEVNDPSIWQKKFNLWRGSILGLSHDVLQVLWFRPSTQDSTGRYKNLFFV
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01-WAY-1991 (Rel. 18, Last sequence update)
11-WAR-2004 (Rel. 43, Last amotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase) (Albino-1
                                                                                                                                   Gaps
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora,
NCBI_TaxID=5141;
                                                                                               25.3%; Score 686; DB I; Length 583; 30.4%; Pred. No. 7e-44;
                                                                                                                Local Similarity 30.4%; Pred. No. 7e-44; nes 157; Conservative 112; Mismatches 227; Indels
                                                               BOESF682B12FB591 CRC64;
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                                                               65983 MW;
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                                                             583 AA;
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                Transmembrane.
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TRANSMEM 53:
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P21334;
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                                                                 SEQUENCE
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Matches
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INDUCTION: By photoinduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
25.1%; Score 681; DB 1; Length 59
Best Local Similarity 32.2%; Pred. No. 1.7e-43;
Matches 166; Conservative 106; Mismatches 216; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 POTENTIAL.
66367 MW; OFF3DF07328ED784 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                 PIR, A35919; A35919. Anino oxidase. InterPro; IRR002937; Amino oxidase. InterPro; IRR00150; Bac_Dhytoene_dh. InterPro; IRR000205; NAD BS. InterPro; IPR000151; Phytn dehydro. Pfam; PF01593; Amino oxidaše; 1. Projom; PD139017; Phytn dehydro; 1. PROSITE; PS00982; PHYTOZNE DH; 1. Carotenoid biosynthesis; Oxidoreductase
                                                                                                                                                                                                                                                                                                                                                         EMBL; MS7465; AAA33555.1; -.
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         | : || || : || || 366 RVDSTAAPEGKDSVVVLVPVGHLLEEDRHASQAHQLSASRNGHISSASPPDQPGLTPTEK 425
                                                                                                                                                                          ------HNRFBBLANCYLVGGGTHPGS 473
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                                                                                - DWQAHCQNVREQVLDTLGARLGLSDIRAHIBCEKIITPQTWETDBHVYKGATFSLSHKF
                                                                                                             MEDLINE=96(62243; PubMed=7592436; MEDLINE=96(62243; PubMed=7592436; MEDLINE=96(62243; PubMed=7592436; Misawa N., Satoml Y., Kondo K., Yokoyama A., Kajiwara S., Saito T., Ohtani T., Miki W.; Satoml Y., Kondo K., Yokoyama A., Kajiwara S., Saito T., Ohtani T., Miki W.; Satomlani P., Miki W.; "Structure and functional analysis of a marine bacterial carotenoid biosynthesis gene cluster and astaxanthin biosynthetic pathway proposed at the gene level."; J. Bacteriol. 177:6575-6584(1995).

-!- FUNCTION: This enzyme converts phytoene into lycopene via the intermediaries of phytofilene, zeta-carotene and neurosporene by the introduction of four double bonds (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD
NP_BIND 12 45 FAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141; Conservative 110; Mismatches 227; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Carotenoid biosynthesis. Involved in astaxanthin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biosynthetic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Protecobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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28.6%; Pred. No. 6.3e-38;
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InterPro; IRR002937; Amino oxidase.
InterPro; IRR0029150; Bac phytoene dn.
InterPro; IPR008151; Bhytn dehydro.
Pfam; PF01593; Amino oxidase; 1.
ProDom; PD139017; Phytn dehydro; 1.
PROSITE; PS00982; PHYTOENE DH; 1.
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                                                                                                                                                                                                                                                                 GLPTIYESARISAKLI 489
                                                                                                                                                                                                                                                                                                             545 GVPICLAGGALVARQI 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agrobacterium aurantiacum.
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                       445 SOMLYWRP----
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P54978;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 EMP-ELCERRSEDYLEPLPLSPMYRLLYDDRDIP-VYSDRENMRABLQRVFDEGTDGYEQ 125
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                                                                                                                                                                                                                     STRAIN=ATCC 1836;
MEDINE-9383691,
Daub M.B.;

"Isolation, sequence, and characterization of the Cercospora
nicochiane phytoene dehydrogense gene.";

"Isolation, microbiol, 60.2766-2771(1994).

"Intermediary of phytofluene by the symmetrical introduction of the double bonds at the C-11 and C-11' positions of phytoene.".

"COPACTOR: FAD (Probable).

"Isolation of the C-11 and C-11' positions of phytoene.".
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoche dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
PbH1.
Cercospora nicotianae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Dothideomycotes et Chaetothyriomycetes incertae sedis;
NCBI_TaxID=29003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.4%; Score 607; DB 1; Length 621; 27.2%; Pred. No. 6.5e-38;
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InterPro; IPR008151; Bhytn dehydro.
ProDom; PD139117; Phytn dehydro, 2.
PROSITE; PS00902; PHYTOENE_DH; 1.
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PIR; T48646; T48646.
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621 AA;
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Best Local S
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                                                                                                                                179 QEKMRLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLMRIAAAMAQVIAENG 238
                                                                                                                                                                                                                                                                                          GEIHINSEIESLIIENGAAKGVKLOHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTPE 298
                                                                                                                                                                                                                                                                                                                       303 SLNAKRWSWSLFVLHFGLREAPKDVAHHTILFGPRYKELVNEIFKGPKLAEDFSLYLHSP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 SASDDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 CTIDPEMAPPGMSTHYVLAPVPHLGRADIDWAVEGPRYADRILASLEERL-IPNLRANLT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEKIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELANCYLVGGGTHPGSGLP 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-SDRENMRAELORVFDEGTDGY
                                                                                           EQFMEQERKRFNALYPCITRDYSSLKSFLSL-DLIKALPWL----AFPKSVFNNLGQYFN
                                                                                                                                                                                                                      299 NLKQREYSCSTFMLYLGL-DKIYDLPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQNA
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MEDLINE-30333;

MEDLINE-3004881; PubMed-8917308;

Schumann G., Nurnberger H., Sandmann G., Kruegel H.J.;

Schumann G., Nurnberger H., Sandmann G., Kruegel H.J.;

Schumann G., Nurnberger H., Sandmann G., Kruegel H.J.;

Mactivation and analysis of cryptic crt genes for carotenoid biosynthesis from Streptomyces griseus.";

Mol. Gen. Genet. 252:658-666(1996).

-!- FUNCTION: This enzyme converts phytocene into zeta-carotene via tintermediary of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11' positions of phytoene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1911;
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InterPro; IPR002937; Amino oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Carotenoid biosynthesis.
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482 GVVGSAKATAQVM 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 MIFDNKTLTDDFSFYVQNASASDDSLAPAGKSALYVLVPMPNNDSG---LDWQAHCQNVR 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 HVVVGAGLAGLAALHLLGAGRRVTVVEREDVPGGRAGLLBSGGFRIDTGPTVLTMPDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 SVFNNLGQYFNQEKMRLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 RAMADAASDAGAVLRYGQRVTRL-------BRSGDRVTAVVTDQEHIPCDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 V--KPGVLKKY-----TPENLKQREYSCSTFWLYLGLDKIY-DLPHHTIVFAKDYTTNIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398 DELLAEL-ERREMPGLGAAIBBEGLVTPVDWTAQGKA-AGTPFSVAHTFPQTGPFRPRNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 HIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFLLMKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 LDEMFELCERRSEDYLEFLPLSPMYRLLY-DDRDIFVYSDRENMRAELQRVFD-EGTDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 RRIKIWIERLYRVQMRRPIDTNFDSPLQLAHPDLAR-LAALGGFGRLDA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 AAMAQVIAENGGEIHINSEIBSLIIENGAAKGVKLOHGAELRGDEV-IINADFAHAMTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 EQVLDTLGARLGLSDIRAHIECEKIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNR
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-!- FUNCTION: This enzyme converts phytoene into zeta-carotene via intermediary of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11' positions of phytoene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
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Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=38315;
                                                                                                                                                                                                                                                                                                                                                                       FAD; Flavoprotein;
(T) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  507;
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 144; Conservative 82; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                        FAD (ADP PART) (POTENTIAL)
FBB97F7FE696B2AC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.7%; Score 508; DB 1; 28.0%; Pred. No. 1.3e-30;
InterPro; iPR000205; NAD BS;
InterPro; iPR008151; Phytn dehydro.
Pfam; PF01291; Amino oxidase; 1.
ProDom; P0139017; Phytn dehydro; I.
PROSTIE; PS00982; PHYTOENE DH; I.
Carotenoid blosynthesis; Oxidoreductase; FAI NP BIND 12 45.
SEQUENCE 507 AA; 54509 MM; FBB97F7FE6966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508 AA
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P54971;
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                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 ------EQFMEQERKR-----FNALYPCITRDYSSLKSPLSLDLIKALPWLAFPK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 SVFNNLGQYFNQEKMRLAFCFQSKYLGMSPWBCPALFTMLPYLEHEYGIYHVKGGLNRIA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 AAMAQVIAENGGEIHIMSEIESLIIENGAAKGVKLOHGAELRGDEVIINADFAHAMTHLV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 RAMADAAADAGASFRYGQSVTRL-BRSGDRVTAVVTDQERIACDAVVITPDLPVSYRLLG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                                                                                                                                                                     288 KPGVLKKYTPENLKQREYSCSTPMLYLGLDKIY-DLPHHTIVFAKDYTTNIRNIFDNKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 TDDFSFYVQNASASDDSLAPAGKSALYVLVPMPNNDSG----LDWQAHCQNVREQVLDTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARLGLSDIRAHIECEKIITPQTWETDEHVYKGATPSLSHKFSQMLYWRPHNRFEELANCY
                                                                                                                                                                         InterPro; IPR002937; Adrida, reductase.
InterPro; IPR002937; Admino Oxidase.
InterPro; IPR002937; Admino Oxidase.
InterPro; IPR002151; Bay Divtoene_dh.
InterPro; IPR008151; Phytin_dehydro.
InterPro; IPR008151; Phytin_dehydro.
Pfam; PF01293; Amino Oxidase; 1.
PRINT; PR00419; ADXRDTASE.
PROSITE; PS00982; PHYTOENE_DH; 1.
PROSITE; PS00982; PHYTOENE_DH; 1.
Carotenoid biosynthesis; Oxidoreductase; PAD; Plavoprotein; NAD.
                                                                                                                                                                                                                                                                                                                                                                                             48;
        -!- PATHWAY: Carotenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                             18.2%; Score 493; DB 1; Length 508; 27.2%; Pred. No. 1.8e-29; ive 88; Mismatches 233; Indels 4
                                                                                                                                                                                                                                                                                                                      AD (ADP PART) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                         FAD
                                                                                                                                                                                                                                                                                                                                   508 AA; 54610 MW;
COFACTOR: FAD (Probable).
                                                                                                                                                              EMBL; D55723; BAA09537.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         138, Conservative
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | ::| |:: | ::| | : | | EFHDLSARLYDAF---DREWRAARPDLRAIATGALKAPRTWPALLPGWTLDRLLRL--- 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 IIIVGAGPGGLCACMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFLLMKGVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sphaeroides.",
J. bacterid. 177:2064-2073 (1995)
-!- FUNCTION: CONVERTS HYDROXYNBUROSPCRENE TO DEMETHYLSPHEROIDENE
METHOXYNBUROSPORENE TO SPHEROIDENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AJ010302; CAB39731, ALT_SEQ.

PIR, 523633; S23633.

InterPro: IPR002937, Amino oxidase.

InterPro: IPR003150; NaD Bs.

InterPro: IPR003055; NaD Bs.

Pfam; PF01593, Amino oxidase; 1.

PROSITE; PS00982; PHYTORNE Ds.

Photosynthesis; Carotenoid biosynthesis; oxidoreductase; PAD; Plavoprotein; NAD.

Oxidoreductase; PAD; Plavoprotein; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE=5518279; PubMed=7721699;
Lang H.P., Cogdell R.J., Takaichi S., Hunter C.N.;
"Complete DNA sequence, specific Tn5 insertion map, and gene assignment of the carotenoid biosynthesis pathway of Rhodobacter
                                                                                    Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATC. 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE=92307398; PubMed=1612412;
MEDLINE=92307399. PubMed=1612412;
Gari E., Toledo J.C., Gibert I., Barbe J.;
"Nucleotide sequence of the methoxyneurosporene dehydrogenase grown Rhodobacter sphaeroides: comparison with other bacterial carotenoid dehydrogenases.";
FEMS Microbiol. Lett. 72:103-108(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: FAD (Probable).
-!- PATHWAY: Carotenoid and chlorophyll biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
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A - G (IN REF. 2).
T - P (IN REF. 2).
L -> M (IN REF. 2).
L -> I (IN REF. 2).
L -> I (IN REF. 2).
H -> I (IN REF. 1).
PHGA - ATCP (IN REF. 1).
W; 622279314158235 CRC64;
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98; Mismatches 243; Indels
28-FBB-2003 (Rel. 41, Last annotation update)
Methoxyneurosporene dehydrogenase (EC 1.14.99.-).
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Matches 115, Conserv
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67

495 AA

STANDARD;

CRID RHOSH Q01671; 01-JUL-1993 16-OCT-2001

SSULT 13

(Rel. 26, Created) (Rel. 40, Last sequence update)

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164 AFPKSVFNNLGQYFNQEKMRLAPCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGL 223
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                                                            224 NRIAAAMAQVIAENGGEIHLNSEIESLIIENGAAKGVKLQHGAEERGDEVIINADFAHAM
                                                                                   289 AGCLGDGPQDAVPEDRIHPRSLSAWTWS-YAARASGPPLVHHNVFFADDPRREFGPIAAG
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                   THLVKPGVLKKYTPENLKQREYSCSTFMLYLGLDKIYDLPHHTIVFAKDYTTNIRNIPDN
                                                                                                                                                                                                                                                         404 ARLGLSDIRAHIECEKIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELANCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90368827; PubMed=2144293;
Bartley G.E., Schmidhauser T.J., Yanofsky C., Scolnik P.A.;
Carotenoid desaturases from Rhodobacter capsulatus and Neurospora crassa are structurally and functionally conserved and contain domains homologous to flavoprotean disulfide oxidoreductases.";
J. Biol. Chem. 265:16020-16024(1990).
-:-PUNCTION: CONVERTE HYDROXYBERDSORENE TO DEMETHYLSPHEROIDENE OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89313663; PubMed=2747617; Marstrong G.A., Alberti M., Leach F., Hearst J.B.;
Mucleotide sequence, organization, and nature of the protein products of the carotenoid biosynthesis gene cluster of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales,
Rhodobacteraceae, Rhodobacter.
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-!- PATHWAY: Carotenoid and chlorophyll biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
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01-AUG-1990 (Rel. 15, Last sequence update)
28-F8B-2003 (Rel. 41, Last annotation update)
Methoxyneurosporene dehydrogenase (RC 1.14.99--).
                                                                                                                                                                                                                                                                                                                                                                                                                                        494 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=SB1003 / St Louis, and BEC404;
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InterPro; IPR002937; Amino_oxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 ADFAHAMTHLVKPGVLK-----KYTPENLKQREYSCSTFMLYLGLDKI-YDLPHHTI
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            InterPro; IPR008151; Phyth dehydro.
Propin 191591; Amino oxidase; 1.
Probom; PD139017; Phyth dehydro: 1.
PROSTE; P800982; PHYTOENE DH; 1.
Photosynthesis; Chlorophyl biosynthesis; Carotenoid biosynthesis; Oxidoreductase; RD; Flavoprotein; NAD.
NP BIND 8 PAD; PRO (ADP PART) (POTENTIAL).
SRQUENCE 494 AA; 52312 MW; D1180A023FFBB5A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 SLSHKPSQMLYWRPHNRFEELANCYLVGGGTHPGSGLPTIYBSARISAKLI 489
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Streptomycineae, Streptomycetaceae, Streptomyces.
NCBL_TaxID=1916;
                                                                                                                                                                                           Length 494;
                                                                                                                                                                                       12.0%; Score 325; DB 1; Length 49 23.9%; Pred. No. 7e-17; ive 94; Mismatches 222; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burnett W.V., Henner J., Eckhardt T.;
"The nucleotide sequence of the gene coding
secreted protein from Streptomyces lividans.
Nucleic Acids Res. 15:3926-3926(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469
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InterPro; IPR008150; Bac phytoene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87231086; PubMed=3453116;
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01-JAN-1988 (Rel. 06, Last seq
01-OCT-1996 (Rel. 34, Last ann
                                                                                                                                                                                                              Best Local Similarity 23.99
Matches 127; Conservative
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                                                                                                                                                                                           Query Match
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PIR; S09192; S0948356.1; -.
InterPro; IPR000759; Adrndx_reductase.
InterPro; IPR008151; Phytn_dehydro.
PRINTS; PR00419; ADXRDIASE.
PRINTS; PR00419; ADXRDIASE.
SEQUENCE 469 AA; 49740 MW; C2AE7533C7C701CB CRC64;

ユダナ・アアーサイ サハー Tキハーハつ・日ご

T 1/:23:06 2004

MOD MAR

56 GPTFLLMKGVLDBMFELCERRSEDYLEPL-PLSPNYRLLYDDRDIFVYSDRENMRAELQR 114 STANDAGE SANDELTAAVELARGEPVAVPEAQGTVGGGARTEELTLPGFRHDPCSAAHPLGIN 64 8 IIVGAGPGGLCAGMLLSQRGFKVSIFDKHABIGG--RNRPINMNGFTFD-----T

Gaps

Query Match 6.5%; Score 175; DB 1; Length 469; Best Local Similarity 21.8%; Pred. No. 1.2e-05; Matches 118; Conservative 70; Mismatches 221; Indels 132;

115 VFDEGTDGYEQFMEQERKRFNALYPCITRDYSSLKSFLSLDLIKALP--

165 PPKSVFNNLGQYFNQEKMRLAFCFQSKYLGMSP---WECPALFTMLPYLEHEYGIYHVKG 221

159 LPPSTW--LMRRFRDEKAKTLFAGLVAHV-MAPLGGFATGAIGLVFALAAHARGWPVARG 215

222 GINRIAAAMAQVIAENGGEIHLINSEIESL-----IIENGAAKGVKL----OHGAEL 268

269 RGDEVIINADFAHAMTHLVKPGVLKKYTPENLKQREYSCSTFMLYLGLDKIYDLPHHTIV 328

R 467 467 earch completed: February 29, 2004, 14:44:59 ob time : 12.6124 secs

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4 protein - protein search, using sw model

Pebruary 29, 2004, 14:34:14 ; Search time 14.2234 Seconds
(without alignments)
3455.835 Million cell updates/sec US-09-941-947A-22
2711
1 MANTKHIIIVGAGPGGLCAG......KHRVRFKDIAHSAWLKKAKA 511 .tle: irfect score: iquence: : uo ui

BLOSUM62 Gapop 10.0 , Gapext 0.5 oring table:

283366 segs, 96191526 residues arched: stal number of hits satisfying chosen parameters:

.nimum DB seg length: 0 ximum DB seg length: 2000000000

st-processing: Minimum March 0%
Maximum March 100%
Listing first 45 summaries

tabase :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	phytoene dehydroge	phytoene dehydroge			റ	hypothetical prote	cen	phytoene dehydroge								phytoene dehydroge			phytoene dehydroge			phytoene dehydroge		phytoene dehydroge	hydroxyneurosporen	hypothetical prote		phytoene desaturas	methoxyneurosporen
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	Score	929.5	915.5	883.5	825.5	794.5	794	783.5	743	737	735	725	713.5	704.5	702.5	700.5	686	681	673	651.5	613.5	607	969	564.5	547.5	504	502.5	85	472.5	404
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392.5 354 332.5				0 0 0 4 4 4 0 0 8
30 31 32		9 B B B	4 4 4 4 2 1 2 2	4 4 4 5 4 5

ALIGNMENTS

RESULT 1 AH1199 Phycone dehydrogenase homolog lmo1000 [imported] - Listeria monocytogenes (strain EGD-e CiSpecies: Listeria monocytogenes CiDate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 CiAccesion: AH1199 Ridlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker CiAccesion: AH1199 Ridlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker CiAccesion: AH199 Alythie: Comparative genomics of Listeria species. Alythie: Comparative genomics of Listeria species. Alythie: Comparative genomics of Listeria species. Alythie: Comparative genomics of Listeria species. Alythie: DNA Alythie: DNA Alythie: DNA Alythie: DNA Alythie: DNA Alythie: DNA Alythie: DNA Alythie: DNA Alythie: Comparative genomics of Listeria Species. CiGenetics: Tealininary Alycoss: Teference number: AB1077; MUID:21537279; PMID:11679669 Alythie: Comparative genomics of Listeria Species CiGenetics: Tealininary Alythie: Comparative genomics of Listeria Species CiGenetics: Algebra: Tealin EGD-e CiGenetics: Algebra: Tealin EGD-e	Query Match 34.3%; Score 929.5; DB 2; Length 490; Best Local Similarity 37.6%; Pred. No. 4.3e-62; Matches 184; Conservative 98; Mismatches 199; Indels 9; Gaps 1;	5 KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTPDTGPTFLLMKG 64 	65 VLDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVYSDRENWRAELQRVFDEGTDGYR 124 [125 QFMEQERXRFNALYPCITRDYSSLKSFLSLDLIKALPWLAFPKSVFNNLGQYFNQERWRL 184	185 AFCROSKYLGMSPWECPALFTWLPYLEHBYGIYHVKGGLARIAAAMAQVIAENOGEIHLN 244 187 AFSLQMRYLGMSPWDIPAAYSIIPFSEYYYGTFHPIGGQNKIVEAMQQVVTENKGKFFFN 246	245 SEIESLIIENGAAKGVKLOHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTPENLKQRE 304	305 YSCSTFMLYLGLDKIYDLPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQNASASDDSL 364 	365 APAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIECEKIITPQ 424
RESULT AH1199 AH1199 C)Spec C,Spec C,Acce R,Glan A,Athirl A,Athirl A,Acce A,Acce A,Acce A,Acce A,Acce C,Gene C,Gene	Que Bes Mat	රු සි	දු ද	& 점	දි දි	දි පි	& a	ò

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N;Alcernate names: phytoene desaturase
C;Species: Myxococcus xanthus
C;Species: Myxococcus xanthus
C;Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 29-Sep-1999
C;Accession: S35306; S27594
R;Fontes, M; Ruiz-Vasquez, R; Murillo, F.J.
EMBO J: 12, 1265-1275, 1993
A;Title: Growth phase dependence of the activation of a bacterial gene for carotenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                 C;Species: Heliobacillus mobilis ctum - netiobacillus mobilis C;Date: 02-Sep-2000 #text_change 15-Sep-2000 C;Accession: T31463 mobilis c;Date: 02-Sep-2000 #text_change 15-Sep-2000 C;Accession: T31463 but to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
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                                                                                                                                                                      probable diapophytoene dehydrogenase crtN - Heliobacillus mobilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-517 <XIO>
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                 472 NAQIATKKFLQKEK 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ohytoene dehydrogenase homolog lin0999 [imported] - Listeria innocua (strain Clip11262)
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TWETDEHVYKGATFSLAHKFSQMLYWRPHNRFEELANCYLVGGGTHPGSGLPTIYESARI 484
                                                                                                                                           V.Cross-references: GB:AL592022; PIDN:CAC96230.1; PID:g16413458; GSPDB:GN00178
V.Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LMKGVLDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVYSDRENMRAELQRVFDEGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 37.4%;
Matches 185; Conservative
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                                                                                                                                                                                                                                485 SAKLISQKHR 494
                                                                                                                                                                                                                                                                                       ATOKFLOKEK 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Residues: 1-488 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           %;Gene: lin0999
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Gene: carc

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A; Molecule type: DNA
A; Residues: 1-517 < R607-
A; Residues: 1-517 < R607-
A; Cross-references: EMBL: 221955; NID: 9577589; PIDN: CAA79956.1; PID: 9288221
A; Experimental source: strain DK1050
B; Botella, J.A.; Murillo, F.J.; Ruiz-Vazquez, R.
Bur. J. Botechen: 33, 238-248, 1995
A; Title: A cluster of structural and regulatory genes for light-induced carotenogenesis
A; Reference number: 867950; MUID: 96061955; PMID: 7588751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 GVKIHIHSPVHQIWIEQGQVRGIELADASRHQFDTVVINADFAYAVRHLLEPISARGRYTD 297
                                                                                                                                                                                                                                    64 GVLDEMFELCERRSEDYLEFLPLSPMYRL-LYDDRDIFVYSDRENWRAELQRVFDEGTDG 122
                                                                                                                                                                                                                                                                    298 NKLGOMOFSCSTFMLYLGINRRYEDLPHHOIYL---SDNIRRLERPWYDDSALDETDPP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRIVVVGAGVGGLAAAARLAHQGFDVQVFEKTQGPGGRCNRLQVDGFTWDLGFTIVLMPE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CjSpecies: Myxococcus xanthus
CjDate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 29-Sep-1999
CjAccession: 832169; 867952
RjBotella, Jr, Murillo, F.; Ruiz-vazquez, R.
Submitted to the EMBL Data Library, March 1993
A.Pescription: Mucleotide and deduced protein sequences of a carotenoid gene
                                                                                                                                                               122 FDRWYSEHIRKYBLGYKPYLAGPARSIFGYLRPDELMKFLSFRPW----ENLYQHFWRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 ODERLVYALSYPSKYLGWHPTVASSVFSLIPFELEFSGGVWHPVGGFRALAQGEANAAQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 GGEIHLNSEIESLIIENGAAKGVKLOHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHABIGGRNRPINMNGFTFDTGPTFLLMXG
                                                                                                                                                                                                                                                                                                                                                123 YEQFMEQERKRFNALY-PCITRDYSSLKSFLSLD-LIKAL---PWLAFPKSVFNNLGQYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 NOEKWRLAFCFOSKYLGMSPWECPALFTMLPYLEHBYGIYHVKGGLNRIAAAMAQVIAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 ENLIGREYSCSTEMLYLGLDKIY-DLPHHTIVFAKDYTTNIRNI----FDNKTLTD-DFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412 RAHIECEKIIIPQIWEIDEHVYKGAIFSLSHKPSOMLYWRPHNRFBELANCYLVGGGTHP
                                                                                                                               4 TKHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHABIGGRNRPINMNGFTFDTGPTFLLMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FYVQNASASDDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDI
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29.3%; Score 794; DB 2; Length 51
Best Local Similarity 35.8%; Pred. No. 7.4e-52;
Matches 177; Conservative 106; Mismatches 201; Indels
                       Length
                                                                        Indels
                    cch 29.3%; Score 794.5; DB 2; al Similarity 35.4%; Pred. No. 6.4e-52; 177; Conservative 102; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473 GSGLLTILEASRSAAGFIHO 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 GSGLPTIYESARISAKLISQ 491
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A;Residues: 9-37;462-488 <BOW>
C;Superfamily: phytoene dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S32169
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                       Query Match
Best Local S
Matches 177
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Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GTDGYEQFWEQERKRFNALYP---CITRDYSSLKSFLSLDLIKALPWLAFP-----KS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KPGVLKKYTPENLKQREYSCSTFMLYLGLDKIY-DLPHHTIVFAKDYTTNIRNIFDN 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 ABAREG -- SRLIDAALERAKYSCSTFWAYYGLDTVYAD5PHHLIYLSESARRIDRDALED 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 RHVDLEDPPFYVCNPGVTDPSGAPAGHSTLYVLVPTPNTGRPVDWVKTEQALRERIPAML 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GARLGLSDIRAHIECEKIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFBELANC 462
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                                                                                                                                                                                                                                                                                                                                                                                                         SVRHVIVVGAGPGGGSAAINLAGQGFRVTVVEKDAVPGGRMKGLTLGASGEYAVDTGPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 LLMKGVLDEMFELCERRSEDYLEFLPLSPMYRL-LYDDRDIFVYSDRENMRAELQRVFDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 VFNNLGQYPNQEKMRLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAA
                                                                              Cross-references: EMBL:M94727; NID:g150079; PIDN:AAA25390.1; PID:g150080
Genetics:
                                                                                                                                                                                                                                                                                                                                                                             3 NIKHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHABIGGRNRPINMNG---FTFDTGPTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XTL-TDDFSFYVQNASASDDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDTL
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                 Length 529;
                                                                                                                                                                                                                                                                 Query Match 30.5%; Score 825.5; DB 2; Length!
Best Local Similarity 35.1%; Pred. No. 3.3e-54;
Matches 179; Conservative 106; Mismatches 192; Indels
Reference number: S35306; MUID:93223667; PMID:8467787
                                                                                                                                                                                   Superfamily: phytoene dehydrogenase
Keywords: carotenoid biosynthesis; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLVGGGTHPGSGLPTIYESARISAKLISQK 492
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Genome: plasmid
Superfamily: phytoene dehydrogenase
                                                 Molecule type: DNA
Residues: 1-529 <FON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-499 <KUR>
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Molecule type: DNA
                       Accession: S35306
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A;Accession: A32617
A;Nolecule type: DNA
A;Residues: 1-524 - CBAR>
A;Residues: 1-524 - CBAR>
A;Cross-references: GB.J04969; NID:g340554; PIDN:AAA50313.1; PID:g556397
B;Armstrong, G.A.; Alberti, M.; Leach, F.; Hearst, J.E.
Mol. Gener. 216, 254-268, 1989
A;Aritle: Nucleotide sequence, organization, and nature of the protein products of the A;Reference number: S04401; MUD:89313663; PMID:2747617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetic characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131
                                                                                                                                                                                           298 ENLKOREYSCSTEMLYLGLDKIY-DLPHHTIVFAKDYTTNIRNI-----FDNKTLTD-DFS 351
                                                                                                                                                                                                                                                                                                                                                                                                                                       RAHIECEKIITEQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELANCYLVGGGTHP 471
                                                                                                                                                                                                                                                                                   411
                                                                    NQEKMRLAPCFQSKYLGMSPWECPALPTML.PYLEHEYGIYHVKGGLMRIAAAMAQVIAEN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NiAlternate names: phytoene desaturate
C;Species: Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Accession: A33617; Soduto E-vision 21-May-1990 #text_change 29-Sep-1999
C;Accession: A33617; Soduto P.A.
G;Accession: A33617; Solnik, P.A.
J;Bartley, G.E.; Scolnik, P.A.
J;Tille: Carotenoid biosynthesis in photosynthetic bacteria. Genetic charact
A;Reference number: A32617; MUID:89327279; PMID:2546948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 MEQERKRENALYPCITRDYSSLKSFLSL-DLIKALP---WLAFPKSVFNNLGQYFNQEKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 VVIGAGLGGLAAAMRLGAKGYKVTVVDRLDRPGGRGSSITKGGHRFDLGPTIVTVPDRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 IIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFLLMKGVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 EMPELCERRSEDYLEFLPLSPMYRLLYDDRDIP-VYSDRENWRAELQRVFDEGTDGYEQF
FDRMYSEHIRKYELGYKPYLAGPARSIPGYLRPDDLMKFLSFRPW----ENLYQHFWRFF
                                                                                                                                                             GGETHINSELESLITENGAAKGVKLQHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTP
                                                                                                                                                                                                                                                                                                                                                                                 178 ODERLUYDLRYPSKYLGMHPTVASSVFSLIPFLEFSQGVWHPVGGFRALAQGLANAAQDL
                                                                                                                                                                                                                                                                                                                                                 PYVQNASASDDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVRBQVLDTLGARLGLSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A;Residues: 1-524 <ARM>
A;Cross-references: BMB-X52291; NID:g45996; FIDM:CAA36533.1; PID:g45998
A;Atote: translation of codons 1-33 is not given
A;Note: the authors translated the codon GTG for residue 34 as Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 524;
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Best Local Similarity 32.8%; Pred. No. 5.2e-48;
Matches 162; Conservative 103; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.4%; Score 743; DB 2; 32.8%; Pred. No. 5.2e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: phytoene dehydrogenase
C;Keywords: carotenoid biosynthesis; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492
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lant Mol. Biol. 24, 369-379, 1994

lilin: A novel carotenoid biosynthesis gene coding for zeta-carotene desaturase: funct
likeference number: 843324; MUID:94154256; PMID:8111038
likeference number: 843324
likeference number: 843324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Albrecht, M., Linden, H.; Sandmann, G. 3ur. J. Biochem. 236, 115-120, 1996
); Title: Biochemical characterization of purified zeta-carotene desaturase from Anabaena 1; Reference number: S62214; MUID:96184887; PMID:8617254
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                                                                                                                                                                                                                                                 248 YGAPVERILIDGGRIRGVRIBGGEVVBADAVLCNADIPYAYEKLIDP---KAITILKRKEK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                  DSIAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIECE-KI 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 ITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFBELANCYLVGGGTHFGSGLPTIYE 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || | :::|:||||:||||:423 STPDDWAGTFNIARGSGFGLSQNFTQIGPFRPSNQDARVKNLFFVGASTQPGTGLPTVL1 482
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                                                                                                                             EQFMEQERKRF-NALYPCITRDYSSLKSFLSIDLIKALPWLAFPKSVFNNLGQYFNOBKM 182
                                                                                                                                                                                                                                                                                                              243 INSEIESLIIENGAAKGVYLQHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTPENLKQ 302
                                                                                                                                                                                                                                                                                                                                                                                                         REYSCSTEMANIGEDKIY-DEPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQNASASD 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;/Variety: PCC 7120
//Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 TKHIIIVGAGPGGLCAGMLLSQRGPKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFLLMK
                                    VLDEMFELCERRSEDYLEFLPLSPMYRLLYDDR-DIFVYSDRENMRAELQRVFDEGTDGY
                                                               RLAFCFOSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIABNGGBIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N. Residues: 1-499 <LIN>
N. Cross-references: GB:D26095; NID:g439477; PIDN:BAA05091.1; PID:g439478
N. Experimental source: PCC7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.9%; Score 783.5; DB 2; Best Local Similarity 35.0%; Pred. No. 4.3e-51; Matches 175; Conservative 103; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: phytoene dehydrogenase seywords: carotenoid biosynthesis; membrane bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | | :: : | :: | 483 SARLVTERLMTWAH 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S43324; S62214
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C;Accession: T50745
R;Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A;Ittle: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides A;Attle: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides A;Atcesence number: 222222; MUID:20115911; PMID:10648776
                                                                                                                       468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIWKTCGRDPDADVELKPIDPFYEVRWPDGSHFTVRQSTBAMKAEVARLSPCDVAGYEKF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAENGGEIH 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEQERKRENALYPCITRDYSSLKSFLSL-DLIKALP---WLAPPKSVFNNLGQYFNOEKM 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRWSMGLFVWYFGTKGTKGMWPDVGHHTIVNAPRYKGLVEDIFLKGKLAKDMSLYIHRPS 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIRAHIECEKIITPQTWETDEHVYK-GATFSLSHKFSQMLYWRPHNRFEELANCYLVGGG 468
309 RRWSMGLFVWYFGTKGTKGMWPDVGHHTIVNAPRYKGLVEDIFLKGKLAKDMSLYIHRPS 368
                                                                                                                                                                                                                                                                                                                                                 phytoene dehydrogenase (EC 1.3.-.-) [imported] - Rhodobacter sphaeroides C.Species: Rhodobacter sphaeroides C.Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 IIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFLLMKGVLD
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14 IVIGSGLGGLAAAMRLGAKGWRVIVIDKLDVPGGRGSSITQEGHRFDLGPIIVIVPQSLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 ASDDSLAPAGKSALYVLVPMPNNDSG--LDWQAHCQNVREQVLDTL-----GARLGLS
                                                                      369 ITDPTVAPEGDDTFYALSPVPHLKQAQPVDWQAVAEPYRESVLEVLEQSMPGIGERIGPS
                                                                                                                         110 DIRAHIBCEKIITPQTWETDEHVYK-GATFSLSHKFSQMLYWRPHNRFEELANCYLVGGG
                                       359 ASDDSLAPAGKSALYVLVPMPN--NDSGLDWQAHCONVREQVLDTL-----GARLGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-518 <-GTO-
A;Cross-references: EMBL:AF195122; PIDN:AAF24289:1
A;Experimental source: strain 2.4:1
                                                                                                                                                                                                           THPGSGLPTIYESARISAKLISQKHRVR 496
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THPGAGVPGVIGSABVMAKLAPDAPRAR 506
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C;Superfamily: phytoene dehydrogenase
C;Keywords: oxidoreductase
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Best Local Si
Matches 170
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Accession: 849620
Lang, H.P.; Cogdell, R.J.; Takaichi, S.; Hunter, C.N.
Ubmitted to the EMBL Data Library, November 1994
Description: The complete DNA sequence, specific TNS insertion map and gene assignment
Reference number: 849619
Accession: 849620
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                                                    302 OREYSCSTEMLYLGLD---KIY-DLPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVONA 357
                                                                                                                                                                                                                      415
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                          RLAFCFOSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGINRIAAAMAOVIAENGGEIH 242
                                                                                                         LNSEIESLII-ENGAAKGVKLQHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTPENLK 301
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                                                                                                                                                                                                                                                                           SASDDSLAPAGKSALYVLVPMPN--NDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ytoene dehydrogenase (BC 1.3.-.-) - Rhodobacter sphaeroides
Alternate names: phytoene desaturase
Species: Rhodobacter sphaeroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
Molecule type: DNA
Residues: 1-518 < LAN>
Cross-references: EMBL:X82458; NID:g575405; PID:g575407
Genetics:
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Superfamily: phytoene dehydrogenase
Keywords: oxidoreductase
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A;Accession: A39273
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                       hytoene dehydrogenase [imported] - Rubrivivax gelatinosus ; Species: Rubrivivax gelatinosus ; Species: Rubrivivax gelatinosus ; Species: Rubrivivax gelatinosus ; Species: Rubrivivax gelatinosus ; Species: 21-0ul-2000 #sequence_revision 21-3ul-2000 #text_change 28-Jul-2000 ; Accession: T50910 #sequence_revision 21-3ul-2000 #text_change 28-Jul-2000 ; Accession: T50910 #species of Rubrivivax gelatinosus Photosynt ; Reference number: 225270 #species of Rubrivivax gelatinosus Photosynt ; Reference number: 225270 #species of Rubrivivax gelatinosus Photosynt ; Accession: T50910 #species of Rubrivivax gelatinosus Photosynt ; Molecule type: DNA #species DNA #species in 11 knd *species                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 RVSFCTTPLDFQHRLLSYKGAGFGLEPLLLQSAYFRPHNRSEDVKNLFMVGASTHPGAGV 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMPELCERRSEDYLEFLPLSPMYRLLYDDRDIFVYS-DRENMRAELQRVFDEGTDGYBQF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 MEGERKRENALYPCITRDYSSL--KSFLSL-DLIKALP-----WLAPPKSVFNNLGOY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 FNQEKMRLAFCFQSKYLGMSPWECPALFTMLPYTEHBYGIYHVKGGLNRIAAAMAQVIAE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGGEIHLNSEIESLIIENGAAKGVKLQHGAELRGDEVIINADFAHAMTHLVKPGVLKKYT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 MGGTMRLKAEVKRIEVDNGVATGVTLADGERIPADIVVCNGDTGYLYKNLVDARWRKHWT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 PENLKOREYSCSTFMLYLGLDKIY-DLPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQ 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 NASASODSLAPAGKSALYVLVPMPNNDSGLDWQAHCONVREQVLDTLGARLGLSDIRAHI 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 LVVGSGFGGMAAAVRLAAKGYRVTVLEKLDAPGGRAYVHRREGHVFDAGFTTVTVPYLFD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i.Species: Etwinia herbicola
i.Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 29-Sep-1999
Abceseium: S52866
Abceseium: S52866
Abceseium: S7.7. Lai, E.M.; To, K.Y.; Chang, Y.S.; Liu, S.T.
follow, Genet. 245, 417-423, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 IIVGAGPGGLCAGMILSQRGFKVSIFDKHAEIGGRNRPINANGFTFDTGPTFLIMKGVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
26.7%; Score 725; DB 2; Length 51
Best Local Similarity 32.4%; Pred. No. 1.1e-46;
Matches 158; Conservative 98; Mismatches 208; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ohytoene dehydrogenase (EC 1.3.-.-) - Erwinia herbicola
Superfamily: phytoene dehydrogenase
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N;Alternate names: phytoene desaturase
C;Species: Erwinia herbicola
C;Species: Erwinia herbicola
C;Accession: A39273; A31120
R;Armstrong, G.A.; Alberti, M.; Hearst, J.B.
R;Armstrong, G.A.; Alberti, M.; Hearst, J.B.
A;Title: Conserved enzymes mediate the early reactions of carotenoid biosynthesis: A;Reference number: A39273; MUID:91088634; PMID:2263648
                                                                                                                                                                                             PID:g148397
Library, April 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 ROFLDYSRAVFKEGY -----LKLIGTVPFLSFRDMLRAAPQLAKLQAWRTVYSKVAS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 BORMEQERKRENALYPCITRDYSSLK----SFLSL-DEIKALPWLA---FPKSVFNNLGQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YVQNASASDDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQVLDTLGARLGLSDI 411
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A; Title: Transcriptional activation of flanking sequences by Th1000 insertion. A; Reference number: $52583; MUID:95107237; PMID:7808390
A; Recession: $52586
A; Accession: $52586
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-492 < LIN>
A; Residues: 1-492 < LIN>
A; Ross-references: RMB:M90698; NID:g148393; PIDN:AAA21263.1; PID:g148397
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April C; Superfamily: phytoene dehydrogenase
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFNQBKWRLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLWRIAAAMAQVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 AIBELFTLAGKQIKOYVELLPVAPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVEGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 ENGGEIHIMSEIBSLIIENGAAKGVKLQHGAELRGDEVIINADFAHAMTHLVK--PGVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 KYTPENLKQREYSCSTFMLYLGLDKLYD-LPHHTIVFAKDYTTNIRNIFDNKTLTDDFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHARIGGRNRPINMXGFTFDTGPTFLLMKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 RAHIECEKIITPOTWETDEHVYKGATFSLSHKPSOMLYWRPHNRFEELANCYLVGGGTHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 VLDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-SDRENMRAELORVFDEGTDGY
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A;Residues: 1-492 <ARM>
A;Cross-references: GB:W38423; NID:g148401; PIDN:AAA24820.1; PID:g148402
A;Note: the authors translated the codon CAG for residue 181 as Phe, TCC
                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                           Length 492;
                                                                                                                                                                                                                                                                                                                                                     Query Match
26.3%; Score 713.5; DB 2; Length
Best Local Similarity 31.7%; Pred. No. 7.9e-46;
Matches 158; Conservative 107; Mismatches 208; Indels
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C;Superfamily: phytoene dehydrogenase
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phytoene dehydrogenase (EC 1.3.-.-) crt1 - Erwinia uredovora
CiSpecies: Erwinia uredovora
CiDate: 31-May-1991 #sequence_revision 31-May-1991 #text_change 20-Jun-2000
CiAccession: D37802
R:Misawa, N.; Nakagawa, M.; Kobayashi, K.; Yamano, S.; Izawa, Y.; Nakamura, K.; Harashim, J. Barteriol. 17. 6704-6712, 1990
A;Title: Blucidation of the Erwinia uredovora carotenoid biosynthetic pathway by function.
                                                                                              FMEQERKRFNALYPCITR------DYSSLKSFLSLDLIKALPWLAFPKSVFNNL 173
                                                                                                                           GQ----YFNQEKMRLAFCPQSKYLGMSPWBCPALFTMLPYLEHEYGIYHVKGGLNRIAAA 229
                                                                                                                                                                                                             MAQVIAENGGEIHLNSBIESLIIENGAAKGVKLQHGAELRG-DEVIINADFAHAMTHLVK 288
                                                                                                                                                                                                                                                                                                                                                                                                         288 DFAPIKKYPPHKIADLDYSCSAFLMYIGIDIDVTDQVRLHNVIFSDDFRGNIEBIFEGR- 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEMFELCERRSEDYLEFLPLSPMYRLLYDDRD-IFVYSDRENMRAELQRVFDEGTDGYEQ 125
                                       LTDDFSFYVQNASASDDSLAPAGKSALYVLVPMP--NWDSGLDW--QAHCQNVREQVLDT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGARLGLSDIRAHIECEKIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELAN 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 LATIEVPEDÍKSHÍVSÉTÍFTÞNDFEQTYHAKFGSAFGLMPTLAGSNYYRÞQNVSRDYKD 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 BOFMBOERKRENALYPCITRDYSSLK----SPLSL-DLIKALPWLA---FPKSVFNNLGQ 175
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                                                                                                                                                                                                                                                                                                              289 P-GVLXKYTPENLKQREYSCSTFMLYLGLD-KIYD-LPHHTIVFAKDYTTNIRNIFDNKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 VLDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-SDRENMRAELORVFDEGTDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AIEBLPALAGKQLKEYVBLLPVTPFYRLCWESGKVFNYDNDQTRLEAQIQQFNPRDVEGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFLLMKG
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A;Residues: 1-492 <MIS>
A;Cross-references: GB.190087; NID:g216681; PIDN:BAA14127.1; PID:g216685 C;Superfamily: phytoene dehydrogenase C;Reywords: oxidoreductase C;Reywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 CYLVGGGTHPGSGLPTIYESARIS 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 LYFAGASTHPGAGVPIVLTSAKIT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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Cross-references: GB:BA000018; PID:gl3702511; PIDN:BAB43652.1; GSPDB:GN00149
Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nalene synthase [imported] - Staphylococcus aureus (strain N315)
Species: Staphylococcus aureus
Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 02-Aug-2002
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                                            Query Match 26.0%; Score 704.5; DB 2; Length Best Local Similarity 31.7%; Pred. No. 3.7e-45; Matches 158; Conservative 102; Mismatches 213; Indels
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Keywords: carotenoid biosynthesis; oxidoreductase
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Molecule type: DNA
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295 C94 KYTPENLKQREYSGSTEMLYLGLDKIYD-LPHTIVFAKDYTTNIRNIEDNKTLTDDESF 352

296 C-SNKLQTRRMSNSLFVLYFGLARHTUGLAHTUCFGFRYRELIDBIFNHDGLAEDFSL 350

297 Q-SNKLQTRRMSNSLFVLYFGLAHTHDQLAHTUCFGFRYRELIDBIFNHDGLAEDFSL 350

298 Q-SNKLQTRRMSNSLFVLYFGLAHTHDQLAHTUCFGFRYRELIDBIFNHDGLAEDFSL 350

299 G-SNKLQTRRMSNSLFVLYFGLAHTHDQLAHTUCFGFRYRELIDBIFNHDGLAEDFSL 350

290 Q-SNKLQTRRMSNSLFVLYFGLAHTHDQLAHTUCFGFRYRELIDBIFNHDGLAEDFSL 350

291 VAADAGASDDSLAPAGKSALYULAPVPHLGTANTLDWTVEQPKLRDRIFFAULGHY-MPGL 409

292 G-SNLCTTPROTTPEPTDGLAYHGGAFSVEPVLTQSAWFRPHNRFEELANCYLVGAGTHP 471

203 G-SGLEPTTYRSARISAKLI 489

204 QAGIPGVIGSAKATAGIAM 487
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Search completed: February 29, 2004, 14:52:39 Job time: 17.2234 secs

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Sequence 16, Appl
Sequence 76, Appl
Sequence 22, Appl
Sequence 4, Appli
Sequence 19519, Ap
Sequence 19519, Ap
Sequence 20438, Ap
Sequence 7750, Ap
Sequence 32, Appl
Sequence 12, Appl
Sequence 234, Appl
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Sequence 540, Appl
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1 MANTKHIIIVGAGFGGLCAG......KHRVRFKDIAHSAWLKKAKA 511
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	QY 241 IHLNSBIESLIIRNGAAKGVKLOHGABLRGDEVIINADE :AAWTHLVKPGVLKKYTPENL 300	OY 301 KOREYSCSTEMLYLGLDKIYDLPHHIVPAKDYTTHIRN FDNKTLIDDESFYYQNASAS 360	Qy 361 DDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVL ILGARLGLSDIRAHIECEKI 420	QY 421 ITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFBEL JCYLVGGGTHPGSGLPTIYE 480	OY 481 SARISAKLISOKHRVRFKDIAHSAMLKKAKA 511	RESULT 3 US-09-941-947A-22	; Sequence 22, Application US/09941947A ; Publication No. US20030003528A1 ; GENERAL INPORMATION: ; APPLICANT: Brzostowicz, Patricia C. ; APPLICANT: Cheng, Qiong	APPLICANT: Dicosimo, Deana J. APPLICANT: Mofflas, Mattheos APPLICANT: Miller, Edward S. Jr. APPLICANT: Odom, J. Martin	APPLICANT: ROUVIERS, PICTOR 5: TITLE OF INVESTOR TO SUBJECT OF INVESTOR TO SUBJECT OF THE PREPROPULE. CIAOLS ITS MAN	CURRENT FILING DATE: 2001-09-01; PRIOR APPLICATION NUMBER: 60/229,907	; PRIOR FILING DATE: 2000-09-01 ; PRIOR PAPLICATION NUMBER: 60/229,858 ; NUMBER OF SEQ ID NOS: 60	; SOFTWARE: Microsoft Office 97 ; SEQ ID NO 22 ; LENGTH: 511 ; TYPE: PRT	, ORGANISM: Methylomonas 16a US-09-941-947A-22	Score 2711; DB 10 Length 511; red. No. 3.8e-270	racties 511; Conservative 0; Mismatches 0; Indels 0; Gaps 1 MANTKHIIIVCAGPGELCAGMELSQRGFKVSIFDKHARI: BRNRPINMNGFTFDTGPTFL 60	1 MANTKHIIIVGAGPUGECAGMELSBRGFKVSIFDKFAEL SRNRPINMNGFTFDTGFTF 61 IMKGVLDEMFELCERREDYLEFLPLSPMYRLLYDDRDI YYSDRENMRAELQRYFDEGT 	LWKGVIDEMFELCERRSEDYLEFLFLSPMYRLLYDDRDT DGYBQFWRQERKRFNALYPCITRDYSSLKSFLSLDLIKA	DD 121 DGYRQFWEGERKRFNALYPCITRDYSSLKSFLSLDLIKA: PWLAFPKSVFNNLGQYFNQE 180 QY 181 KWRLAFCFQSKYLGMSPWECPALFTMLFYLEHEYGIYFV: 3GINRIAAAMAQVIAENGGE 240	Db 181 KWRLAFCFQSKYLGMSPWECPALFTMLPYLBHBYGIYHV GGLNRIAAAWAQVIAENGGE 240
DD 61 LWKGVLDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVYSDRENMRAELQRYFDBGT 120	CY 121 DGYEQFWEGERKRFNALYPCITRDYSSLKSFLSLDLIKALPWLAFPKSVFNNLGGYFNGE 180 121 DGYEQFWEGERKRFNALYPCITRDYSSLKSFLSLDLIKALPWLAFPKSVFNNLGGYFNGE 180	OY 181 KMRLAFCFOSKYLGMSPWECPALFTMLPYLEHBYGIYHVKGCLNRIAAANAQVIAENGGE 240 DD 181 KGRLAPCFOSKYLGMSFWECPALFTMLPYLEHBYGIYHVKGCLNRIAAANAQVIAENGGE 240	OY 241 IHLNSEIBSLIIENGAAKGVKLOHGAELROBEVIINADFAHAMTHUVRPGVLKKYTPENL 300 DD 241 IHLNSEIBSLIIENGAAKGVKLOHGAELROBEVIINADFAHAMTHUVRPGVLKKYTPENL 300	Oy 301 KQREYSCSTEWLYLGLDXIYDLPHHIUVPAKDYTYNIRNIFDNKTLTDDFSFYVQNASAS 360	OY 361 DDSLAPAGKSALYUVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIECEKI 420	Qy 421 ITPQTWETDEHVYKGATFSLSHKFSQMLYMRPHNRFEELANCYLVGGGTHPGSGLPTIYE 480	Cy 481 SARISAKLISQKHRYRFKDIAHSAWLKKAKA 511 	RESULT 2 US-09-934-868-76 Sequence 76, Application US/09934868 Patent No. US20020137190A1	GENERAL INFORMATION: APPLICANT: Koffas, Mattheos APFLICANT: Odom. James M	; APPLICANT: Schenzle, Andreas J ; TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN ; FILE REFERENCE: CL1596 US NA	CURRENT APPLICATION NUMBER: US/09/934,868 CURRENT FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: 06/229,858 PRIOR FILING DATE: 2000-09-01	NUMBER OF SEQ ID NOS: 81 SOFTWARE: Microsoft Office 97 SEQ ID NO 76 LENGTH: 511	; TYPE: PRT ; ORGANISM: Methylomonas 16a ; FRATURE:	; OTHER INFORMATION: Amino acid sequences encoded by CRIN1 US-09-934-868-76	Query Match 100.0%; Score 2711; DB 9; Length 511; Best Local Similarity 100.0%; Pred. No. 3.8e-270; Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy I MANTKHIIIVGAGPCCLCAGMILSORGFRVSIEDKHAEIGGRNRPINMAGFTEDTGPTFL 60	2) 61 LAMKGVLDEWFELCERRSEDYLAFLPPLSPMYRLLYDDRDIFVYSDRENMRAELQRVFDBGT 120	2y 121 DGYEQFMEQERKRENALYPCITRDYSSLKSFLSLDLIKALPWLAFPKSVFNNLGQYFNQE 180 121 DGYEQFWEQERKRENALYPCITRDYSSLKSFLSLDLIKALPWLAFPKSVFNNLGQYFNQE 180	KORLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAENGGE

Db 161 DDSLAPAGKSALYVLVPMFNNDSGLDWQAHCQNVR Qy 421 ITPQTWETDEHVYXGATFSLSHKFSQMLYWRPHNRI Db 421 ITPQTWETDEHVYXGATFSLSHKFSQMLYWRPHNRI Qy 481 SARISAKLISQKHVRFKDIAHSAWIKKAKA 511 Db 481 SARISAKLISQKHVRFKDIAHSAWIKKAKA 511	RESULT 5 US-10-369-493-8951 Sequence 8951, Application US/10369493 Fublication No. US20030233675A1 GENERAL INFORMATION: APPLICANT: Gao, Yongwei APPLICANT: Hinkle, Gregory J.	HYPLICANT: STATE, STEVEN C. APPLICANT: Goldman, Barry S. APPLICANT: Chen, Xianfeng ITTLE OF INVENTION: EXPRESSION OF MICROBIAL PRC ITTLE OF INVENTION: PLANTS WITH IMPROVED PROPE FILE REPERENCE: 38-10(52052)B CURRENT PILING DATE: 2003-02-28 FRIOR APPLICATION NUMBER: US 60/360,039 FRIOR PILING DATE: 2003-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 8951 LENGTH: 494 ITYPE: BRT CORGANISM: Chloroflexus aurantiacus US-10-369-493-8951	Query Match	Qy 67 DEMFELCERRSEDYLEFLPLSPWYRL-LYDDRDIFV	125	QY 180 EKMRLAFCFQSKYLGMSPWECPALFTWLPYLEHEYG	QY 240 EIHLNSEIBSLIIENGAAKGVKIQHGAELRGDBVIII	OY 300 INQREYSCSTEMIALGLDKIYD-LPHHTIVFAKDYTF	OY 350 PSFYVQNASASDDSLAPAGKSALYVLVPMPNDSGLI	QY 410 DIRAHIBCEKIITPOTWETDEHVYKGATFSLSHKFS(Cy 470 HPGSGLPTIYESARISQ 491
2Y 241 IHLANSHESLIIENGAAKGVKLOHGABLRGDEVIINADFAHAMTHLVKEGVLKKYTPENL 300 241 IHLANSHESLIIENGAAKGVKLOHGABLRGDEVIINADFAHAMTHLVKPGVLKKYTPENL 300 241 IHLANSHESLIIENGAAKGVKLOHGABLRGDEVIINADFAHAMTHLVKPGVLKKYTPENL 300 2y 301 KQREYSCSTFMLYLGLDKTYDLPHHTIVFAKDYTTVNIRNIFDNKTLTDDFSFYVQNASAS 360	361 DDSLAPAGKSALYULUNNINGGLINGHILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	17 on, Kelley aTION OF CA 0/358,917	NUMBER OF SEQ ID NOS: 28 SOFTWARE: Microsoft Office 97 SEQ ID NO 4 LENGTH: 511 TYPE: PRT ORGANISM: Methylomonas sp.16a	Query Mato Best Local Matches 5	1 MANTKHIIIVQAGPGGLCAGMLLSQRGFYVSIFDKHAELGGRNRPINMNGFTFDTGPTFL			y 181 KWRLAFCPQSKYLGMSPWECPALFTWLPYLEHBYGIYHVKGGLMRIAAAMAQVIAENGGE 240	/ 241 IHLNSEIESLIIENGAAKGVKLOHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTPENL 300 241 IHLNSEIESLIIENGAAKGVKLOHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTPENL 300	/ 301 KOREYSCSTFMLYLGLDKIYDLPHHTIVPAKDYTTNIRNIFDNKTLTDDFSFYVQNASAS 360	361 DDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDYLGARLGLSDIRAHIECEKI 420

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PROTEZN IN PLANTS FOR PRODUCTION OF PREATIF.
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-76;
189; Indels 31; Gaps 12;
                       RREBLA CYLVGGGTHPGSGLPTIYE 480
REQVLE LGARLGLSDIRAHIBCEKI 420
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DLTSNI. AFKAQLAR-FDPALPAEFE 123
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OGIWHP GGPRALAAGLAKAATDLGV 239
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Warner S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: WINGRIP S.
FILER REFERENCE: 38-10 (5.052) B
FILER REFERENCE: 38-10 (5.052) B
FILER APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DAIR: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 18983
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Best Local Similarity 35.4%; Pred. No. 1.3e-72;
Matches 177; Conservative 102; Mismatches 200;
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US-10-369-493-18983
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Best Local Similarity
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APPLICANT: CAO, YONGWEI
APPLICANT: GAO, YONGWEI
APPLICANT: STATEM, Gregory J.
APPLICANT: Statem, Steven C.
APPLICANT: Galdman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE SEPRENCE: 38-10 ($2052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
FRIOR FILING DATE: 2002-02-21
SEQ ID NOS: 47374
SEQ ID NOS: 47374
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; Sequence 19519, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:
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Publication No. US20030233675A1
GENERAL INFORMATION:
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Sequence 20438, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXERSSION OF MICROBIAL PROTEIN: IN PLANTS FOR PRODUCTION OF TILLE REFERENCE: 38-10(52052)B
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, ORGANISM: Rhodobacter sphaeroides US-10-369-493-7750
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ORGANISM: Pantoea stewartii
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US-09-941-947A-32
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LENGTH: 492
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APPLICANT: Cao, Yongwei
APPLICANT: Alater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10 (52022) B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
NUMBER: OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                          66 IDEMFELCERRSEDYLEFLFLSPMYRLLYDDRDIFVYS-DRENMRAELQRVFDEGTDGYB 124
                                                                                                                                                                                                                                                                                                                                                                                                                    125 QFMEQERKRFNALYPCI-TRDYSSLKSFLSLDLIKALPWLAFPKSVPNNLGQYFNQEKAR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 LAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAENGGBIHL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 QVESFHPLLIGGNPFMSSSVYCLITYLEKÇMGVHSAMGGTGALVTGLVNLIBGQGNTIRY 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 RYSMSLFVWYFGTKRRYBDVGHYILLGPRYKELISDIFSRKVVAEDFSLYLHRPTATDP 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 SLAPQGCDTFYVLSPVPNLLGDTDWHTKAETYRASIAKMIGATV-LPDLENQIATSKITT 428
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                                                                                                                                                                                                                                                                                                                                      6 HIIIVGAGFGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFLLMKGV
                                                                                                                                                                                                                               28.3%; Score 767; DB 15; Length 498; 32.1%; Pred. No. 8.9e-70;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                           Query Match 28.3%; Score 767; DB Best Local Similarity 32.1%; Pred. No. 8.9e-Matches 157; Conservative 105; Mismatches
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20438
LENGTH: 498
                                                                                                                                                                   ORGANISM: Rhodopseudomonas palustris
IS-10-369-493-20438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7750, Application US/10369493
Publication No. US20030233675A1
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LENGTH: 518
TYPE: PRT
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                                                                                                                                                         14 LVIGSGLGGLAAAMRLGAKGWRVTVIDKLDVPGGRGSSI3 3GHRFDLGPTIVTVPQSLR 73
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Publication No. US20030003528A1

Publication No. US20030003528A1

APPLICANT: Broostcwicz, Patricia C.

APPLICANT: Dicosimo, Deana J.

APPLICANT: Dicosimo, Deana J.

APPLICANT: Dicosimo, Deana J.

APPLICANT: Miller, Edward S. Jr.

APPLICANT: Miller, Edward S. Jr.

APPLICANT: Miller, Edward S. Jr.

APPLICANT: Miller, Edward S. Jr.

APPLICANT: Miller, Edward S. Jr.

APPLICANT: Miller, Edward S. Jr.

APPLICANT: Miller, Edward S. Jr.

APPLICANT: Miller, Edward S. Jr.

APPLICANT: MOVIER: B.

TILL OF INVENTION: CARCIFROID PRODUCTION FROM A SI: SLE CARBON SOURCE

FILE REFERENCE: CLisqui US NA

CURRENT FILING DATE: 2001-09-01

PRIOR FILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01

SOUTHARE NICROSCH Office 97
                                                                                                                                                                                                                                                                                                                                                                                                        183 RLAFCFOSKYLGMSPWECPALFTWLPYLEHBYGIYHVKGG NRIAAAMAQVIAENGGEIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 ITDPTVAPEGDDTFYALSPVPHLKQAQPVDWQAVAEPYRE:\VLEVLEQSMPGIGERIGPS
                                                                                                                      8 IIVGAGPGGLCAGMLLSORGFKVSIFDXHABIGGRARPIN ANGFFEDTGPTFLLAMKGVLD
                                                                                                                                                                                                                                         68 EMPELCERRSEDYLEFLPLSPMYRLLYDDRDIF-VYSDRE MRAELQRVFDEGTDGYEQP
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                                                            Gaps
                                                            34;
      ength 518
                                                               Indels
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Query Match 27.3%; Score 740; DB 15; Best Local Similarity 33.7%; Pred. No. 5.8e-67; Matches 171; Conservative 96; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 THPGSGLPTIYESARISAKLISQKHRVR 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THPGAGVPGVIGSAEVMAKLAPDAPRAR 506
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RAFLDYSRAVFNEGY------LKLGTVPFLSFKDMLRAAPQLAKLQAMRSVYSKVAG 172 471 62 AIEELFALAGKQLKDYVELLPVTPFYRLCWESGKVFNYDDDQAQLEAQIQQFNPRDVAGY 121 124 EQFMEQERKRFNALYPCITRDYSSLK---SFLSL-DLIKALPWLA---FPKSVFNNLGQ 175 176 YFNQEKWRLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIA 235 236 ENGGEIHLASEIESLIIENGAAKGVKLOHGAELRGDEVIINADFAHAMTHLVK--PGVLK 293 294 KYTPENLKQREYSCSTFMLYLGLDKLYD-LPHHTIVFAKDYTTNIRNIFDNKTLTDDFSF 352 353 YVQNASASDDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQVLDTLGARLGLSDI 411 VLDEMFELCERRSBOYLEFLPLSPMYRLLYDDRDIFVY-SDRENMRAELQRVFDEGTDGY 123 2 KPTVIGAGFGGLALAIRLQAAGIPVLLLEQRDXPGGRAYVYQEQGFTFDAGFTVTDPS 61 5 KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMAGPTFDTGPTFLLMKG 64 5 KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHARIGGRNRPINMNGFTFDFGPTFLLMKG 64 412 RAHIECEKIITPQTWETDEHVYKGATFSISHKFSQMLYWRPHNRFEELANCYLVGGGTHP 65 VLDEMPELCERRSEDYLEFLPLSPMYRLLXDDRDIFVY-SDRENMRAELQRVFDEGTDGY 25; Gaps Query Match 25.9%; Score 703.5; DB 14; Length 492; Best Local Similarity 31.7%; Pred. No. 3.1e-63; Matches 158; Conservative 105; Mismatches 210; Indels 25; DB 10; Length 492; APPLICANT: Brosscowicz, Patricia
APPLICANT: Brosscowicz, Petricia
APPLICANT: Picaraggio, Stephen
APPLICANT: Picaraggio, Stephen
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Encoding Carotenoid Compounds
TITLE OF INVENTION: Genes Encoding Carotenoid Compounds
FILE REPREBENCE: CL1876 US NA
CURRENT APPLICATION NUMBER: US/10/218,118
CURRENT FILING DATE: 2002-08-13
FRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97 Query Match 25.9%; Score 703.5; DB 10; Best Local Similarity 31.7%; Pred. No. 3.1e-63; Matches 158; Conservative 105; Mismatches 210; US-10-218-116-8 ; Sequence 8, Application US/10218118 ; Publication No. US20030148319A1 ; GENERAL INFORMATION: |:|:| : ||: GAGIPGVIGSAKATAGLM 487 , ORGANISM: Pantoea stewartii US-10-218-118-8 SEQ ID NO 8 ઠે 8 ò 셤 ઠે 셤 δ 용 ਨੇ 용 쉱 ਨੇ ਨੇ

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Š	PCITRDYSS
qq	122 RAFLDYSRAVFNEGYLKLGTVPFLSFKDML AAPQLAKLQAMRSVYSKVAG 172
ζ q	176 YFNQEKMRLAFCFQSKYLGMSPWBCDALFTWLPYLEHEY IYHVKGGLARIAAAMAQVIA 235
È	ENGGEIHINSEIESLIIENGAAKGYKLQHGAELRGDEVI NADFAHAWTHLVKPGVLK 29
Dp	DLGGEVVTLNARVSHMETVGDKTQAVQLEDGRRFETCAVA: NADVVHTYRDLLSQHPAAAK 29
දු දු	294 KYTPENLKQREYSCSTEMINLGLDKIYD-LPHHTIVFAK. YTTNIRNIFDNKTLTDDPSF 352 : : : : :
È	DDSLAPAGKSALYVLVPMPN-NDSGLDWQAH QNVRE
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à	RAHIECEKIITPOTWETDEHVYKGATESLSHKFSQMLYW PHNRFEBLANCYLVGGGTHP 47.
Q	RSQLVTHRMFTPFDFRDBLNA
& 8 8	472 GSGLPTIYESARISARLI 489
RESULT 12 US-10-358- ; Sequence; ; Publicat APPLICA APPLICA APPLICA APPLICA FITTE CURRENT CURRENT PRIOR P P PRIOR P P P P P P P P P P P P P P P P P P P	917-12 Lin Pornation US. Lin Pornation US. ANT. Cheng. Qiong ANT. Cheng. Qiong ANT. Tao, Luan ANT. Tao, Luan CERENCE: CL1929 US. EVERNENCE: CL1929 US. EVERNENCE: CL1929 US. EVERNENCE: CL1929 US. EVERNENCE: CL1929 US. EVERNENCE: CL1929 US. EVERNENCE: CL1929 US. EVERNENCE: CL1929 US. EVERNENCE: CL1929 US. EVERNENCE: CL1929 US. EVERNENCE: CL1929 US. EVERNENCE: CL1929 US. EVERNENCE: 2002-02 EVERNENCE: CONSERVENCE EVERNENCE: CL1929 US. EVERNENCE: CONSERVENCE EVERNENCE: CONSERVENCE EVERNENCE: CL1920 US. EVERNENCE: CONSERVENCE EVERNENCE: CL1920 US. EVERNENCE: CONSERVENCE EVERNENCE: CL1920 US. E
අය	123 FLIDVYKKYBIARRYFLERTYRKPSDFYNMTSLV; 3AKLKTLNHA 167
දු පු	174 GQYENQEKMRLAFCFQSKYLGMSPWECPALFTMLP: GHEYGIYHVKGGLMRIAAA 229

KIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEE ANCYLVGGGTHPGSGLPTI SDDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQV? DTLGARLGLSDIRAHIECE ORGANISM: Deinococcus radiodurans 61 LMKGVLDBMFELCER-479 YESARISAKLI 489 ||:|:| |: 477 LASAKITANLM 487 360 419 152 g g 셤 ò 셤 ሯ 성 음 ઠે q Š ∂ ઠે APPLICANT: Cac, Yongwei
APPLICANT: Cac, Yongwei
APPLICANT: Cac, Yongwei
APPLICANT: Galdman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10(52052)8
CURRENT PELLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
SNUMBER OF SEQ ID NOS: 47374
SEQ ID NO 234
LENGTH: 491 MAQVIAENGGEIHLNSEIESLIIENGAAKGVKLOHGAELRG-DEVIINADFAHAMTHLVK 288 346 LIDDFSFYVQNASASDDSLAPACKSALYVLVPMP--NNDSGLDW--QAHCQNVREQVLDT 401 402 LCARLGLSDIRAHIECEKIITPOTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELAN 461 407 LATIEVPEDIKSHIVSETIFTPNDFEQTYHAKFGSAFGLMPTLAQSNYYRPQNVSRDYKD 466 125 123 126 FMEQERKRENALYPCITRDYSSLKSFLSL-----DLIKALPWLAFPKSVFNNLGQYFNQE 180 99 63 7 IIIVGAGPGGLCAGMLLSQRGFKVSIFDKHABIGGRNRPINMNGFTFDTGPTFLLMKGVL 4 IPVIGSGFGSIALAIRLQAANIPTLLIDKRDKPGGRAYVYQDKGFFFDAGPTVITDPSAI 67 DEMPELCERRSEDYLBFLPLSPMYRLLYDDRDIFVY-SDRENMRAELQRVFDEGTDGYEQ 3. 5. Query Match 25.8%; Score 699.5; DB 15; Length 491; Best Local Similarity 30.5%; Pred. No. 7.9e-63; Matches 150; Conservative 109; Mismatches 217; Indels 15; 467 LYFAGASTHPGAGVPIVLTSAKIT 490 462 CYLVGGGTHPGSGLPTIYESARIS 485 Sequence 234, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION: TYPE: PRT ORGANISM: Xenorhabdus nematophilus }-10-369-493-234 -10-369-493-234 64

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235 ----AAKGVKLQHGAELRGDEVIINADFAHAMTHLVKPGVLXXXTPENLKQREYSCSTF 310 KSALYVLVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGL:)IRAHIBCEKIITPQTWBT 428 151 179 ISL------DLIKALPWLAFPKSVFNNLGQ: NQEKMRLAFCFQSKYLGM 195 SPWECPALFTWLPYLEHRYGIYHVKGGLNRIAAAMAQVIA: NGGEIHLNSEIESLIIENG 255 311 MLYLGLDKIYDLP--HHTIVFAKDYTTNIRNIFDNKTLTDL SFYVQNASASDDSLAPAG 368 92 73 93 IXDDRDIPVY-SDRENMRABLQRVFDEGTDGYEQFWEQERKAFNALYPCITRDYSSLKSF 14 ARRYALVIGAGFGGLALGIRLQSLGFDTTLLERLDGFGG-AYQKRIPDGYVFDMGFTVL -- RSEDYLEFLPLSPMYRL 2 ANTXHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGG: -NRPINMNGFFFDTGPTFL Query Match 24.0%; Score 651.5; DB 15; Length 548; Best Local Similarity 29.7%; Pred. No. 8.4e-58; Matches 161; Conservative 96; Mismatches 215; Indels 71; 256 8 8 8 8 & 8 g ð

KOREYSCSTEMLYLGLDKIY-DLPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQNASA 359 KEKKMSNSLPVIYFGLNKLHIQLAHHTICFGNRYKELLIDDIFEGNSIPGDFSLYLHSPSV 357

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 MEGERKRFNALYPCI-TRDYSSIKSFLSLDLIKALPWLAPPKSVFNNLGQYFNQEKMRLA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 FCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAENGGEIHLNS 245
429 DEHVYKGATFSLSHKFSOMLYWRPHNRFBELANCYLVGGGTHPGSGLPTIYESARISAXL 488
                     67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 494;
                                                                                                                                                                                                  Sequence 5, Application US/09547267

Sequence 5, Application US/09547267

Patent No. US20020147371A1

GENERAL INFORMATION: Hommann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Passier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: PREMENTATIVE CAROTENOID PRODUCTION
NAMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: FIDOPPY disk
COMPUTER: IBM PC compatible
OPETATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN R-Blease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
PILING DATE:
PROSIFICATION INVERE: US/09/547,267
FILING APPLICATION DATA:
PRILING APPLICATION NUMBER: 08/660,645
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.6%; Score 640.5; DB 9; Best Local Similarity 30.9%; Pred. No. 9.7e-57; Matches 150; Conservative 98; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        494 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-547-267-5
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IS-09-547-267-5
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Db 183 FSFHTLLVGGNPFSTSSIYALIHALERRGGVNFAKGGTN(LVAGMVALFERLGGTLLLAN 242

Qy 246 BIESLIIBNGAAKGVKLQHGAELRGDEVIINADPAHAMT: LVKPGVLKKYTPENLKQREY 305

243 RVTRIDTEGDRATGVLLDGRQLRADTVASNGDVMHSTR. LGHTRRGTKAALLIMRQRW 302

Qy 305 SCSTFMLYLGLDK-ILDGRQLRADTVASNGDVMHSTR. LGHTRRGTKAALLIMRQRW 302

Qy 305 SCSTFMLYLGLDK-ILDGRQLRADTVASNGDVMHSTR. LGHTRRGTKAALLIMRQRW 302

Qy 305 APAGKSALLYLDEPHHTVPROXTTWIRNIPDN: LTDDFSPYVQNBASADDSL 364

Db 303 SMSLFVLHFGLSKRPENLAHHSVIRGPRYKGLVNBIENGERLDFSRYLHSPCYTDPSL 365

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Qy 365 APAGKSATHYVLAPVPHLGRADVDWBAEARGYAERIFEEL-SRRAIPDLAKHLTVSRIFSP 421

Qy 424 QTWSTDSHYYKGATFSLSHKRSQMLYWRPHNRFEELANC: LVGGGTHPGAGLPTIYSGAR 481

Qy 484 ISAKLI 489

Qy 484 ISAKLI 489

Cy 484 ARAQVW 487

Search Completed: Pebruary 29, 2004, 15:27:50

Job time: 37.9275 secs
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Sequence Sequence Sequence

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181 KARLAFCEQSKYLGMSPWECPALFTMLPYLEHBYGIYHVK 3LARIAAAMAQVIAENGGE 240
181 KARLAFCEQSKYLGMSPWECPALFTMLPYLEHBYGIYHVK 3LARIAAAMAQVIAENGGE 240
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GENERAL INFORMATION:
APPLICANT: Koffas, Mattheos
APPLICANT: Schenzle, Amarian
APPLICANT: Schenzle, Amarian
APPLICANT: Schenzle, Amarias J.
APPLICANT: Schenzle, Amarias J.
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
TILE OF INVENTION: Cheng, Olong
TILE REFERENCE: Clidet US NA
CURRENT ELLING DATE: 2001-08-22
CURRENT FILING DATE: 2001-08-22
FRIOR FILING DATE: September 1, 2001
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 16
LENGTH: 511
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                                           US-08-808-931-8
US-08-808-333-8
US-09-102-4208-8
US-09-102-4208-8
US-09-102-4208-8
US-09-105-28-8
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US-08-808-331-4
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US-08-808-333-4
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·09-489-039A-9181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/09934903
Patent No. 6660507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Methylomonas 16a
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                                                                                                                                                                                   February 29, 2004, 14:35:44 ; Search time 15:5283 Seconds (without alignments) 1698.885 Million cell updates/sec
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2711
1 MANTKHIIIVGAGPGGLCAG.......KHRVRFKDIAHSAWLKKAKA 511
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Sequence 8
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/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PcTUS_COMB.pep:*
                          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-198-452A-958
US-09-489-039A-13710
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US-07-783-705A-4
US-09-091-725-17
US-08-660-645A-5
US-09-298-718-5
US-09-946-969-5
US-09-940-832-4
US-08-980-832-4
US-08-995-726-8
US-08-096-043-8
US-08-096-043-8
US-08-096-043-8
US-08-096-043-10
US-08-096-043-10
US-08-096-043-10
US-08-996-043-18
US-08-936-165A-462
US-09-934-903-18
US-09-9443-184-55
US-09-443-184-55
US-09-443-184-55
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  M protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match
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241 IHINSEIESLIIENGAAKGVKLQHGAELRGDEVIINADPAHAMTHLVKPGVLKKYTPENL 300
                                                                                      KOREYSCSTPMLYLGLDKIYDLPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQNASAS 360
                                                                                                                                                                      DDSLAPAGKSALYVLVPWPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAFIECEKI 420
                                                                                                                                                                                                                          ITPOTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELANCYLVGGGTHPGSGLPTIYE 480
                                                                                                                                               DDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIECEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Miseaw, No. 5429939ihiko

APPLICANT: Miseawin, Kazuo

APPLICANT: Kobayashi, Kazuo

APPLICANT: Vamano, Shigeyuki

TITLE OF INVENTION: DNA SEQUENCES USEFUL FOR THE

TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ladas & Parry

STREET: 26 West 61 Street

CITY: New York

STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIF: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720Kb storage
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.8%; Score 700.5; DB 1; Best Local Similarity 31.5%; Pred. No. 4.4e-62; Matches 157; Conservative 103; Mismatches 213;
                                                                                                                                                                                                                                                                                                           SARISAKLISQKHRVRFKDIAHSAWLKKAKA 511
                                                                                                                                                                                                                                                                                                                                               SARISAKLISOKHRVRFKDIAHSAWLKKAKA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
SOFTWARE:
SOFTWARE:
N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/783,705A
FILING DATE: 19911023
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-103078
FILING DATE: 02-APR-1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 05-MAR-1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 19-APR-1990
APPLICATION NUMBER: 37,738
FILING DATE: 19-APR-1990
APPLICATION NUMBER: 33,778
FILING DATE: 12-APR-1990
APPLICATION NUMBER: 33,778
FELEPHONE: 212-709-1935
FELEPHONE: 212-709-1935
FELEPHONE: 212-709-1935
FELEPHONE: APPLICATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TURNER: ANTO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/07783705A
Patent No. 5429939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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Indels

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62 AIBBLFALAGKQLKEYVELLPVTPFYRLCWESGKVFNYD: DQTRLEAQIQQFNPRDVBGY 121
                                                                                                                                                                                                                                                 122 RQFLDYSRAVFKBGY-----LKLGTVPFLSFRDME: AAPQLAKLQAWRSVYSKVAS 172
                                                                                                                                                                                                                                                                                                                                                        124 EQFMEQERKRENALYPCITRDYSSLK----SFLSL-DLI.ALPWLA---FPKSVFNNLGQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                236 ENGGEIHLNSEIESLIIENGAAKGVKLQHGAELRGDEVI WADFAHAMTHLVK--PGVLK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411
                                                                                                          65 VLDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-. DRENMRAELQRVFDEGTDGY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412 RAHIECEKIITPQTWETDEHVYKGATFSLSHKFSQMLYW: PHNRFEELANCYLVGGGTHP 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRATVYEDQGFTFDAGFTVITDPS 61
5 KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRN PINMNGFTFDTGPTFLLMKG 64
                                                                                                                                                                                                                                                                                                                        176 YFNOEKMRLAFCFQSKYLGMSPWECPALFTMLPYLEHEY : IYHVKGGLNRIAAAMAQVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 YVQNASASDDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQVLDTLGARLGLSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Improved methods for transforming Phaffia and recombinant DNA for use therein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUTY: Washington & Foerster 11pp STREEF: 2000 Pennsylvania Avenue, N.W.

STREEF: 2000 Pennsylvania Avenue, N.W.

STATE: DC

COUNTRY: United States of America

ZIP: 20006-1888

COMPUTER: ELOSPY disk

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.2 (BPO)

CURRENT APPLICATION DATA:

RELIGNED DATE: 23-DBC-1996

CLASSIPICATION: 435

PRICH DATE: 22-DBC-1995

FILING DATE: 22-DBC-1995

APPLICATION NUMBER: EP 95203620.0

FILING DATE: 22-DBC-1995

APPLICATION NUMBER: EP 95203620.0

FILING DATE: 12-DBC-1995

APPLICATION NUMBER: BP 96200943.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: BP 96200943.7 FILING DATE: 11-APR-1996 ATTONIEY/ACENT INFORMATION:
NAME: E. VICTOR DONAINE REGISTRATION NUMBER: 35,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09091725; Patent No. 6329141; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 GSGLPTIYESARISAKLI 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 GAGIPGVIGSAKATAGLM 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Im
TITLE OF INVENTION: and
NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAEN--GGE 240
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                                                                                                                                                                                                                                                                                                                                                   8 IIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFLLMKGVLD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 EMPELCERRSEDYLEPLPLSPMYRLLYDDRDIFVYS-DRENMRAELQRVPDEGTDGYEQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 IHLNSEIESLIIE--NGAAKGVKLQHGAELRGDEVIINADFAHAMTHLV-----KP
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                    Length 582;
                                                                                                                                                                                       Query Match 24.8%; Score 673; DB 4; Length 58 Best Local Similarity 30.6%; Pred. No. 3.5e-59; Matches 155; Conservative 109; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08660645A
Patent No. 6087152
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Passamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVERTION: FERNENTATIVE CAROTENOID PRODUCTION
NUMBER OF SECURICES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WMBER: US/08/660,645A
FILING DATE: 07-UUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVGASTHPGTGVPIVLAGAKLTANOV 516
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COUNTRY: USA
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-091-725-17
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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JS-08-660-645A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 HDYAREVYREGYLKLGTTPP--LKLGOMLNAAPALMRLOARSVHSWVARFIQDPHLRQA 182
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Patent No. 612413
GEBERAL INFORMATION:
APPLICANT: Holmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES:
ADDRESSER: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                          23.6%; Score 640.5; DB 3; 30.9%; Pred. No. 5.3e-56; ive 98; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 IIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPIN
PRIOR APPLICATION DATA:

APPLICATION NUMBER: BP 95108888.9
FILING DATE: 09-7UN-1995
ATTORNEY AGENT INFORMATION:
NAME: POKTAS, BTUCE A.
REGISTRATION NUMBER: 23.748
REFERENCE/DOCKET NUMBER: RAM 6002/170
TELECOMMUNICATION INFORMATION:
TELEFANCE; (201) 235-2363
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              494 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 150; Conserv
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                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
23.6%; Score 640.5; DB 3;
Best Local Similarity 30.9%; Pred. No. 5.3e-56;
Matches 150; Conservative 98; Mismatches 231;
                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: RAN 6002/170 TELECOMMUNICATION INFORMATION: TELEPHONE: (201) 235-2801 TELEPHONE: (201) 235-2363 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                : 340 Kingsland Street
Nutley
                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: POKTAS, Bruce A.
REGISTRATION NUMBER: 32,748
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 494 amino acids TYPE; amino acid
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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                                             USA
                                           COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 RVTKIDTEGDRATGVTLLDGRQLRADTVASNGDVMHSYRELLGHTRRGRTKAAILNRQRW 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCSTEMLYIGLDK-IYDLPHHTIVPAXDYTTWIRNIFDN:TLTDDFSFYVQNASASDDSL: 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 EMPELCERRSEDYLEFIPLSPMYRLLYDDRDIFVY-SDRENNRAELQRVFDEGTDGYEQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 MEQERKRFNALYPCI-TRDYSSLKSFLSLDLIKALPWLA PKSVFNNLGQYFNQEMMRLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                         APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: PERMENPATIVE CAROTENOID PROJUCTION
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.6%; Score 640.5; DB 3; Best Local Similarity 30.9%; Pred. No. 5.3e-56; Matches 150; Conservative 98; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POKTAS, BILDCE A;
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMINICATION INFORMATION:
TELEPHONE: (201) 235-2363
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/546,969
FILING DATE:
                                                                                                                                                                                                                                                                         Hoffmann-La Roche Inc
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
RESULT 6
US-09-546-969-5
US-09-546-969-5
Sequence 5, Application US/09546969
Patent No. 6207409
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                            340 Kingsland Street
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-STREET: 340 Kingslam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                       STATE: N
COUNTRY:
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COUNTRY:
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                                                                                                                             483
303 SMSLFVLHFGLSKRPENLAHHSVIFGPRYKGLVNEIFNGPRLPDDFSMYLHSPCVTDPSL 362
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                                                                                                                                                   BMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-SDRENMRAELQRVFDEGTDGYEQF 126
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                                       365 APAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIBCEKIITP
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Sequence 4, Application US/08980832B
GENERAL INFORMATION.
APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Vari
TILE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentive Carotenoid
CURRENT APPLICATION NUMBER: US/08/980,832B
CURRENT FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Flavobacterium sp. R1534
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Matches 150, Conservative
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68 EMPRICERRSEDYLEFLPLSPMYRLLYDDRDIPVY-SDRENMRABLQRVFDEGTDGYRQF 126
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                                                                                                APPLICANT: Passamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PROUGTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
Sequence 5, Application US/09547267
Patent No. 6613543
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REFERENCE/DOCKET NUMBER: RAN TELECOMUNICATION INFORMATION: TELEPHONE: (201) 235-2363
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                               Hohmann, Hans-Peter
                                                                                                                                                                                                                                                                                   STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
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TYPE: amino acid
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Matches 150; Conservative
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COMPUTER READABLE FORM:
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                                                    GENERAL INFORMATION:
APPLICANT: Hohman
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TOPOLOGY: lir
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482 ATAOVM 487
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STREET: < ...
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                                                                              363 APEGMSTHYVLAPVPHLGRADVDWEAEAPGYAERIFEEL-ERRAIPDLRKHLTVSRIFSP 421
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Fermentative Carotenoid Production
TITLE REFERENCE: 15464 US (C38435/125944)
CURRENT APPLICATION NUMBER: US/09/920,923B
CURRENT FILING DATE: 2001-08-02
PRIOR PILING DATE: 1997-12-01
                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09920923B Patent No. 6677134 GENERAL INFORMATION:
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// ORGANISM: Flavobacterium sp. R1534
US-09-920-923B-4
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SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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Matches 150; Conservative
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US-09-920-923B-4
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                                                                                                          174 GOYFNQBKMRLAFCFQSKYLGMSPWBCPALFTMLPYLEHSYGIYHVKGGLNRIAAAMAQV 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Amoco Corp., Patents and Licensing Dept 200 E Randolph St
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FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION DATA:
APPLICATION ANDRER: US/08/095,726
FILING DATE: 21-UUL-1993
CLASSIFICATION: 435
                                                                                                                                                     APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Proffitt, John H
APPLICANT: Proffitt, John H
APPLICANT: Varger, James G
APPLICANT: Yen, Huel-Che B
TITLE OF INVENTION: Beta-Carotene F
TITLE OF INVENTION: Genetically En
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.24
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
Sequence 8, Application US/08095726
Patent No. 5530188
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ZIF. 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 30.39
Matches 152; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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VIDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-SURENMRAELQRVFDEGTDGY 123
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STREET: 120
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ZIP: 606
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                                                          291 QKRAARLERKSMSINSIFVLYFGLNQPHSQLAHHTICFGPRYREJIDBIFTGSALADDFSL 350
                                                                                                                           410 RSQLVTQRIFTRQ---TSRHAWIAILGSLFIEPPSLTQGLFAANATRH---SNLYLVAAG 463
231 FIDLGGEIELNARVEELIVVADNRVSQVRLADGRIFDTDAVASNADVVNTYKKLLGTIPVG 290
                                  294 KYTPENLKOREYSCSTFMLYLGLDKIY-DLPHHTIVPAKDYTTWIRNIFDNKTLTDDFSF 352
                                                                                                                                                                                  RAHIECEKIITPOTWETDEHVY---KGATFSLSHKFSOMLYWRPHNRFEELANCYLVGGG 468
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Mukharji, Indrani
APPLICANT: Yarger, James G
APPLICANT: Yarger, James G
APPLICANT: Yer, Huei-Che B
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/785,568
FILING DATE: 30-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530189val B
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Parentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NOMER: US/08/096,043
FILING DATE: 22-UU-1993
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                        464 THPGAGIPGVVGLAESTASLM 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: FLOPPY DISK
MEDIUM TYPE: PC COMPALIATE
PC-DOS/MS_DC
                                                                                                                                                                                                                                                                                                                                                                                 Seguence 8, Application US/08096043
Patent No. 5530189
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amino acid
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Best Local Similarity 30.3%
Matches 152; Conservative
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LENGTH: 489 amino acid
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APPLICANT: Ausich
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STREET: 200 -
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S-08-096-043-8
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APPLICANT: BILINGARIA, Indexed and APPLICANT: Mukharji, Indexed and APPLICANT: Mukharji, Indexed and APPLICANT: Proffit, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huei-Che B.
TITLE OF INVENTION: Biosynthesis of Zeaxanthin and
TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: | : | | | | | : | : | : | : | | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
122 RRFLAYSQAVFQ-----EGYLRLGSVPFLSFRÖMLRAGFQLLKLQAW----QSVYQSV 170
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MEDIUM TYPE: Floppy disk
COMFUTER: ENDORY disk
COMFUTER: IBM GOOD COMPUTER:
COMFUTER: IBM PC-DOS/NG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SUBTRARE: Patentin Release #1.0, Version #1.30
CURRENT AFPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
CLASSIFICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: US 0F-RE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,674
FILING DATE: US 03-NG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 03-NG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 03-NG-1990
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120 S. Riverside Plaza, 22nd Floor
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Brinkhaus, Priedhelm :
Mukharji, Indrani
Proffitt, John H.
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413
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Best Local Similarity 30.3%; Pred. No. 2.5e-53;
Matches 152; Conservative 97; Mismatches 218; Indels
APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATE: APPLICATION NUMBER: US 07/487,613
PILING DATE: 02-MAR-1990
ATTORNEY AGENT INFORMATION:
NAME: Ganson, Edward P.
REGISTRATION NUMBER: 29,381
REFERRENCE/DOCKET NUMBER: AMO-006.1
TELEPHONE: (312) 655-1501
INFORMATION FOR SEG ID NO: 8: SRQUENCE CHARACTERIZIOS.
INFORMATION FOR SEG ID NO: 8: SRQUENCE CHARACTERIZIOS.
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Brinkhaus, Friedhelm L
Mukharji, Indrani
Profflit, John H
Yarger, James G
Yen, Huei-Che B
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Patent No. 5530188
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yarger, James G.
APPLICANT: Yarger, James G.
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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127 MEGERKRENALYPCITRDYSSLKS--FIGL-DLIKALP------WLAFPKSVFNNLGQY 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 LGGEIELMARVEELVVADDNRVSQVRLADGRIFDTDAVASNADVNTYKKLLGTIPVGQKR 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 NASASDDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCONVREQVLDTLGARLGLSDIRAH 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 EMFELCERRSEDYLEFLPLSPWYRLLYDDRDIFVY-SDREENORVFDEGTDGYEOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 22.5%; Score 611; DB 1; Langth 48
Best Local Similarity 30.3%; Pred. No. 5e-53;
Matches 151; Conservative 97; Mismatches 216; Indels
Beta-Carotene Biosynthesis i
Genetically Engineered Hosts
                                                                                                                                                                                                                     GSGLPTIYESARISAKLI 489
                                                                           ADDRESSEE: Amoco Corp., P. STREET: 200 E Randolph St CITY: Chicago
                                                                                                                               STATE: IL
CCUNTRY: USA
ZIP: 60600-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-095-726-10
   TITLE OF INVENTION: BEI
TITLE OF INVENTION: GEI
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472
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us-08-096-623A-10

Sequence 10, Application Us/08096623A

Patent No. 5684238

GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Proffitt, John H.
APPLICANT: Yen, Huei-Che B.
ITILE OF INVENTION: Biosynthesis of Zeaxanthin and
ITILE OF INVENTION: Biosynthesis of Zeaxanthin in Genetically Engineered Hosts
NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Karz, Ltd.
STREET: 120 S. Riverside Plaza, 22nd Floor
CITY: Chicago
STRATE: IL
COUNTRY: USA
                                                                                                                                            356 NASASDDSIAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQVLDTIGARLGLSDIRAH 414 : | | | | | : | | | : : | | | : : | | | 354 SPCYTDPSLAPPPCASFYVLAPVPHIGNAPLDWAQEGPKLRDRIERY-WPGLRSQ 412
                                                294 AARLERKSMSNSLFVLYFGLNQPHSQLAHHTICFGPRYRESIDEIFTGSALADDFSLYLH 353
                                                                                                                                                                                                                                                                                                                                                                 413 LVTQRIFTRQ---TSRHAWIAILGSLFIBPPSLTQGLFAANATRH---SNLYLVAAGTHP 466
                                                                                                                                                                                                                                                                                                     415 IECEKIITPQTWETDEHVY---KGATFSLSHKFSQMLYWERPHRRFEELANCYLVGGGTHP 471
297 PENLKQRBYSCSTFMLYLGLDKIY-DLPHHTIVFAKDYTTWIRNIFDNKTLTDDFSFYVQ 355
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MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
RIGHTON APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 08-DEB-1991
APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
RIGHTON APPLICATION DATA:
APPLICATION NUMBER: US 07/562,551
FILING DATE: 18-MAY-1990
RIGHT APPLICATION NUMBER: US 07/487,613
FILING DATE: 18-MAY-1990
APPLICATION NUMBER: US 07/487,613
FILING DATE: 02-MAR-1990
APPLICATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
REGISTRATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
TYPE: amino acid
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                                                        Sequence 10, Application US/08096043
Sequence 10, Application US/08096043
Sequence 10, Sapulas
GENERAL INFORMATION:
APPLICANT: Autich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Broffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yarger, John H
APPLICANT: Yarger, John H
APPLICANT: WINGERT, John H
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APPLICANT: Yarger, John H
APPLICANT: Yarger
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ZIP: 60680-0703

COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,043
FLING DATE: 22-UUL-1993
CLASSIPRICATION: 435
PRIOR APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: US
TLING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: GABLOWAY, NO. 5530189VALB
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
467 GAGIPGVVGLAESTASLM 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 3128567180
TELEPAX: 3128564972
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 489 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
IS-08-096-043-10
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34; Gaps
                                                                                               22.5%; Score 611; DB 1; Length 489; 30.3%; Pred. No. 5e-53; Artive 97; Mismatches 216; Indels
                                                                                                 Query Match
Best Local Similarity 30.3%
Matches 151; Conservative
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-096-623A-10
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68 EMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-SDRENMRAELQRVFDEGTDGYEOF 126 127 MEGERKRFNALYPCITRDYSSLKS--FLSL-DLIKALP------WLAFPKSVFNNLGQY 176 5 VVIGAGEGGLALAIRLQAAGIPTVLLBQRBKPGGRAYVWHDQGFTFDAGFTVITDPTALE 64 8 IIVGAGPGGLCAGMILSQRGFKVSIFDXHAEIGGRNRPINMNGFTFDTGPTFLIMKGVLD 67 125 ਨੇ Ωp ò 용

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415 IECEKIITPOTWETDEHVY---KGATFSLSHKFSOMLYWRPHNRFEELANCYLVGGGTHP 471

GSGLPTIYESARISAKLI 489 |:|:|: GAGIPGVVGLAESTASLM 484 472 467

Search completed: February 29, 2004, 14:54:51 Job time : 18.5283 secs

	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
M protein - pr	M protein - protein search, using sw model
inon:	February 29, 2004, 14:26:38; Search time 60.417 Seconds (without alignments) 2389.754 Million cell updates/sec
itle: erfect score: equence:	US-09-941-947A-22 2711 1 MANTKHIIIVGAGPGGLCAGKHRVRFXDIAHSAWLKKAKA 511
coring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
sarched:	1586107 segs, 282547505 residues

sarched:

otal number of hits satisfying chosen parameters:

ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 sed inimum DB s iximum DB s

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* .: geneseqp1980s:* :: geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* atabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	uoı	Methylomo	High grow	Methylomo	Methylomo	Listeria	Protein e	Anabaena	Photorhab	Pantoea s	Pantoea s	Pantoea s	Staphyloc	Staphyloc	Polypepti	C. utilis	Protein e	Erwinia u	Erwinia u	Phaffia d	Blakeslea	Flavobact	Flavobact	Erythroba	Phytoene	Phytoene
	Description	Aae22309	Abg61588	Aau80332	Ada14534	Abb49224	Abu32531	Aar64269	Abm70123	Aae22314	Aa016021	Abp96688	Abm72613	Ada14542	Aar07466	Aaw82257	Aaw87889	Aaw99099	Aay26333	Aaw22499	Abp97465	Aaw00871	Aaw69532	Aar95697	Aaw01122	Aaw00173
SUMMAKIBS	91	AAE22309	ABG61588	AAU80332	ADA14534	ABB49224	ABU32531	AAR64269	ABM70123	AAB22314	AA016021	ABP96688	ABM72613	ADA14542	AAR07466	AAW82257	AAW87889	AAW99099	AAY26333	AAW22499	ABP97465	AAW00871	AAW69532	AAR95697	AAW01122	AAW00173
	DB	'n	Ŋ	ß	9	Ŋ	ø	7	9	Ŋ	v	9	9	ø	~	N	N	7	N	7	9	(7)	7	N	N	7
	Length	511	511	511	511	490	490	499	494	492	492	492	502	502	492	492	492	492	492	582	582	494	494	526	489	489
d	Ouery Match	100.0	100.0	100.0	100.0	34.3	34.3	28.9	26.3	25.9	25.9	25.9	25.9	25.9	25.8	25.8	25.8	25.8	25.8	24.8	24.0	23.6	23.6	23.0	22.6	22.6
	Score	2711	2711	2711	2711	929.5	929.5	783.5	713	703.5	703.5	703.5	702.5	702.5	700.5	700.5	700.5	700.5	700.5	673	651	640.5	638.5	624.5	614	614
	esult No.	1	7	m	4	Ŋ	و	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23.	24	25

Aaw32472 Erwinia h Aar13985 Phytoene_ Aar1398 Phytoene Aaw01123 Phytoene				Aab76640 Corynebac Aab76641 Corynebac Aag90440 C glutemi Aau34200 Staphyloc
AAW32472 AAR13985 AAR13984 AAW01123	AAW00174 AAW32475 AAB22310 ABG61589	AAU80333 ADA14538 ABU43877	ADA14544 ABM72616 AAB85728 AAO15518	AAB 76640 AAB 76641 AAG90440 AAU34200
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4. 4. 4. 4 60 60 60 6 60 60 60 6	4 4 4 4 0 8 8 9 9 2 9 7 7	497 497 502	5 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	57.44 57.448 53.448
222.6	1222 1222 2222 2024 4	44.00.6	18.5 17.8 17.8	17.7 17.7 17.7 16.5
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22 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	, w w w w	. W W W .	0 8 8 4 4 2 8 6 0 1	4 4 4 4 5 6 4 8

ALIGNMENTS

Carotenoid; isopentenyl pyrophosphate; antheraxanuhin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electru-optic application; aquaculture; enzyme; diapophytoene dehydrogenase; CrtN1. Methylomonas 16a sp. diapophytoene dehydrogenase (CrtN1) enzyme. AAE22309 standard, protein, 511 AA. (first entry) (revised) 07-AUG-2003 25-JUL-2002 AAE22309; RESULT 1

Methylomonas sp. WO200218617-A2. 07-MAR-2002.

(DUPO) DU PONT DE NEMOURS & CO E I. 01-SEP-2000; 2000US-0229858P. 04-SEP-2001; 2001WO-US027420.

Koffas M, Miller ES; Q, Dicosimo DJ, K, Rouviere PE; Brzostowicz PC, Cheng Q, Odom JM, Picataggio SK,

WPI; 2002-351711/38. N-PSDB; AAD35507.

Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon the caroter substrates,

Claim 37; Page 127-129; 156pp; English.

The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule controling an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by

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the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Methylomonas lea sp. diapophytoene dehydrogenase (CrtM1) enzyme used in the invention. (Updated on 07-AUG-2003 to correct OS field.) using microorganism having a nucleic acid molecule encoding enzymes in

Sequence 511 AA;

180 420 420 ITPOTWETDEHVYKGATFSLSHKFSOMLYWRPHNRFRELANCYLVGGGTHPGSGLPTIYE 480 ITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFBELANCYLVGGGTHPGSGLPTIYE 480 9 9 1 MANTKHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFL LMKGVLDEMFELCERRSEDYLEFILPLSPMYRLLYDDRDIFVYSDRENMRARLQRVFDEGT KQREYSCSTFMLYLGLOKIYDLPHHIIVFAKDYTTNIRNIFDNKTLTDDFSFYVQNASAS DDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIBCEKI DGYEQFMEQERKRFNALYPCITRDYSSLKSFLSLDLIKALPWLAFPKSVFNNLGQYFWQE KWRLAFCFQSKYLGMSPWECPALFTWLPYLEHEYGIYHVKGGLNRIAAAMAQVIAENGGE KMRLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAENGGE IHLNSEIESLIIENGAAKGVYLQHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTPENL KOREYSCSTFMLYLGLDKIYDLPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQNASAS DDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIECEKI 1 MANTKHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFL LMKGVLDEMFELCERRSEDYLBFLPLSPMYRLLYDDRDIFVYSDRENMRAELORVFDEGT Gaps ô 100.0%; Score 2711; DB 5; Length 511; 100.0%; Pred. No. 6.4e-265; ive 0; Mismatches 0; Indels 0. SARISAKLISOKHRVRFKDIAHSAMLKKAKA 511 SARISAKLISQKHRVRFKDIAHSAWLKKAKA 511 511; Conservative Local Similarity 61 61 121 121 181 241 301 481 Query Match 181 241 301 361 363 481 ਧੋ ≥ ≥ ū \geq Đ. ñ Ω. ≿ ð 2 ≥, ≿ ď ⋩ S

ABG61588 standard; protein; 511 AA (first entry) (revised) 07-AUG-2003 27-AUG-2002 RESULT 2 ABG61588

High growth methanotrophic bacterial strain polypeptide #38.

High growth methanotrophic bacterial strain, Cl carbon substrate; enzyme; methano! Embden-Meyerhof carbon flux pathway; 168 RNA; pyrophospbate dependent phosphofrutchinase; nitrogen-containing compound; ammonia; nitrate; nitrite; nitrogen; pigment; oxygen; landfill; methane-containing environment; waste water treatment system; isoprenoid; nitrous oxide; terpenoid; animal feed; carotenoid; exopolysaccharide.

Methylomonas sp.

WC200220728-A2

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The invention relates to a high growth methanotrophic bacterial strain, which grows on a Cl carbon substrate e.g. methane and methanol, and comprises a functional smadern Meyerboc Carbon flux pathway comprises a comprise a functional smadern Meyerboc Carbon flux pathway comprises a functional smadern Meyerboc Carbon of Lathway compound, or protein and for the biotransformation of a nitrogen-containing compound, production of a feed product comprising a protein, carbohydrates and a production of a feed product comprising a protein, carbohydrates and a production of a feed product comprising a protein, carbohydrates and a nitrites in methane-containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are present. The bacterial strain of the invention c.n be used as a centrifying agent for the conversion of nitrates are present. The bacterial strain of the invention c.n be used as a demittifying agent for the conversion of nitrates and a wide oride with methane or methanol as a carbon source. It is also used in the production of biomass including proteins, carbohydrates and a wide compounds, useful as pigments for insprenoid and carotenoid compounds, useful as pigments and as monomers in polymeric materials and compounds, useful as pigments and as monomers in polymeric materials and an invention (Updated on 07-MUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                   New high growth methanotrophic bacterial strain, useful for producing single cell proteins, grows on a Cl carbon substrate, and comprises a functional gene encoding in Embden-Meyerhof carbon pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 150-152; 157pp; English.
                                                                                                                                                                   (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                  Schenzle A;
                                                                                                                   01-SEP-2000; 2000US-0229858P.
                                                                       28-AUG-2001; 2001WO-US026827
                                                                                                                                                                                                                  Koffas M, Odom JM,
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                          14-MAR-2002
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100.0%; Score 2711; DB 5; Length 511; 100.0%; Pred. No. 6.4e-265; ive 0; Mismatches 0; Indels 0; Local Similarity 100. Query Match

1 MANTKHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHAEIGGRNRPINMNGFTFDTGPTFL

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180 240 120 240 241 IHINSEIESLIIENGAAKGVKLQHGAELRGDEVIINADFAHAMTHLVKPGVLKKYTPENL 300 KQREYSCSTFMLYLGLDKIYDLPHHTIVFAKDYTTNIRNEPDNKTLTDDFSFYVQNASAS 360 9 241 IHLNSEIESLIIENGAAKGVKLQHGAELRGDEVIINADFAGAMTHLVKPGVLKKYTPENL 300 301 KOREYSCSTFMLYLGLDKIYDLPHHTIVFAKDYTTNIRNIFDNKTLTDDFSFYVQNASAS 360 1 MANTECHIIIVGAGEGGCCAGMLLSQRGFKYSIFDKEAEIGGRNRPINMNGFTFDTGPTFL 61 LMKGVLDBMFELCERRSEDYLBFLPLSPMYRLLYDDRDIFVYSDRENMRAELQRVFDEGT DGYEQFMEQERKRFNALYPCITRDYSSLKSFLSLDLIKAL PWLAFPKSVFNNLGQYFNQE 121 DGYEQFMEQERKRENALYPCITRDYSSLKSFLSLDLIKALPWLAFPKSVFNNLGQYFNQE 61 LMKGVLDEMFELCERRSEDYLEFILPLSPMYRLLYDDRDIFYYSDRENWRAELQRVFDEGT KWRLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHV; SGLNRIAAAMAQVIAENGGE KORLARCPOSKYLCMSPWECPALFTMLPYLEHEYGIYHVK 3GLNRIAAAMAQVIAENGGE 121 301 181

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ð 음 361 DDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLEFLGARLGLSDIRAHIBCEKI 420

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240 300 360 360 420

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180 180

361 421 421 481 181

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241 IHLNSKIESLIIENGAAKGVKLQHGASLRGDEVIINADFALAMTHLVKPGVLKKYTPENL
                                                                                                  KARLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAENGGE
                                                                                                                                                                    KORLAPCPQSKYLGMSPWECPALFTMLPYLEHBYGIYHVKGGLMRLAAAMAQVIARNGGE
                                                                                                                                                                                                                       THINSELESLI LENGAAKGVKLOHGAELRGDEVI INADFARBATHLVKPGVLKKYTPENL
                                                                                                                                                                                                                                                                                       KQREYSCSTFMLYLGLDKIYDLPHHTIVFAXDYTTNIRNIFDNKTLTDDFSFYVQNASAS
                                                                                                                                                                                                                                                                                                                        301 KOREYSCSTFMLYLGLDKIYDLPHHTIVPAKDYTTNIRNIFDNKTLTDDFSFYVQNASAS
                                                                                                                                                                                                                                                                                                                                                           DDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIECEKI
                                                                                                                                                                                                                                                                                                                                                                               DDSLAPAGKSALYVLVPMPNNDSGLDWQAHCQNVREQVLDYLGARLGLSDIRAHIECEKI
                                                                                                                                                                                                                                                                                                                                                                                                                              421 ITPQTWETDEHVYKGATPSLSHKFSQMLYWRPHNRFEELANCYLVGGGTHPGSGLPTIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                               DGYEQFWEQERKRPNALYPCITRDYSSLKSFLSLDLIKALPWLAFPKSVFNNLGQYFNQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SARISAKLISQKHRVRFKDIAHSAWLKKAKA 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA14534 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid molecule encoding a isoprenoid biosynthetic enzyme, isolated from Methylomonas 16a, useful for the production of isoprenoid
DSSLAPAGKSALYULVPMPNNDSGLDWQAHCQNVREQVLDTLGARLGLSDIRAHIECEKI
                                                    I TPQTWETDEHVY KGATFSLSHKFSQMLYWRPHNR PEBLANCYLVGGGTHPGSGLPTIYE
                                                                                                                                                                                                                                                                                                                                                                             Isoprenoid biosynthetic enzyme; isoprenoid compound; feed additive; keratenoid; pigment; flavour; fragrance; open reading frame 8; ORP8; crtN1; crtN copy1; diapophytoene dehydrogenase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Picataggio SK;
                                                                                                                                                                                                                                                                                                                                                Methylomonas 16a ORF8 crtN1 protein seguence.
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                                                                                                                                          SARISAKLISQKHRVRFKDIAHSAWLKKAKA
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                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schenzle A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koffas M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-383051/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methylomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200220733-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rouviere PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-SEP-2000;
                                                                                                                                                                                                                                                                                                               15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2002.
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Cheng Q,

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omega-aldehyde-functionalised carotenoid;
omega-carboxy-functionalised carotenoid; C30 carotenoid;
carotenoid biosynthesis; antioxidant; microbial; pigment; feed additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding carotenoid biosynthesis enzymes, useful for onalized carotenoids, e.g. pigments and antioxidants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 91-93; 125pp; English
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carotenoid biosynthetic enzyme; CBE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preparing functionalized calso encoded polypeptides.
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Gaps

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Indels

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0; Mismatches

Length 511;

100.0%; Score 2711; DB 5; 100.0%; Pred. No. 6.4e-265;

Query Match 100. Best Local Similarity 100. Matches 511; Conservative

Sequence 511 AA;

ID NO:4

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The present invention describes nucleic acid sequences encoding carotenoid biosynthetic enzymes (CBES). Also described: (1) a CBE polypeptides; (2) a chizeric gene (CG) containing a CBE linked to regulatory sequences; (3) host cell transformed with CG; (4) obtaining a nucleic acid that encodes a CBE; (5) products of method (4); (6) producting an omega-aldehyde-functionalised carotenoid (X); (7) producing an omega-carboxy-functionalised carotenoid (Y); (8) producing an omega-carboxy-functionalised carotenoid (Y); (8) producing Carotenoids (Z); and (9) regulating carotenoid (Y); (8) producing C30 carotenoids, and are potentially useful as pigments and and C30 carotenoids, and are potentially useful as pigments and antioxidants, e.g. as feed additives. The present sequence represents a ctr. NCBE protein isolated from Methylomonas sp. strain 16a, which is used in the exemplification of the present invention.
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100.0%; Pred. No. 6.4e-265;
ive 0; Mismatches 0; Indels 0;
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Best Local Similarity 100.0
Matches 511; Conservative
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SARISAKIJSQKHRVRFKDIAHSAWLKKAKA 511 481 RESULT 5

ABB49224 standard; protein; 490 05-FEB-2002 ABB49224

Listeria monocytogenes protein #1928 (first entry)

Antibacterial; gene therapy, vaccine, biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.

Listeria monocytogenes

WO200177335-A2

18-OCT-2001.

11-APR-2001; 2001WO-FR001118.

(INSP) INST PASTEUR.

Dehoux P; Cossart P; Amend A; Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charloit A, Durant L; Percz-Diaz J, Baquero P, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Rose M, Voss H;

WPI; 2002-010914/01.

Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.

Claim 6; SEQ ID NO 1929; 192pp; French.

The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
it are useful for selecting probes and primers for detecting genes in L.
monocytogenes and related organisms, and for studying genetic
color polymorphisms and other genomes. The present sequence is a protein
encoded by the genome sequence of the present invantion. Proteins
concoded by the genome sequence are useful for raising specific
antibodies, identification of L. monocytogenes and related organisms, and
for biosynthesis and biodegradation, especially biosynthesis of vitamin
BL2. The genome sequence and proteins encoded by it are also useful for
selecting compounds that regulate gene expression and cell replication
and modulate L. monocytogenes. related diseases. In addition, the genome
sequence and proteins encoded by it are useful in pharmaceutical and
vaccines compositions for the treatment or prevention of infections by L.
monocytogenes and related organisms. Note: The sequence data for this
control format directly from WIPO at
the control of the printed specification, but was obtained
the control of the printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences

Sequence 490 AA;

SEIBSLIIENGAAKGVKLQHGAELRGDEVIINADFAHAMTHUVKPGVLKKYTPENLKQRE 304 185 AFCFQSKYLGMSPWECPALFTML.PYLBHEYGIYHVKGGLNRIAAAMAQVIAENGGEIHLN 244 VLDEMPELCERRSEDYLEFIPLSPMYRLLYDDRDIFVYSDRENMRAELQRVFDEGTDGYE 124 125 ÇEMBQERKRFNALYPCITRDYSSLKSFLSLDLIKALPWIARPKSVFNNLGQYFNQEKWRL 184 99 5 KHIIIVGAGPGGLCAGMLLSQRGFKVSIFDKHARIGGRNEEINMNGFTFDTGPTFLLMKG 7 KKIALIGAGPGGLAAGALLSQLGYQVNIYEKNDRIGGRIALHRMSKYSFDVGPSALTMTH Gaps ŝ Indels 34.3%; Score 929.5; DB 5; ilarity 37.6%; Pred. No. 1.5e-84; Conservative 98; Mismatches 199; Local Similarity nes 184; Conserv 245 Query Match

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305 YSCSTFMLYLGLDKIYDLPHHTIVFAKDYTTNIRNIFDNETLTDDFSFYVQNASASDDSL 364

247

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Matches
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
358 APINHSSIRIMVPVPNNTSNIDWKKETPAFRQLVLETVKERLEIPDLESQIEEBYIITPI 417
                                                                                                                                                        484
                                                                    APAGKSALYVLVPMPNNDSGLDWQAHCQNVRBQVLDTLGARLGLSDIRAHIBCEKIITPQ 424
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                                                                                                                                                        425 TWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELANCYLVGGGTHPGSGLPTIYESARI
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Xu HH;
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                                     ABU32531 standard; protein; 490 AA
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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N-PSDB; ;
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Wall D,
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compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for callular proliferation to isolate candidate molecules for rational forgulared for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPD at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 VIDEMFELCERRSEDYLEFIPLSPMYRLLYDDRDIFVYSDRENMRAELQRVFDEGTDGYE 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 34.3%; Score 929.5; DB 6; Length al Similarity 37.6%; Pred. No. 1.5e-84; 184; Conservative 98; Mismatches 199; Indels
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27-AUG-2003
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Length 499;

Sequence 499 AA;

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Query Match

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(KIRI) KIRIN BREWERY WPI; 1995-069305/10. N-PSDB; AAQ80736. 08-JUN-1993;

93JP-00163926

Prodn of bleaching herbicide-resistant plants - by transformation with Erwinia phytoene desaturase gene the

Example 9; Page 11-13; 20pp; Japanese

The sequence of the Anabaena strain PCC7120 epsilon-carotene desaturase protein. The corresponding gene was used in a method for the production of plants resistant to epsilon-carotene desaturase inhibiting herbicides e.g. SAN306H, JBS2, etc., or phytocene desaturase inhibiting herbicides e.g. norflurazone, fluxidone, etc., by introducting into the plant a DNA sequence that encodes a polypeptide, preferably the Erwinia-derived phytoene desaturase e.g. the Euredovora crtI gene, or a variant e.g. the Anabaena sequence given in the specification, having a phytoene to contenting activity. The DNA sequence also contains a sequence coding for a transit peptide. (Updated on 27-AUG-2003 to correct OS field). (Updated on 16-OCT-2003 to standardise OS field)

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                                                                                                                GVLDEMFELCERRSEDYLEFLPLSPMYRL-LYDDRDIFVYSDRENMRAELQRVFDEGTDG 122
                                                                                                                                                                                                                                                                                                                               298 ENLKQREYSCSTFWLYLGLDKIY-DLPHHTIVFAKDYTTRIRNI----FDNKTLTD-DFS 351
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                                                                                                                               62 HLYKELPERAGINFADYVQLKKLEPYTRLKFWDGTQLDITTSDLQSFKTQLATLRSDLPLA
                                                                                                                                                                                          122 FDRWYSEHIRKYELGYKPYLAGPARSIFGYLRPDDLMKFLSPRPM----ENLYQHFWRFF
                                                                                                                                                                                                                                      2 SKKVAIVGAGPGGLATAIRLAGLGYQVBIFEAAERVGGRWAGPEVDSYAFDTGPFILQLP
                                                                                                                                                                    123 YEQEMEQERKRENALY-PCITRDYSSLKSFLSL-DLIKAL ---PWLAFPKSVPNNLGOYF
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                                                                                                                                                                                                                                                                                                                                                                                                  412 RAHIBCEKIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFBELANCYLVGGGTHP
                                                                                                                                                                                                                        178 NOEKONRLAFCFOSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAEN
                                                           4 TKHIIIVGAGPGGLCACMLLSQRGFKVSIFDKHAEIGGRUNPINANGFTFDTGPTFLLMK
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28.9%; Score 783.5; DB 2; 35.0%; Pred. No. 9.2e-70; W. ematches 201;
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                      Best Local Similarity 35.0%; Pred. No. 9.2e
Matches 175; Conservative 103; Mismatches
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(CNRS ) CNRS CENT NAT
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Buchrieser C;
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Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.

Claim 2; SEQ ID NO 3220; 1205pp; French

The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorphisms; for gene analysis and for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or mirroorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. Cemphinant production of the proteins practicularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes by proteins, vectors containing the genes and Ab are also useful the are sensitive to P. luminescens-encoded toxins or antibiotics) and as hopesticides. Other uses of the genes and the proteins are as virulence is subopesticides. Other uses of the genes and the proteins are as virulence luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins

Sequence 494 AA;

24; Query Match 26.3%; Score 713; DB 6; Length 494; Best Local Similarity 31.4%; Pred. No. 1.2e-62; Matches 158; Conservative 109; Mismatches 212; Indels 2

S LVIGAGFGGLALAIRLQSAGIPTCILEQRDKPGGRAYVYKEQGFTFDAGPTVITAPNVIE 64 8 IIVGAGPGGLCAGMLLSQRGFKVSIFDKHARIGGRNRPINMNGFTFDTGPTFLLMKGVLD

EMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-SDRENMRAELQRVFDEGTDGYEQF 126 68

LAFCFOSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIAENGGEIHL 243

SDDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVRBQVLDTLGARLGLSDIRAHIECE 418 360

479 YESARISAKLISOKHRVRFKDIA 501

477 IGSAKATATLM-----LEDIA 492

492 AA. AAE22314 standard; protein; RESULT 9

AAE22314;

(first entry) 25-JUL-2002

Pantoea stewartii phytoene desaturase (CrtL) enzyme.

Carotenoid; isopentenyl pyrophosphate; antheraxan;hin; astaxanthin; danti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; phytoene desaturase; CrtL.

Pantoea stewartii.

WO200218617-A2

07-MAR-2002

04-SEP-2001; 2001WO-US027420.

01-SEP-2000; 2000US-0229858P. 01-SEP-2000; 2000US-0229907P.

(DUPO) DU PONT DE NEMOURS & CO E I.

Koffas M. Miller ES; Dicosimo DJ, Rouviere PE; ò Brzostowicz PC, Cheng Q, Odom JM, Picataggio SK,

2002-351711/38. N-PSDB; AAD35512 Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes ir the carotenoid biosynthetic pathway and which metabolize single carbon substrates.

Claim 19; Page 141-143; 156pp; English.

The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by using microorganism having a mucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which methodises single carbon substrates. The carotenoids have potent anti-oxidant properties useful in intermediates in the synthesis of steroids flavours and tragrances and compounds for potential electro-optic applications. The present sequence is propertied.

Sequence 492 AA;

25; 25.9%; Score 703.5; DB 5; Length 492; larity 31.7%; Pred. No. 1.1e-61; Conservative 105; Mismatches 210; Indels 25, Query Match Best Local Similarity Matches 158; Conservat 5 KHIIIVGAGPGGLCAGMLLSQRGPKVSIPDKHABIGGRNRPINMKGPTFDTGPTFLLMKG

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65 VLDEMFELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-SERENWRAELQRVFDEGIDGY

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124 BOPMEGERKRFNALYPCITRDYSSLK----SFLSL-DLIEALPWLA---FPKSVFNNLGO 175
                                                                                                                                                                                                     176 YFNQEKMRLAPCFQSKYLGMSPWECPALFTMLPYLEHEY IYHVKGGLNRIAAAMAQVIA 235
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                              2 KPITVIGAGEGGLALAIRLOAAGIPVILLEQRDKPGGRAYVYQEQGFTFDAGPTVITDPS
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    YFNQEKMRLAFCFQSKYLGMSPWECPALFTMLPYLEHEYGIYHVKGGLNRIAAAMAQVIA 235
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                                                                                                                                                                                                        ENGGETHINSETESTITENGAAKGVKLOHGAELRGDEVIINADPAHAMTHLVK--PGVLK
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N-PSDB; ACC44762.
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Length 492; Indels

Query Match 25.9%; Score 703.5; DB 6; Best Local Similarity 31.7%; Pred. No. 1.1e-61; Matches 158; Conservative 105; Mismatches 210;

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pyrophosphate synthase (crtE), zeaxanthin glucosyl transferase (crtX), phyropene explase (crtE), zeaxanthin glucosyl transferase (crtX), phyropene synthase (crtX), phyropene synthase (crtX), phyropene synthase (crtX), phyropene synthase (crtX), phyropene synthase (crtX), phyropene synthase (crtX), and beta-carcene hydroxylase (crtZ) enzymes (see ABP96685 to ABP96690) encoded by ACC44759 to ACC44764. (I) can be used for regulating caractenoid biosynthesis is altered in the organism, such that the carctenoid biosynthesis is altered in the organism. (I) and the genes encoding (I) are useful for converting phytoene to the carctenoids, for creating recombinant organisms that have the ability to produce various carctenoid compounds, and also for enhancing or manipulating carctenoid compounds, and also for producing gene products having enhanced or altered activity
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stewartii carotenoid biosynthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.9%; Score 703.5; DB 6; Length 492; 31.7%; Pred. No. 1.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 105; Mismatches 210; Indels
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es 158; Conserva
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Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostrics. The protein is also used in an assay for enzymatic studies and as a target for autibiotics. This sequence represents one of the novel S. aureus proteins of the invention
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preventing Staphylococcal infection, specifically an infection caused by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 DEMFELCERRSEDYLEFLPLSPMYRLLYDDRD-IFVYSDRENMRAELQRVFDEGTDGYEQ 125
                                                                                                                                                                                                   carotenoid biosynthetic enzyme; CBE; omega-aldehyde-functionalised carotenoid; omega-aldehyde-functionalised carotenoid; C30 carotenoid; carotenoid biosynthesis; antioxidant; microbial; pigment; feed additive; CrtN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 FWEQERKRFWALYPCITR--------DYSSLKSFLSLDLIKALPWLAFPKSVFNNL 173
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Best Local Similarity 31.5%; Pred. No. 1.5e-61;
Matches 159; Conservative 108; Mismatches 196; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding carotenoid biosynthesis enzymes, useful for preparing functionalized carotenoids, e.g. pigments and antioxidants,
                                                                                                                                                                                Staphylococcus aureus CrtN protein SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 108-111; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                      ADA14542 standard; protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-FEB-2003; 2003WO-US004150.
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                                                                                                                                   06-NOV-2003 (first entry)
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also encoded polypeptides.
                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheng Q, Norton KC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 502 AA;
                                                                                                                                                                                                                                                                                                                                                                                            WO2003068917-A2.
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168 OQLIEHYIDNEKIQKLLAFQTLYIGIDPKRGPSLYSIIPMIEMMFGVHFIKGGMYGMAQG 227
                                                                                                                           230 MAQVIAENGGEIHLNSEIESLIIENGAAKGVKIQHGAELFG-DEVIINADFAHAMTHLVK 288
                                                                                                                                                                               289 P-GVLKKYTPENLKQREYSCSTFMLYLGLD-KIYD-LPHHTIVFAKDYTTNIRNIFDNKT 345
                                                                                                                                                                                                                                                                                                                                                         288 DFAPIKKYPPHKIADLDYSCSAFLMYIGIDIDVTDQVRLHNVIFSDDFRGNIBBIFEGR- 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene products are useful for the synthesis of carotenoids, useful as food coloring, vitamin A precursor, and possibly in prevention of cancer. See also AAQ06293-9. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 LTDDFSFYVQNASASDDSLAPAGKSALYVLVPMP-~NNDSGLDW-~QAHCQNVREQVLDT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402 LGARLGLSDIRAHIBCEKIITPQTWETDEHVYKGATFSLSHKFSQMLYWRPHNRFEELAN 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407 LATIEVFEDIKSHIVSETIFTPNDFEQTYHAKFGSAFGLMPTLAQSNYYRPQNVSRDYKD 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide with enzymatic activity for the conversion of phytoene into
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                                                                                                                                                                                                      YPNOEKWRLAFCFOSKYLGMSPWECPALFTWLPYLEHEYGIYHVKGGLNRIAAAMAQVIA 235
                                                                                                                                                                                                                            YIEDEHLROAFSFHSLLVGGNPPATSSIYTLIHALEREWGVWFPRGGTGALVQGMIKLFQ 232
                                                                                                                                                                                                                                                                            ENGGETHINSELESLITENGAAKGVKLOHGAELRGDEVIINADFAHAMTHLVK--PGVLK 293
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KHIIIVGAGPGGLCAGMLLSQRGFKVSIPDKHABIGGRNRPINMNGFTFDTGPTFLLMKG
                      EQFMEQERKRENALYPCITRDYSSLK----SFLSL-DLIKALPWLA---FFKSVFNNLGQ
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                                                                  VLDEMPELCERRSEDYLEPLPLSPMYRLLYDDRDIFVY-SDRENMRABLORVFDEGTDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HMG-CoA; 3-hydroxy-3-methylglutaryl coenzyme A reductase; crtI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene useful for increase in carotenoid production carotenoid.
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(first entry)
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This invention describes a novel method for the preparation of carotenoids using genes and proteins isolated from Candida utilis. The

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invention specifically describes the isolation of a 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CAA) reductase protein. This sequence represents the Candida utilis cril protein which is used in the method the invention. (Updated on 17-0CT-2003 to standardise OS field)
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Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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1D G9HWY4 PRELIMINARY; PRT; 295 AA.

C 09HWY4

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DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DE 01-CT-2003 (TrEMBLrel. 15, Last annotation update)

DE Geranyltranstransferase.

C Bedteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

DS Pseudomonadaceae; Pseudomonas.

CNELL AND A.

RADINE-20437337; PubMed=10984043;

RADINE-20437337; PubMed=10984043;

RADINE-20437337; PubMed=10984043;

RADINE-20437337; PubMed=10984043;

RA STOWN CR. C.W. Pham X. V.O.T., Extrin A.L., Mizoguchi S.D., Warrener P., Radickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., R.

STRAIN-ATCC 15692 / PAD1;

RA STOWN CR. C.W. Pham X. C.O. L. Hufnagle W.O., Kowalik D.J., Lagrou M., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Stown C.W., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., R. Brody L.L., Coulter S. N., Folger K.R.-S., Wu Z., Paulsen I.T., R. Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V., Smith R.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V., Smith R. R., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V., R. Coulter genome sequence of Pseudomonas acruginosa PAD1, an opportunistic pathogen.";

RE PREL AROUGHST, PROMOS2; Polyprenyl Synth.

RE PREL REPRO! IPROMOS2; Polyprenyl Synth.

RE PREL PROMOS4; Polyprenyl Synth.

RE PREP PROS1TE; PS0044; POLYPRENYL SYNTHET Z: 1.

RE PROSITE; PS0044; POLYPRENYL SYNTHET Z: 1.

RE PROSITE; PS0043; 31444 MN; EFDFFA6D66FSC126 CRC64;

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55.0%; Score 831; DB 16; Length 295;

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Pseudomonadaceae; Pseudomonas.
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EMBL; ARD167706; AAN66155.1; -...
                       Indels
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60.3%; Pred. No. 1.2e-58;
:ive 33; Mismatches 83;
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PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
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01-JUN-2003 (TrEMBLrel. 24,
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  Best Local Similarity 60.3
Matches 176; Conservative
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MEDLINE=99339254; PubMed=10412909;
Ohto C., Ishida C., Nakane H., Muramateu M., Nishino T., Obata S.
The thermophilic cyanobacterium Synechococcus elongatus has three different Class I prenyltransferase genes.";
Plant Mol. Biol. 40:307-321(1999).
Franc, Rand, Randsefat, J. .
GO, GO:0008299; Prisopremoid biosynthesis; IEA.
InterPro: IPR00092; Polypremoid biosynthesis; IEA.
InterPro: IPR0009949; Terpenoid synth.
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Bacteria, Cyanobacteria, Chroococcales, Synechococcus.
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PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
PROSITE; PS0044; POLYPRENYL SYNTHET 2; 1.
SEQUENCE 300 AA; 32604 MW; CIALC46A20A16FC4 (RC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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58.3%; Pred. No. 3.6e-56;
ive 35; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Farnesyl diphosphate synthase (SelFPS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 58.33
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Land M.

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75 BFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILACDALQALAFBVLANDPGITV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 DAPARLKMITALTRASGSQGWVGGQAIDLGSVGRKLTLPELENMHIHKTGALIRASVNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 ALSKPDLDTCVAKKLDHYAKCIGLSPQVKDDILDIBADTATLGKTQGKDIDNDKPTYPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 ARCGWRLDETQPKLLDHFAKCMGLAFQVIDDILDTBATTAALGKTAGKDARWKPTYVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 VERALDARLPAENILPQTLHQAMRYSVINGGKRTRPLLTYATGQALGLPENVLDAPACAV
                                           Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A., Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.; Complete genome sequence of the ammonia-oxidizing bacterium and obliqate chemolithoautocroph Nitrosomonas europaea."; J. Bacteriol. 185:2759-2773 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Moralli G., Baaham D., Ebrown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Felroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., Warrain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis (serogroup A).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
                     Lamerdin J.E., Larimer F.W., Regala W., Lao V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Indels
                                                                                                                                                                                    J. Bacteriol. 185:2759-2773(2003).
BMBL; BX321860; CAD85071.1, -
GO, GO:000437; F:geranyltranstransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008299; F:isopremoid biosynthesis; IEA.
InterPro; IPR000992; Polyprenyl synt.
InterPro; IPR009999; Terpenoid_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; ALIG5758; CAB84437.1; -.
PIR, BR1796; ER1796.
GO; GO:0004337; F:geranyltranstransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase, Complete proteome.
SEQUENCE 297 AA; 32448 MW; A22BC333E65F3699 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 LGMAGAKOKAQELHEQAVESLTGFGSBADLLRELSLYIIER 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 IGIKQARELAHELRQEATGVINQFGSBALRLQOVIDFIVQR 295
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01-0CT-2000 (TIEMBLrel. 15, Last sequence update)
01-0CT-2003 (TIEMBLrel. 25, Last annotation update)
Geranyltranstransferase (EC 2.5.1.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.2%; Score 787.5; DB 1
56.9%; Pred. No. 3.9e-55;
iive 40; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00348; polyprenyl synt; 1.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serotype 4A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE=2022556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 56.9%
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     meningitidis Z2491.";
Nature 404:502-506(2000)
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              Chain P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 AEDANGAACAVELIHAYSLVHDDLPAMDDDDLRRGQPTTHKAFDEACAILAGDGLGSLAST 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 EVLANDPGITVDAPARKKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENMHIHKT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALIRASVNIAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKD 243
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

IIGR; PSTT00699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 IDNDKPTYPALLGMAGAKQKAQELHEQAVESLTGFGSEADLLRELSLYIIBRTH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria, Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OTV-2003 (TrEMBLrel. 25, Last annotation update)
01-OTV-2003 (TrEMBLrel. 25, Last annotation update)
1SPA OR NEL160.
1SPA OR NEL160.
Nitrosomonas europaea.
Bacteria: Proteobacteria: Betaproteobacteria; Nitrosomonadales;
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56.8%; Pred. No. 2e-55;
tive 36; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase, Complete proteome.
SEQUENCE 295 AA; 31255 MW; 86DAIE6092FB501A CRC64;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
InterPro; IPR000092; Polyprenyl_synt.
InterPro; IPR008949; Terpenoid_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00348; polyprenyī synt; 1.
PROSITE; PS00723; POLYPRENYI SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYI SYNTHET 2; 1.
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STRAIN=ATCC 19718 / IFO 14298;
MEDLINE=22586410; PubMed=12700255;
                                                                                                                                                                                                                                              Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 167; Conservative
                                                                                                            Geranyltranstransferase.
ISPA OR PSPTO0699.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              NCBI_TaxID=323;
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                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=DC3000,
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Q82VD4 ESULT 5

134 134

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InterPro; IPR008949; Terpenoid synth.
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Matches 148; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio vulnificus.
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SEQUENCE 298 AA
                                                                          Transferase;
                                                                                                                                                                151;
                                                                                          SEQUENCE
                                                                                                                                Query Match
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Best Local
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SEQUENCE FROM N.A.

SEQUENCE PROM N.A.

SEQUENCE 23913 / NCPPB 528;

A BUINE-2502145; PubMed=12024217;

A a Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A a Silva A.C.R., Forno J.A., Bertolini M.C., Camargo L.B.A.,

A Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A Camarotte G., Cannavan F., Cardozo J.C., Cambergo L.R., El-Dorry H.,

Raria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Formighieri B.F., Franco M.C., Gregolo C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

A comparison M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machadnis J.M., Menck C.F.M., Maryaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Spinola L.A.F., Tarkita M.A., Tammra R.E., Teixeira B.C., Tezza R.I.D.,

Spinola L.A.F., Tarkita M.A., Tammra R.E., Teixeira B.C., Tezza R.I.D.,

Stubal J.C., Kitajima J.P.;

T. "Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                            243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244
                                                                                                                                                                                                                                                                                                                                                                                                EVLANDPGITVDAPARLKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENMHIHKT 183
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                                                                                                                                                                                                                                              4 LKAYLTVCQERVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLP
                                                                                                                                                                                                                                                                    64 ENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 GALIRASVNLAALSKPDLDTCVARKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 ADNDKPTYVKLMGIZAARSYAHKLVAEAVALIEPFGDKALRIRQLAEFAVARKY 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 IDNDKPTYPALLGMAGAKOKAQELHEQAVESLTGFGSBADLLRELSLYIIERTH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; (pv. campestris).
Kanthomonadaceae; Xanthomonas.
NCBI_TaxID=340;
                                                                                                                                                                                                          ä
                                                                                                                                                              48.3%; Score 729; DB 16; Length 298; 51.4%; Pred. No. 2e-50; 7ative 44; Mismatches 97; Indels
                InterPro, IPR000092; Polyprenyl synt.
InterPro, 1PR008949; Terpenoid synth.
Pfam; PF001348; Polyprenyl synt.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
Transferase; Complete proteome SEQUENCE 298 AA; 32009 MW; 8034853998066085 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mature 417.459-463 (2002).

EMBL, AE012371; AAM41872.1; -.

GO, GO:0010570; F:transferase activity; IEA.

GO, GO:0008299; P:isoprenoid biosynthesis; IEA.

InterPro; IPR000092; Polyprenyl_synt.
GO:0008299; P:isoprenoid biosynthesis; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 AA
                                                                                                                                                                                                        Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geranyltranstransferase.
ISPA OR XCC2600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              host specificities.
                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                124
                                                                                                                                                                  Query Match
                                                                                                                                                                                        Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBP7L1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8P7L1
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253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 VEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEVLANDPGIT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 APACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALAFEVLAN 128
                                                                                                                                                                                                                                                                                                                               71
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                                                                                                                                                                                                                                                                                                             12 RTERQLDACLPSPALAPQRLHAAMRHAVLGGGKRMRPLLVYASGALFGAEEGSLDAPAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 GVLT-GGAGIADOQRLDAFADALGLAFQVRDDILDVESSSAQLGKTAGKDAAQSKSTYPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 RVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLPENVLDAPACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 AALSKPOLDTCVAKKLDHYAKCIGLSPQVKDDILDIEADTATLGKTOGKDIDNDKPTYPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 QERVERALDA---RLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLPENVLD
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        4.
                                                                                                                                                                 Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.8%; Score 707; DB 16; Length 298; 51.6%; Pred. No. 1.2e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CMCP6;
Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
VCBL_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 LIGMAGAKOKAQELHEQAVESLTGFGSEADLLRELSLYIIERTH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 LLGWDGAKTKLAELASHWHALLLPYGESGATLASKGRFA/DRAH 291
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Vibrio vulnificus CMCP6."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; ABO16798; ABO18649.1; -...
EMBL; ABO16799: ABO18849.1; -...
InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synth.
Pfam; PF00348; Polyprenyl synt.
PROSITE; PS00023; POLYPRENYL SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
                                                                                   ; Complete proteome.
291 AA; 30227 MW; 0A20B0797CBB5773 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 AA; 32538 MW; 65E59976E668066C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                        1) Similarity 53.2%; Pred. No. 2.6e-49; St. Conservative 35; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Mismatches
Pfam; PF00348; polyprenyl synt; i.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Geranylgeranyl pyrophosphate synthase.
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294 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLEEL 24, 01-JUN-2003 (TrEMBLEEL 24, 01-OCT-2003 (TrEMBLEEL 25, Geranyltranstransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.1:
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Q87RT9
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
Q8ZRD0
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STRAIN-306 / ATCC 13902 / XV 101;

MEDLINE-2202145; PubMed=12024217;

A da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A ves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A caralila R.M. B., Coutinho L.L., Cursino-Santos J.R., Bl-Dorry H.,

Ferria J.B., Ferreira A.J.S., Ferreira R.C.C., Forber A.I.T.,

Racsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Iemos M.V.F.,

A carali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Mechado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

A moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Spinola L.A.P., Tarkita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

A Trindade dos Santos M., Truffi D., Tsai S.M., White P.F.,

T "Comparison Of the genomes of two Xanthomonas pathogens with differing
                       DPGITVDAPARLKWITALTRASGSOGMVGGQAIDLGSVGRKITLPELENWHIHKTGALIR 188
                                                             189 ASVNLAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKDIDNDK 248
                                                                                                                                                                                       72 VELIHAYSLVHDDLPAMDDDALRRGQPTVHIAFDEATAILAGDALQTRAFELLA---AAS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 VEFIHVYSLIHDDLPAMDNDDLRRGKPICHKAYDEATAILAGDALQALAFEVLANDPGIT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 VDAPARLXMITALTRASGSQGMVGGQAIDLGSVGRKUTLPELENMHIHKTGALIRASVNL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 RVERALDARLPAENILPQTLHQAMRYSVINGGKRTRPLLTYATGQALGLPENVLDAPACA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISPA ÓR XAC2762.
Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ъ.
                                                                                                                                                                                                                                                                            249 PTYPALLGMAGAKQKAQELHEQAVBSLTGFGSBADLLRELSLYIIER 295
                                                                                                                                                                                                                                                                                                                 250 STYPSLLGLEGAMEKAHTLLHEALQALEAIPYNTQHLEEFARYVVER 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404C3E5EDFEBEF67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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46.8%; Score 706; DB 16;
Best Local Similarity 51.7%; Pred. No. 1.4e-48;
Matches 148; Conservative 44; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synth.
Pfam, PF00348; Polyprenyl synt.
PROSITE; PS00434; POLYPRENYL SYNTHET 1: 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Complete proteome.
291 AA; 30516 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xanthomonadaceae; Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geranyltranstransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=92829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8PIY3;
01-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2002
01-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8PIY3
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
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UPPERZOUUXZAUX44444444444444444

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REGUENCE FROM N.A.

REGUENCE FROM N.A.

REGUENCE FROM N.A.

STRAIN-RIMD 2210633 / Serotype 03:K6;

RA MAKIND K., Oshima K., Kirokawa K., Yokoyama K., Uda T., Tagomori K.,

RA MAKIND K., Oshima M., Nakano M., Yokoyama K., Wibota Y.,

Ijima Y., Najima M., Nakano M., Yamashira A., Kihota Y.,

RA Tasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

RI "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

RI "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

RI Iancet 361:743-749(2003)

BR MBL; AP005075; RAC58950.1; -

DR GO; GO:0106740; Firtansferase activity; IEA.

DR GO; GO:0106740; Firtansferase activity; IEA.

DR GO; GO:0106740; Firtansferase activity; IEA.

DR GO; GO:0106949; Firtansferase activity; IEA.

DR InterPro; IPR000092; Polyprenyl synt; 1.

DR PROSTIE: PS00449; Polyprenyl synt; 1.

DR PROSTIE: PS00449; Polyprenyl synt; 1.

DR PROSTIE: PS00449; Polyprenyl synt; 1.

DR PROSTIE: PS00449; Polyprenyl synt; 1.

DR PROSTIE: PS00449; Polyprenyl synt; 1.

RW Transferase; Complete proteoned.

SEQUENCE 294 AA; 32337 MW; ALC1924A66774FDO CRC64;
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                                     194 AALSKPDLDTCVA - - KKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKDIDNDKPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LIVCOERVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLPENVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 DAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEVLA
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                                                                                                                                                                                Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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Last annotation update)
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J., Filtwell T., Hamlin N., Haque A., Hien T.T., White N., Parrar J., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Emmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 185:2330-2337(2003).

EMBL; AL627266; CAD08879.1; -

EMBL; AR016842; AAO70030.1; -

GO; GO:0016740; F:transferase activity; IEA

GO; GO:0016740; F:transferase activity; IEA

GO; GO:000399; F:tsoprenoid biosynthesis;

InterPro; IPR000992; Polyprenyl synt.

InterPro; IPR008949; Terpenoid_Synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00348; polyprenyl synt; 1.
PROSITE, PS00723; POLYPRENYL SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
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01-0CT-2000 (TEMBLrel. 15, Last seq
01-0CT-2003 (TEMBLrel. 25, Last ann
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                                                                 MEDLINE=21534947; PubMed=11677608;
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  [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                              McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 PENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 OLGACVTGANGALSRFI-APLPFON---TPVVBAMOYGALLGGKRLRPFLVYATGQMFGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATLDAPAAAVECTHAYSLIHDDLPAMDDDDLRRGLPTCHIKPGEANAILAGDALQTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 FAIISDAPMPBVADRDRIAMIAELANASGIAGMCGGGALDLAABGGRITLDALERIHRHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGALIRASVNLAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Gaps
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Enterobacteriaceae; Salmonella.
NCBI TaxID=601;
                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
46.7%; Score 705.5; DB 16; Length 299;
Best Local Similarity 52.7%; Pred. No. 1.6e-48;
Matches 156; Conservative 39; Mismatches 94; Indels 7;
                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last semocation update)
Geranyltranstransferase (farnesyldiphosphate synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SE9BF79CCCF0FC3C CRC64;
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Last annotation update)
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EMBL, AE008115, AAL19377.1; .

GO, GO:0016740; F:transferase activity; IEA.

GO: CO:0008299; P:isoprenoid biosynthesis; IEA.

InterPro; IPR000849; Propenoid synth.

Pfam; PF00348; polyprenyl synth.

PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.

PROSITE; PS00444; POLYPRENYL SYNTHET 1; 1.

Transferase; Compute protecome.

SEQUENCE 299 AA; 31986 MW; 5E9BF79CCCF0FC3C C:
299 AA
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TOTAL / SCSC1412 / ATCC 700720,
TOTAL PROPERTY / SCSC1412 / ATCC 700720,
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PRT;
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NCBI_TaxID=602;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-0CT-2003 (TrEMBLrel. 25,
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Salmonella typhi.
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PRELIMINARY;
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                                                                                                                                                  ISPA OR STM0423.
Salmonella typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 STATLDAPAAAVECHAYSLIHDDLPAMDDDDLRRGLPTCHIKFGEANAILAGDALQTLA 121
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STRAIN=TY2 / Arcc 700931,
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., PubMett G. III, Mayhew G.P., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KLKAYLTVCQERVERALDARLPAENILPQTLHQAMRYSVINGGKRTRPLLTYATGQALGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOOLGKSTYPALLGIEQARNKARDLIEDARQSLHQLAAQSLDTSALBALANXIIQR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.7%; Score 705.5; DB 16; Length 299; 52.7%; Pred. No. 1.6e-48;
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Vibrionaceae, Vibrio.
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Last annotation update)
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NCBI_TaxID=83334;
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SEQUENCE 30
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01-MAR-2002
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                       SEQUENCE FROM N.A.

SERAINEEL TOR NIS961 / Serotype 01;

MEDLINE=20406833; PubMed=10952301;

Heidelberg U.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.B., Read T.D., Tettelin H., Richardson D.A.,

Ernolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;

"DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 LTVCQERVERALDA----RLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LSSYÓQRANGQLDQWLARIPFQTL---PLIEAMRYGLLLGGKRARPYLVYITGÓMLGCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CO-92 / Biovar Orientalis;
BIRDINES-1470401; PubMed=115861560;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 DNDKPTYPALLGMAGAKOKAQBLHEQAVESLTGFGSEADLLRELSLYIIER 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 BINKSTYPALLGLEGAQQKAHTLLQBALLALBAIPYNTEHLBEFARYVVER 292
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                                                                                                                                                                                                                             EMEL, AE004177; AAP94052.1; -.

PIR, AB2267; A82267.

TIGR; VCC0890; -.

TIGR; VCC0890; -.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016799; P:isoprenoid biosynthesis; IEA.

InterPro; IPR000949; P:trpenoid synth.

PEAM; PEO0348; POLYPERNYL SYNT; 1.

PROSITE; PS00723; POLYPERNYL SYNTHET 1; 1.

PROSITE; PS00444; POLYPERNYL SYNTHET 2; 1.

ITRANSFERASE; COMPLEE PROTECTOR.

SEQUENCE 294 AA; 32259 MW; E7D33C0FD935CB96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  46.6%; Score 704; DB 16; Length 2: 51.2%; Pred. No. 2e-48; Live 45; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TYEMBLrel. 20, Created)
01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-OCT-2003 (TYEMBLrel. 25, Last annotation update)
Geranyltranstransferase (EC 2.5.1.10).
ISPA OR YPO3176 OR Y1009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306
                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity 51.2
149; Conservative
                                                                                                                                                                                                                   Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                    cholerae. ";
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Best Local S
Matches 149
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68 LSLANLDAPAAAIBCIHAYSLIHDDLPAMDDDDLRRGQPTCHVKFGRAHAILAGDALQTL 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 AFEVLANDPGITVDAPARLKMITALTRASGSQGMVGGQAIDLGSVGRKUTLPELENMHIH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDQQLGKSTYPALLGLDCAQTKAMDLYQEALBALDBLAKQSYNTDSLQALARFIIERNN 306
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).
                                                                                                                                                                                                                                         STRAIN=KINS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=1214430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P. Perna N.T., Rose D.G., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 KOOLAAHOORVNOALLDPIAPLPFGN---SNLIEAMRYGAVIGGKRLRPYLVYATGOMFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 KTGALIRASVNLAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQG
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Bscherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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GO; GO:0004337; F:geranyltranstransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008299; P:isopranoid biosynthesis; IEA.
InterPro; IPR00092; Polyprenyl synt.
InterPro; IPR00092; Perpenoid_synth.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Geranyltransferase (farnesyldiphosphate synthase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of Yersinia pestis KIM.";
V. Bacterlol. 184-4601-4611(2002).
EMBL; AJ41415; CAC92411.1; --
EMBL; AE013704; AAM84590.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEAM, PF00348; polyprenyl synt; i.
PROSITE, PS00723; POLYPRENYL SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
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MEDLINE=21074935; PubMed=11206551;
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16 AA; 32919 MW;
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                                                                                                                                                                                                                               SEQUENCE FROM N.A
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C. STRAIN=0157:H7 / RIND 0509952;
C. STRAIN=0157:H7 / RIND 0509952;
A. MEDIINE-21156231; PubMed=11258796;
A. Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Jarashi H., Honda T., Sasakawa C., Ogasawara M., Tobe T.,
A. Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
A. Lida T., Takami H., Honda T., Sasakawa C., Ogasawara M., Yasunaga T.;
A. Complete genome sequence of enterohemorrhagic Escherichia coli
T. Complete genome sequence of enterohemorrhagic Escherichia coli
T. DNA Res. B.11-2212001).
EMBL; AE005221; AAG54771.1; -.
EMBL; AE005221; AAG54771.1; -.
EMBL; AR005251; AAG54771.1; -.
EMBL; AR005251; AAG54771.1; -.
EMBL; AR005251; BAB33898.1; -.
EMBL; AR00529; Prisoprenoid biosynthesis; IEA.
GO; GO:0016299; Prisoprenoid biosynthesis; IEA.
ELEFPC; IPR000092; Polyprenyl Eynt.
ELEFPC; IPR000094; Polyprenyl Eynt.
ELEFPC; IPR000094; Terponoid Synth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Gaps
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Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Bosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Helch R.A., Blattner F.R.; Helch R.A., Elattner F.R.; Helch R.A., Elattner F.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.; Helch R.A., Blattner P.R.
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46.1%; Score 695.5; DB 16; Length 299;
Best Local Similarity 52.4%; Pred. No. 9.9e-48;
Matches 154; Conservative 35; Mismatches 96; Indels 9;
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Pfam; PP00348; polyprenyl_synt; 1.
PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.
PROSITE; PS00444; POLYPRENYL_SYNTHET_2; 1.
PROSITE; PS00444; PROTECOME.
SEQUENCE 299 AA; 32131 MW; 15BCGBEGEEFFBOCA CRC64;
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geranylgeranyl pyr
farnesyltranstrans
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probable geranylge
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                                                   February 29, 2004, 14:34:14; Search time 8.26685 Seconds (without alignments) 3455.835 Million cell updates/sec
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                                                                                                          1 MSKLKAYLTVCQERVERALD......FGSEADLERELSLYIIERTH 297
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                         283366 seqs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
                                    - protein search, using sw model
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AE1833
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Gapop 10.0 , Gapext 0.5
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T09966
E84566
E83997
G84566
A13285
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A69961
T02429
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3: pir3:*
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AG1607	T06969	\$71230	A89932	F97685	AH2910	B84984	A86732	D97156	G95139	F98007	871231	S04407	A64636	B81261	G71878
7	7	7	N	C)	7	7	7	N	7	0	N	7	7	7	7
293	300	378	293	304	335	282	285	289	291	291	222	289	303	281	303
35.0	34.6	34.6	34.3	34.2	34.2	33.2	32.4	31.6	29.6	29.5	29.5	26.4	25.9	25.1	24.8
529	522.5	522	517.5	517	517	503	488.5	476.5	446.5	445.5	440.5	399	391	379	375
3.0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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M.J., Br
K., Lim,
                                                                                                                                                                      A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor, A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83139
A;Accession: F83139
A;Accession: Preliminary
A;Molecule type: DNA
A;Residues: 1-295 <5TO>
A;Residues: 1-295 <5TO>
A;Residues: 1-295 <5TO>
A;Experimental source: strain PA01
C;Genetics:
geranyltranstransferase PA4043 [imported] - Pseudocconas aeruginosa (strain PAO1)
                                                                                      Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, j. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                   C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_charge 31-Dec-2000
C;Accession: F83139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IAAYQARCQARVDAALDALFVAPREELQRLYBAMRYSVWNGGKRVRFILAYAACBALGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 GALIRASVNIAALSKPOLDTCVAKKLDHYAKCIGLSFQVKDOILDIBADTATLGKTQGKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                             55.0%; Score 831; DB 2; Length 295;
60.3%; Pred. No. 2.6e-58;
ive 33; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.3%
Matches 176; Conservative
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geranyltranstransferase (EC 2.5.1.10) NMA2226 (imported] - Neisseria meningitidis (strai C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: E81796

RESULT 2

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <HEI>
A;Cross-references: GB:AE004173; GB:AE003852; NID:g9655341; PIDN:AAF94052.1; GSPDB:GN00
A;Experimental source: serogroup O1; strain N16961; blotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
C;Accession: A40385
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Vibrio cholerae (strain N16961 serogroup Ol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A82267
R;Heidelberg, J.F.; Bisen, J.A.; Melson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Brindleeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J. R.R.; Mekalanos, J.J.; Venter, J.C.; Praser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                242
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STATEDAPAAAVECHAYSEHHDDEPAMDDDERREEPTCHIKFGBANAILAGDALQTLA 121
                                                                                  PEVLANDPGITVDAPARLKMITALTRASGSOGMVGGQAIDLGSVGRKLTLPELENMHIHK 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 VLANDPGITVDAPARLKMITALTRASGSQGWVGGQAIDLGSVGRKLTLPELENMHIFKTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Vibrio cholerae
C.Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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46.6%; Score 704; DB 2;
Best Local Similarity 51.2%; Pred. No. 2.9e-48;
Matches 149; Conservative 45; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: dimethylallyltranstransferase
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  R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell, Holtroph, S.; Gagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: AB1775; MJID:20222556; PMID:10761919
A;Accession: EB1796
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyacession: AG0554
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Lh, T; Connerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Tile: Complete genome sequence of a multiple drug resistant Salmonella enterica servy A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                     A,Cross-references: GB:AL162758, GB:AL157959; NID:g7380672; PIDN:CAB85437.1; PID:g738084
A,Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            geranyltranstransferase [imported] - Salmonella enterica subsp. enterica serovar Typhi C;Species: Salmonella enterica subsp. enterica serovar typhi A;Note: this species has also been called Salmonella typhi C;Darte: 09-Nov-2001 #seguence_revision 09-Nov-2001 #text_change 18-Nov-2002
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A;Cross-references: GB:AL513382; PIDN:CAD08879.1; PID:g16501691; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVLANDPGITVDAPARLKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENMHIHKT 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.3%; Score 729; DB 2;
51.4%; Pred. No. 3.1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: dimethylallyltranstransferase C;Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: dimethylallyltranstransferase
                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-298 <PAR>
A,Cross-references: GB:AL162758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 51.4%
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                              A; Gene: ispA; NMA2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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A,Status: preliminary
A,Status: DNA
A,Mcd.ecule type: DNA
A,Residues: 1-299 <STO>
A,Cross.references: GB:AE005174; NID:g12513277; PIDN:AAG54771.1; GSPDB:GN00145; UMGP:Z05
A,Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geranyltranstransferase (EC 2.5.1.10) - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Accession: J00665; E64771
R;Fujisaki, S.; Hara, H.; Nishimura, Y.; Horiuchi, K.; Nishino, T.
R;Fujisaki, S.; Hara, H.; Nishimura, Y.; Horiuchi, K.; Nishino, T.
R;Fujisaki, S.; Hara, H.; Nishimura, Y.; Horiuchi, K.; Nishino, T.
R;Fujisaki, S.; Hara, H.; Nishimura, Y.; Horiuchi, K.; Nishino, T.
R;Fujisaki, S.; Hara, H.; Nishimura, Y.; Horiuchi, K.; Nishino, T.
R;Fujisaki, S.; Hara, H.; Nishimura, Y.; Horiuchi, K.; Nishino, T.
R;Reference number: J00664; MUID:91210228; PMID:2089044
R;Reference number: J00665
R;Residues: 1-299 cFUJ.
A;Residues: 1-290 cFUJ.
A;Residues: 1-290 cFUJ.
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A;Residues
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K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                    geranyltranstransferase [similarity] - Bscherichia coli (strain 0157:H7, substrain BDL93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                  124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 VLANDPGITVDAPARLKMITALITRASGSQGWVGGQAIDLGSVGRKLTLPELENMHIHKTG 184
   124 ILSDADMPEVSDRDRISMISELASASGIAGMCGGQALDLDASGKHVPLDALERIHRHKTG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Accession: G85538
R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                        /Species: Bscherichia coli
.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #tex:_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 NVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDBATAILAGDALQALAFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIRASVNIAALSKPOLDTCVAKKLDHYAKCIGLSFQVKODILDIEADTATLGKTQGKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 ALIRASVNIAALSKPDEDTCVAKKIDHYAKCIGLSPQVKDDILDIEADTATLGKTQGKDI
                                                                                                                                                                                                                                                297
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                                                                                                                                                                                        245 DNDKPTYPALLGMAGAKQKAQELHEQAVESLTGFGSEA---DLLRELSLYIIER 295
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                                                                                                                                                                                                                            244 QLGKSTYPALLGLEQARKKAQDLIDDARQSLKQLAEQSIDTSALEALADYIIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 QLGKSTYPALLGLEQARKKAQDLIDDARQSLKQLAEGSIDTSALEALADYIIQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.1%; Score 695.5; DB 2 52.4%; Pred. No. 1.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: ispA
C;Superfamily: dimethylallyltranstransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: G85538
                                                                 185
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;Molecule type: DNA
;Residues: 1-306 <KUR>
;Cross-references: GB:AL590842; PIDN:CAC92411.1; PID:g15981114; GSPDB:GN00175
;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLANDPGITVDAPARLKMITALTRASGSQGWVGGQAIDLGSVGRKLTLPELENMHHKTG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQAL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFEVLANDPGITVDAPARLKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENMHIH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTGALIRASVNLAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIBADTATLGKTQG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTGALIRAAVRIGAQAAGEAGRKTILSLDRYAEAIGLARQVQDDILDVIGDIATIGKRQG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1.299 «HAY»
;Cross-references: GB:BA000007; PIDN:BAB33898.1; PID:g13359932; GSPDB:GN00154
;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFE 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOIDNDKPTYPALLGMAGAKQKAQELHEQAVESLTGFGSEA---DLLRELSLYIIERTH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDQQIGKSTYPALLGLDCAQTKAMDLYQEALBALDBLAKGSYNTDSLQALARFIIERNN 306
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                          Fitle: Genome sequence of Yersinia pestis, the causative agent of plague. Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 KAYLIVCQERVERAL --- DARLPAENILPQILHQAMRYSVINGGKRIRPILITYAIGQALG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95; Indels
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46.1%; Score 695.5; DB 2
Best Local Similarity 52.4%; Pred. No. 1.4e-47;
Matches 154; Conservative 35; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
46.5%; Score 702.5; DB
Best Local Similarity 52.5%; Pred. No. 4e-48;
Matches 157; Conservative 38; Mismatches 5
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                                                                                                                                                                                                                                                                                                           ;Superfamily: dimethylallyltranstransferase;Keywords: transferase
413, 523-527, 2001
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F;223-227/Region: DDXXD motif

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geranyltranstransferase (farnesyl-diphosphate synthase) XF0661 [imported] - Xylella fas
C,Species: Xylella fastidiosa
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: D82778
R,anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque R,anonymous, The Xylella fastidiosa.
A,Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A,Reference number: A82515; MUID:20365717; PMID:10910347
A,Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                     61 GLPENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKFTCHKAYDEATAILAGDALQA 120
                                                                                                                                                                                                                                                                                                                       121 LAFEVLANDPGITVDAPARLKMITALTRASGSQGMVGGQAIDIGSSVGRKUTLPELENMHI 180
                                                                                                                                                                                                                                                                                                                                                 HKTGALIRASVNLAALSKPDL-DTCVAKKLDHYAKCIGLSFQVKDDILDIBADTATLGKT
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                                                                                                                      1 MSKLKAYLTVCQERVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQAL
                                                                                                                                                                   1 MGHFSEBLQQVQTRINRFLBAQFSGIBSHNAPLLBAMKYALLLGGKRVRPFLVYATGQML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 KAYLTVCQERVERALDARLPABNILPQTLHQAMRYSVINGGKRTRPLLTYATGQALGLPE
                       Length 295;
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44.7%; Score 675; DB 2;
Best Local Similarity 50.2%; Pred. No. 5.6e-46;
Matches 149; Conservative 37; Mismatches 99
                     44.8%; Score 677; DB 2; 49.0%; Pred. No. 3.9e-46;
                                                                         50; Mismatches
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                                                                         Conservative
                       Query Match
Best Local Similarity
Matches 145; Conserv
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A;Molecule type: DNA
A;Residues: 1-291 <SIM>
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                                                                                                                                                                 Cross-references: GB:AE000148; GB:U00096; NID:g1786614; PIDN:AAC73524.1; PID:g1786623; A:Zxperimental source: strain K-12, substrain MG1655; Comment: This enzyme catalyzes the condensation of isopentenyl diphosphate with dimeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               v; Description: catalyzes condensation of isopentenyl diphosphate with dimethylallyl diph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Figure 26), 496-512, Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Puhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

**Authors: Gnehm, C.L.; McDonald, D.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, *Iffle, Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

**Accession: C64123
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\Cross-references: GB:U32822; GB:L42023; NID:91574265; PIDN:AAC23087.1; PID:91574277;
                                                                                                                                                                                                                                                                                                                                               ;Pathway: isoprenoid biosynthesis
;Superfamily: dimethylallyltranstransferase
;Suporfas: ATP; isoprenoid biosynthesis; nucleotide binding; P-loop; transferase
;84-93/Region: aspartate-rich
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2.Species: Haemophilus influenzae
3.Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 NTEDAPAAAVECIHAYSLIHDDEPAMDDDDERRGEPTCHVKRGBANAILAGDALQTLARS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDBATAILAGDALQALAFE 124
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                                                               Accession: E64771; Status: nucleic acid sequence not shown; translation not shown; Molecule type: DNA
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Science 277, 1453-1462, 1997
A,Title: The complete genome sequence of Escherichia coli K-12.
A,Reference number: A64720; MUID:97426617, PMID:9278503
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Fj241-248/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
45.8%; Score 691.5; DB 2
Best Local Similarity 52.0%; Pred. No. 2.8e-47;
Matches 153; Conservative 36; Mismatches 96
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A.Cross references: EMBL:D90899, GB:AB001339; NID:g1651650; PIDN:BAA16690.1; PID:g16517.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: geranyltranstransferase
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A.Reference number: A85001; MUID:20083488; PMID:10617193
A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
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                                            A; Reference number: S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                                  40.2%; Score 606.5; DB 2;
47.2%; Pred. No. 1.5e-40;
tive 42; Mismatches 97;
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45.9%; Pred. No. 3.1e-40;
tive 51; Mismatches 99
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Best Local Similarity 47.29
Matches 143; Conservative
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Best Local Similarity 45.9°
Matches 136; Conservative
                                                                                                                    A; Molecule type: DNA
A; Residues: 1-302 < KAN>
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A,Status: preliminary
A,Molecule type: DNA
A;Residues: 1-371 <ST
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"Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vertile. Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
"Accession: F81217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Cross-references: GB:AE002383; GB:AE002098; NID:g7225484; PIDN:AAF40715.1; PID:g722548; EXperimental source: serogroup B, strain MC58
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, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
NA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                       | Jeranyltranstransferase NMB0261 [imported] - Neisseria meningitidis (strain MC58
| Species: Neisseria meningitidis
| Jate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                               185 ALIRASVNIAAL----SKPDIDTCVAKKIDHYAKCIGLSFQVKDDILDIEADTATLGKTQ 240
                  VLANDPGITVDAPARLKMITALTRASGSQGWVGGQAIDLGSVGRKLTLPBLBNMHIHKTG 184
                                                                                                                                              RGKPTCHKAYDBATAILAGDALQALAFEVLANDPGITVDAPARLKMITALTRASGSQGMV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGQAIDLGSVGRKLTLPELENMHIHKTGALIRASVNLAALSKPDLDTCVAKKLDHYAKCI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRYAALDGGKRIRPMLVLAASELGEAVHEAVEQAMAAIEMIHVYSLVHDDM9AMDNDSLR 60
                                                                                                                                                                                                                241 GKDIDNDKPTYPALLGMAGAKQKAQELHEQAVESLTGFGSEADLLRELSLYIIERTH 297
                                                                                                                                                                                                                                                eranylgeranyl pyrophosphate synthase - Synechocystis sp. (strain PCC 6803) Alternate names: hypothetical protein slr0739 Species: Synechocystis sp. , Nariety: PCC 6803 , Nariety: PCC 6803 #Sequence_revision 25-Apr-1997 #text_charge 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 MRYSVINGGKRIRPILIYATGQALGIPENVIDAPACAVEFIHVYSLIHDDIPAMDNDDLR
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44.2%; Score 668; DB 2; Length 25
Best Local Similarity 52.5%; Pred. No. 1.7e-45;
Matches 137; Conservative 39; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: dimethylallyltranstransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | : | | | | | : | : | : | | : | PFGDKALRLRQLAEFAVARKY 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFGSEADLLRELSLYIIERTH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .; Molecule type: DNA
.; Residues: 1-259 <TET>
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               125
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VLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEV 125
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A;Residues: 1-366 <BON>
A;Cross-references: EMBL;X98795; NID:g1419757; PIDN:CAA67330.1; PID:g1419758
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LASATSSEV - SPARVVRAVGELAKAI GTEGLVAGOVVDISSEGLDLNNVGLEHLKFIHLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 LANDPGITVDAPAR-LKMITALTRASGSQGMVGGQAIDLGSVGRKLT---LPELENWHIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 AYLTVCOERVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 KTGALIRASVNIAALSKPDLDICVAKKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Genome: nuclear
C;Superfamily: geranyltranstransferase
C;Keywords: carotenoid biosynthesis; chloroplast; transferase
                                                                                                                                                                                                                                                                                                                                               / Match 39.1%; Score 590.5; DB 2, Local Similarity 45.6%; Pred. No. 3.6e-39; les 135; Conservative 52; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 29, 2004, 14:52:36
Job time : 11.2669 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                farnesyltranstransferase (SC 2.5.1.29) precursor - pepper
NyAlternate names: geraralygevanyl diphosphate synthase; geranylgeranyl pyrophosphate syn
C.Species: Capsicum annuum (pepper)
C.Date: 15-Uul-1995 #sequence_revision 21-Uul-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title: Structure of a functional geranylgeranyl pyrophosphate synthase gene from Capsi
Reference number: SS3722; MUID:95195169; PMID:7888631
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                                                                                                                                                   KTGALIRASVNIAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIRADTATLGKTQG 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S KAYLTVCQERVERALDARLPAENILPQTLHQAMRYSVINGGKRTRPLLTYATGQALGLPB 64
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C,Keywords: carotenoid biosynthesis; chloroplast; chromoplast; transferase
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A,Status: nucleic acid sequence not shown; translation not shown
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Title: Structure of a functional geranylgeranyl pyrophosph
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Best Local Simi
Matches 139,
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farmesyltranstransferase (EC 2.5.1.29) precursor, chloroplast - white mustard N.Alternate names: geranylgeranyl-diphosphate synthase; geranylgeranyl-pyrophosphate synt C.Species: Sinapis alba (white mustard) C.Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C;Accession: T10452 R;Bonk, M.; Hoffmann, B.; von Lintig, J.; Schledz, M.; Al-Babili, S.; Hobeika, E.; Klein Bur. J. Bicchem. 247, 942-950, 1997 A;Title: Chloroplast import of four carotenoid biosynthetic enzymes in vitro reveals dif A;Reterence number: Z17023; MUID:97433278; PMID:9288918 A;Accession: T10452 A;Status: preliminary; translated from GB/EMBL/DD5J

E.; Klein

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Length Indels

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P55539 rhizobium s
04520 bradyrhizob
08291 bacillus st
04269 catharanthu
062126 micrococus
06428 bacillus su
P48368 cyanophora
08840 buchnera ap
P57537 buchnera ap
P57537 buchnera ap
P67537 chodobacter
06692 aquifex aeo
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                                                                                             1 MSKLKAYLTVCQERVERALD......FGSEADLLRELSLYIIERTH 297
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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                                                                                                                                    141681 seqs, 52070155 residues
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                                                                                                                                                                                                                                                                                                                                                                   ISPA BRAJA
ISPA BACST
GGPP CATRO
ISPA MICLU
ISPA BACSU
CRTE CYAPA
ISPA BUCAP
ISPA BUCAL
CRTE RHOCA
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Match Length DB
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PREA_CYACA	COO1 YEAST	GGPP MOUSE	GGPP_BOVIN	GGPP HUMAN	GGPP GIBFU	GGPP NEUCR	FPP2 ARATH	FPP2 PARAR	FPP1 ARATH	FPPS SCHPO	PPPS_MAIZE
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323	473	300	294	300	418	428	342	342	384	347	350
14.1	13.5	12.0	11.5	11.5	11.4	10.2	8.3	8.2	7.6	7.6	7.5
213.5	203.5	181	174	173	172	154	125.5	124.5	115.5	114.5	113.5
34	35	36	37	38	39	40	41	42	43	44	45

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ROBERTS D., Allen B., Araujo R., Aparicio A., Chung E., Davis K., Duncts D., Allen B., Araujo R., Kalman S., Kong C., Kurdi O., Duncan M., Federspiel N., Hyman R., Kalman S., Kong C., Kurdi O., Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate = diphosphate + trans, trans-farnesyl diphosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Geranyltranstransferase (EC 2.5.1.10) (Farnesyl-diphosphate synthase)
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Blattner PubMed=9278503;

Blattner P.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

Blattner P.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

Man B., Shao Y.,

"The complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91210228; PubMed=2089044;
Pujisaki S., Hara H., Nishimura Y., Horiuchi K., Nishino T.;
Cloning and nucleotide sequence of the ispå gene responsible for
farnesyl diphosphate synthase activity in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bscherichia coli,
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Bscherichia.
VGBL_TaxID=562;
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ALIGNMENTS
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EMBL; U8264; AAB41177.1; -.
PIR; JQ0665; JQ0665;
SWISS-2DPAGE; P22999; COLI.
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                                                                                                                                                                                              STANDARD;
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ISPA OR B0421.
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                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                          LEACVKQANQALSRFIAPLPFQN---TPVVETMQYGALLGGKRLRPFLVYATGEMFGVST 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate = diphosphate + trans,trans.farnesyl diphosphate. --- SUBCELLULAR LOCATION: Cytoplasmic. --- SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                              8 LIVCQERVERALD -- - ARL PAENIL POTLHQAMRYSVINGGKRIR PLLIYATGQALGLPE
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10-CCT-2003 (Rel. 42, Last annotation update)
Geranyltranstransferase (BC 2.5.1.10) (Farnesyl-diphosphate synthase)
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STRAIN=Rd / KW30 / ATCC 51907;
MEDLINE=59350630; PubMed=754900;
Reliachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
Kerlavage A.R., Sult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M.,
Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hamma M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Gnehm C.L., Rcitchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 DNDKPTYPALLGMAGAKQKAQELHEQAVESLTGFGSEA---DLLRELSLYIIER 295
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                45.8%; Score 691.5; DB 1; Length 299; 52.0%; Pred. No. 9.4e-47; ive 36; Mismatches 96; Indels 9.
                     InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synth.
InterPro; IPR008949; Terpenoid synth.
PROSITE; PS00444; POLYPRENYL SYNTHET_2; I.
PROSITE; PS00723; POLYPRENYL SYNTHET_1; I.
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10-OCT-2003 (Rel. 42, Last and
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
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BEDLINES-20083488; PubMed=10617198;
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
Pairris B., Ansorge W., Brandt P., Grivell L., Rieger M., Weiler P., Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller P.
Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
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MEDLINE-99186754; PubMed-8016276;
Scolnik P.A., Bartley G.E.;
"Mucleotide sequence of an Arabidopsis cDNA for geranylgeranyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match
Local Similarity 49.0%; Pred. No. 1.2e-45;
Los 145; Conservative 50; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                  295 AA; 32407 MW; A64DE650266E670F
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PIR; C64123; C64123.
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GGPS1 OR AT4G36810.
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A Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Wo P., Hobleisel J., Zimmermann W., Wedler H., Ridley P., Langham S.-A. McCullagh E., Bilham I., Robben J., Vandenbussche F., Backen M., Welleins I., Voer M., Bastiaens I., Aert R., Defcor E., Weizenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Melzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Melzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Mooijman P., Klein Lankborst R., Rose M., Hauf J., Xoetter P., Berceiser S., Hempel S., Peldpausch M., Milar M., Milar M., Bener M., Dedrett R., Petter R., Degett J., Galen J., Villarroel R., De Glercq R., Van Montagu M., Rogers U., Gronin A., Quail M.A., Deray-Allen S., Van Montagu M., Rogers U., Hall S., Kay M., Lenmard N., McLay K., Mayes R., Pettett A., Rajandream M.A., Lyne M., Lenmard N., McLay K., Mayes R., Pettett A., Rajandream M.A., Lidhe D., Lighori R., Pether T., Herzl A., Gabel C., Fuchs M., Patrann B., Granderath K., Dauner D., Herzl A., Borses C., Gelhan M., Lenmard N., Meller-Aner S., Gabel C., Fuchs M., Patrann B., Granderath K., Dauner D., Herzl A., Massenet C., Quigley F., Clabauld G., Muenlelen S., Patrans B., Schaeler M., Bargues M., Pether R., Schmidt M., Bargues M., Tarol J., Torres A., Ghebon T., Weber N., Patrans B., Charles S., Francs P., Bielke C., Cheffors T., Weber R., Berger C., Monfort A., Casacubarta B., Gharan S., Tarishman D., Hassen D., Lemcke K., Mewes E.-W. Stocker S., Beva B., Johnson D., Wesser T., Heijnen L., Schwarz S., Scholler P., Hobert S., Francs P., Bielke C., Arishman D., Hassen D., Lemcke K., Mewes E.-W. Stocker S., Donnson D., Marchis B., Madren D., Abbort A., Scholler P., Cotton M., Joshu K., Marchis B., Madren M., Marry J., Sheet P., Cotton M., Dohott A., Scott K., Johnson D., Mirx P., Bertjach M., Spiech J., Marchises B., Madren M., Marry J., Sheet P., Cotton M., Worden S., Woldy N., Hassgers M., Brenner M., Bertjack M., Marry M., Marry M., Marry M., Marry M., Marry M., Marry M., Marry M., Marry M., Marry M., Marry 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i - SUBCELLULAR LOCATION: Chloroplast. -i - SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme in plant terpenoid biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L25813; AAA32797.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 402:769-777(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Monomer.
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GGPP ठ 유 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ -I- FUNCTION: Catalyzes the trans-addition of the three molecules of IPP onto DMAPP to form geranylgeranyl pyrophosphate.
-I-CATALYTIC ACTIVITY: Dimethylallyl diphosphate + isopentenyl diphosphate = diphosphate + geranyl diphosphate + isopentenyl diphosphate = diphosphate + faranyl diphosphate + isopentenyl diphosphate + trans.trans.farnesyl diphosphate + isopentenyl diphosphate + trans.trans.farnesyl diphosphate + isopentenyl diphosphate = diphosphate + geranylgeranyl diphosphate.
-I-CATALYTIC ACTIVITY: Trans.trans.farnesyl diphosphate + isopentenyl diphosphate = diphosphate + geranylgeranyl diphosphate. InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synth.
Pfam; PF00348; Polyprenyl synt; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
Transferase; Isoprene biosynthesis; Carotenoid biosynthesis; CAB16803 PIR; F85434; F85434. AL161590;

EMBL;

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                                                                                                                                                                                                                                                                                                                                                                                                                    126 LANDPGITVDAPAR-LKMITALTRASGSQGMVGGQAIDLGSVGRKLT---LPELENMHIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta,
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Capsicum.
                                                                                                                                                                                                                                                                                                                                  66 VLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 KDLIADKLTYPKIMGLEKSREPAEKLNREARDOLLGFOSDKVAPLL-ALANYIAYR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Mol. Biol. 27:425-428(1995).
-!- FUNCTION: Catalyzes the trans-addition of the three molecules of IPP onto DWAPP to form geranylgeranyl pyrophosphate.
-!- CATALYTIC ACTIVITY: Dimethylallyl diphosphate + isopentenyl diphosphate = diphosphate + geranyl diphosphate.
-!- CATALYTIC ACTIVITY: Geranyl diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Badillo A., Steppuhn J., Dervere J., Camara B., Kuntz M.;
"Structure of a functional geranyigeranyl pyrophosphate synthase gene
from Capsicum annuum.";
                                                                                                                                                                                                               Gaps
                                            PYROPHOSPHATE SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Geranylgeranyl pyrophosphate synthetase, chloroplast precursor (GGPP synthetase) (GGPS) [includes: Dimethylallyltransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10); Farnesyltranstransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 KDIDNDKPTYPALLÆMAGAKOKAQELHEQAVESLTGFGSE--ADLLRELSLYIIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a cDNA for the plastid-located geranylgeranyl pyrophosphate synthase from Capsicum annuum: correlative increase enzyme activity and transcript level during fruit ripening."; plant J. 2:25-34(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuntz M., Roemer S., Suire C., Hugueney P., Weil J.H., Schantz R.
                                                                                                                                                                                                             10;
                                                                                                                                                                     Length 371;
                                                                                                                                                                                                             99; Indels
                                                             R -> S (IN REF. 1).
A -> R (IN REF. 1).
A -> S (IN REF. 1).
; BFA8088A75B6A005 CRC64;
                                                                                                                                                               40.0%; Score 604; DB 1;
45.9%; Pred. No. 7.9e-40;
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(Rel. 22, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                           51; Mismatches
                        CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Yolo Wonder;
MEDLINE=95195169; Pubmed=7888631;
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MEDLINE=93272043; PubMed=1303794
                                                                                                                           40174 MW;
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  peptide.
                                                                                                                                                                                   Best Local Similarity 45.7
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                            371
108
141
192
    Transit
                                                                                                                           371 AA;
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SEQUENCE FROM N.A.
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Chloroplast;
TRANSIT
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10-0CT-2003
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CONFLICT
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PIR, T10452; T10452.
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ses 135, Conserv
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                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 VLAND-PGITVDAPARL-KMITALTRASGSQGWVGGQAIDLGSVGR-KLTLPELENMHIH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
CATALYTIC ACTIVITY: Trans-farnesyl diphosphate.
diphosphate + isopentenyl diphosphate + isopentenyl diphosphate = diphosphate + geranylgeranyl diphosphate.
APTHANY: First committed step in carotenoid biosynthesis. Key enzyme in plant terpenoid biosynthesis. Key SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KAYLTVCQERVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLPE
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Geranylgeranyl pyrophosphate synthetase, chloroplast precursor (GGPP synthetase) (GGPS) [Includes: Dimethylallyltransferase (EC 2.5.1.1);
Geranyltransferase (EC 2.5.1.10); Farnesyltransferase
GGPS1 OR GGPS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GERANYLGERANYL PYROPHOSPHATB SYNTHETASE: 2D527F5E43A29C6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDIDNDKPTYPALLGMAGAKOKAQELHEQAVESLTGFGS-EADLLRELSLYIIER 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDLVVDKTTÝPKILGLEKAKEFAABINREAKQQLEGFDSRKAAPLIALADÝIAYR 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sinapis alba (White mustard) (Brassica hirta).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Sinapis.

(NCBI_TAXID=3728,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synth.
Pfan; PF00348; polyprenyl synt; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
PROSITE; PS00733; POLYPRENYL SYNTHET 1; 1.
Transferase; Isoprene biosynthesis; Carotenoid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 369;
                                                                                                                      SUBCELLULAR LOCATION: Chloroplast. SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.5%; Score 596; DB 1; Length 36 Best Local Similarity 47.1%; Pred. No. 3.3e-39; Matches 139; Conservative 45; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLOROPLAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast; Transit peptide.
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ID GGPP SINAL
AC Q43133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                                                                                                                                                                                                                                                                                                LEUNCTION: Catalyzes the trans-addition of the three molecules of iPDMCTION: Catalyzes the trans-addition of the three molecules of iPD onto DMAPP to form geranylgeraryl pyrophosphate.

-!-CATALYTIC ACTIVITY: Dimethylallyl diphosphate + isopentenyl diphosphate = diphosphate + geranyl diphosphate + isopentenyl diphosphate + isopentenyl diphosphate + trans.trans.farneyl diphosphate + trans.trans.farneyl diphosphate + isopentenyl diphosphate + isopentenyl diphosphate + isopentenyl diphosphate = diphosphate + geranylgeranyl diphosphate + isopentenyl diphosphate = diphosphate + geranylgeranyl diphosphate.

-!-CATALYTIC ACTIVITY: frans.trans.farnesyl diphosphate.

-!-CATALYTIC ACTIVITY: frans.trans.farnesyl diphosphate.

-!-CATALYTIC ACTIVITY: frans.trans.farnesyl diphosphate.

-!-CATALYTIC ACTIVITY: frans.trans.farnesyl diphosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ? 366 GERANYLGERANYL PYROPHOSPHATE SYNTHETASE. 366 AA; 39432 MW; 1EADBFD9C4CF4F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE-97433278; PubMed-2288918;
Bonk M., Hoffmann B., von Lintig J., Schledz M., Al-Babili S.,
Hobeika E., Kleinig H., Beyer P.,
Chlocroplast import of four carotenoid biosynthetic enzymes in
reveals differential fates prior to membrane binding and oligom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Program Projates and Project Structure of the Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Projates Pr
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45.6%; Pred. No. 8.8e-39;
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InterPro; IPR008949; Terpenoid Synth.
                                                                                                                                                                                                                                                                                                                                        assembly.";
Eur. J. Biochem. 247:942-950(1997).
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P55539;
01-NOV-1997 (Rel. 35, Created)
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Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
           synthase)
                                         FPPS OR BLR2148.
                                                                                                                                                                                    NCBI_TaxID=375;
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           synthase)
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           g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBE cutstation the Buropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 KRVEQALARLICAEDHGETEIMAAMRYATIHGGKRIRALICLAAGALADTPAHILDDVGA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 AVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEVLANDPGI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 TVDAPA--RLKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENWHIHKTGALIRAS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 VRMGALCAIAEDAADATLYCALDHYSACFGLALQVVDDILDATADTATLGKTPGKDAAAQ 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 337:394-401(1997)
-!- CAPALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate
= diphosphate + trans.trans-farnesyl diphosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the PPP/GGPP synthetase family.
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable geranyltranstransferase (EC 2.5.1.10) (Farnesyl-diphosphate
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal
Perret X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPTYPALLGMAGAKQKAQELHEQAVESLTGFGSEAD----LLRELSLYIIE 294
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                                                                                                                                                                                                               Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98; Indels
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InterPro; IPR000949; Perpenoid synth.
InterPro; IPR000949; Perpenoid synth.
PR03138; Polyprenyl_synt; I.
PR031TE; PS00444; POLYPRENYL_SYNTHET_2; I.
PR031TE; PS00723; POLYPRENYL_SYNTHET_1; I.
Transferase; Isoprene biosynthesis; Plasmid.
SEQUENCE 332 AA; 34688 MM; EE68C1547449AA87 CRC64;
                                                                                                                                                                                                                                                                                   Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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38.6%; Score 583; DB 1;
Best Local Similarity 45.7%; Pred. No. 3e-38;
Matches 133; Conservative 46; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000082; AAB91752.1; -.
                                                                                                                                                                             (strain NGR234).
                                                                                                             synthase) (FPP synthase).
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                                                                                                                                                                             Rhizobium sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizolum japonicum USDA110.";
DNA Res. 9:189-197(2002).
-!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate = diphosphate + trans.trans.transeyl diphosphate.
-! SUBCELLULAR LCCATION: Cytoplasmic [Potential]).
-!- SUBCELLULAR LCCATION: Cytoplasmic Potential).
-!- SIMILARITY: Belongs to the PPP/GGPP synthetase family.
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MEDINE=89322110; PubMed=9655913;
MIJN RE., van Berkum P., Lovins K.W., Keister D.L.;
"Identification and sequencing of a cytochrome P450 gene cluster from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 ERVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLPENVLDAPAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., Kobara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada
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                             STRIN-USDA 110;
Tully R.B., Keister D.L.;
"Cloning and mutagenesis of a cytochrome P-450 locus from Bradyrhizobjum japonicum that is expressed anaerobically and
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InterPror, IRR00082; Polyprenyl synt.
InterPror, IRR008949; Terpenoid synth.
Pfam; PF00348; polyprenyl synt; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
Transferase; Isoprene blosynthesis; Complete proteome.
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                                                                                                                                                    symbiotically.";
Appl. Environ. Microbiol. 59:4136-4142(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                       Bradyrhizobium japonicum.";
Biochim. Biophys, Acta 1398;243-255(1998).
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BAC47413.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22484998; PubMed=12597275;
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Matches 133; Conservative 4
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SEQUENCE FROM N.A.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable geranyltranstransferase (RC 2.5.1.10) (Farnesyl-diphosphate

332 AA

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SPA_BRAJA 1D 169A BRAJA 1C 045220; 71 01-NOV-1997 (77 10-NOV-1997 (77 10-NOV-1997 (77 10-NOV-1997 (78 10-NOV-1997 (79 10-NOV-1997 (79 10-NOV-1997 (79 10-NOV-1997 (70 10-NOV-

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VNLAALSKPDLDTCVAK----KLDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKDIDND 247
                           217 VRMGALCAVGVNAAHAALYCALDHYSACFGLALQVIDDILDVTADTAALGKTPGKDAAAQ 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                MUTAGENESIS OF CYSTEINE RESIDUES.
MUTAGENESIS OF CYSTEINE RESIDUES.
MEDINE=95001990; PubMed=7918490;
KOyama T., Obata S., Saito K., Takeshita-Koike A., Ogura K.;
Koyama T., Obata S., Saito K., Takeshita-Koike A., Ogura K.;
Structural and functional roles of the cysteine residues of Bacillus stearchermophilus farnesyl diphosphate synthase.";
Biochemistry 33:12644-12648(1994).
-!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentemyl diphosphate = diphosphate LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the FPF/GGPP synthetase family.
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
8
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MEDLINE=9252788; PubMed=8486607;
Koyama T., Obata S., Osabe M., Takeshita A., Yokoyama K.,
Uchida M., Nishino T., Ogura K.,
"Thermostable farnesyl diphosphate synthase of Bacillus
stearchermophilus: molecular cloning, sequence determination,
overproduction, and purification.";
J. Blochem. 113:355-363(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.2%; Score 577; DB 1; Length 297; 44.8%; Pred. No. 7.7e-38; ative 42; Mismatches 114; Indels
                                                                                                                                                                                                                                              (FPP synthase).
Bacillus stearothermophilus.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Geobacillus.
                                                                          277 KPTCASIMGLQBARQFALDLLRDAGEAIAPLGPRAERLAQL
                                                         248 KPTYPALLGWAGAKQKAQELHEQAVESLTGFGSEADILREL
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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Best Local Similarity 44.81
Matches 133; Conservative
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4 LKAYLTVCOERVERALD --- ARLPAENILPQTIHQAMRYSVLNGGKRTRPLLTYATGQAL

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                                                                                                                                                                                                                           121 LAFBVLANDPGITVDAPARLKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPBLENMHI 180
                                                                                                                                                                                                                                                                                                                                                                                                                           |||| ::: ||: || GAADARQTRELDEFAAHLGLAFQIRDDILDIEGAEBKIGKPV 240
                                                                                                                                                                                                                                                                        181 HKTGALIRASVNLAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQ 240
                                                                             GLPENVIDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQA 120
61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GKDIDNDKPTYPALLGMAGAKOKAQELHEQAVESLTGFGSEADLLRELSLYIIBRTH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Bukaryota, Viridiplantae, Streptophyta; Bukaryothyta; Trachleophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; asterids;
Spermatophyta; Apocynaceae; Rauvolfioldeae; Vinceae;
                                                                                                                      62 GKDPAVGLPVACAIEMIHTYSLIHDDLPSWDNDDLRRGKPTNHKVFGEAMAILAGDGLUT
6 VEQFINEQKQAVETALSRYIERLEG----PAKLKKAMAYSLEAGGKRIRPLLLLSTVRAL
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
46-OCT-2003 (Rel. 25, L.1);
46-OCT-2003 (Rel. 25, L.1);
46-OCT-2004 (Rel. 25, L.2);
46-OCT-2004 (Rel. 25, L.2);
46-OCT-2004 (Rel. 25, L.2);
46-OCT-2005 (Rel. 25, L.2);
46-OCT-2005 (Rel. 25, L.2);
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STRAIN-cv. G. Don c20;
Bantignies B., Liboz T., Ambid C.;
"Nucleotide sequence of a Catharanthus roseus geranylgeranyl pyrophosphate synthase gene.";
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InterPro; IPR008949; Terpenoid_synth.
Pfam; PF00348; polyprenyl synt; 1.
PR0SITE; PS00742; PULYPRENYL SYNTHET_1; 1.
TRANSIE; PS00444; POLYPRENYL SYNTHET_2; 1.
Transferase; Isoprene biosynthesis; Carotenoid biosynthesis;
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291 AA; 32362 MW; 797125AB71B5674A CRC64;

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SEQUENCE
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                                                                                                                                                                                                                                                                                      67 KAYMIGKANSVNKALEDAVLVRE---PLKIHESMRYSLLAGGKRVRPMLCIAACELFGGT 123
                                                                                                                                                                                                                                                                                                                                                                    64 ENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDBATAILAGDALQALAF 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 KTGALIRASVNIAALSKPDLDTCVAKKIDHYAKCIGLSFQVKDDILDIEADTATLGKTQG 241
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                                                                                                                                                                                                                                                        5 KAYLTVCQERVERAL-DARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLP 63
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"Molecular cloning, expression, and characterization of the genes encoding the two essential protein components of Micrococcus luteus B.P. 26 hexaprenyl diphosphate synthase.",
J. Bacteriol. 180:1578-1581(1998)
-!-CYTALWITT. CATTIVITY: Geranyl diphosphate + isopentenyl diphosphate = diphosphate + trans, trans-farnesyl diphosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                             40 CHLOROPLAST (POTENTIAL).
357 GERANYLGERANYL PYROPHOSPHATE SYNTHETASE.
38786 MW, 81C52FDEALEO6FA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Geranyltranstransferase (EC 2.5.1.10) (Farnesyl-diphosphate synthase)
                                                                                                                                                                                                     10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 KDIDNDKPTYPALLGMAGAKQKAQBLHEQAVESLTGFGSE-ADLLRELSLYIIER 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Micrococcus luteus (Micrococcus lysodeikticus).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Micrococcus.
                                                                                                                                            Length 357;
                                                                                                                                      Query Match 38.1%; Score 575; DB 1; Length 357 Best Local Similarity 47.1%; Pred. No. 1.4e-37; Matches 139; Conservative 43; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synth.
Pfam, PP00348; Polyprenyl synt, 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
Transferase; Isoprene biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=B-P 26;
MEDLINE=98175686; PubMed=9515931;
Chloroplast, Transit peptide. TRANSIT 1 40 CEAIN 41 357 SEQUENCE 357 AA, 38786 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB003187; BAA25265.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                             357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FPP synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISPA MICLU
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70 PACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDBATAILAGDALQALAFEVLAND 129
                                                                                                                                                                                                       70
                                                             71 ---ALEMIHTYSLIHDDLPAMDNDDYRRGKLTNHKRFDEATAILAGDALLTDAFQCILN-
                                                                                                                                                          "systematic sequencing of the 283 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many sporulation genes.";
                                                                                                                                            130 PGITVDAPARLKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENMHIHKTGALIRA
                                                16 BRALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQAL-----GLPENVLDA
                                                                                                                                                                                        SVNLAALSKPDLDTCVAKKLDHYAKCIGLSPQVKDDILDIBADTATLGKTQGKDIDNDKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97124195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Greated)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Geranyltranstransferase (EC 2.5.1.10) (Farnesyl-diphosphate synthase)
                         20; Gaps
 Length 291;
                                                                                                                                                                                                                                                               244 TYVSLÍGLEASKÓLLNDKLTETYDALKTLOPINDNÍKTLITÝIVER 289
                         92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                                                                                                        TYPALLGMAGAKQKAQELHEQAVESLTGFGSBADLLRELSLYIIER
37.5%; Score 566; DB 1;
45.5%; Pred. No. 5.4e-37;
tive 44; Mismatches 92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                crobiology 142:3103-3111(1996)
Query Match
Best Local Similarity 45.5'
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JH642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              (FPP synthase).
Yold OR BSU24280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=168 /
                                                                                                                                                                                                                                                                                                                         BACSU
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Glaucocystophyceae; Cyanophoraceae; Cyanophora.
                       Eukaryota; Glauc
NCBI_TaxID=2762;
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                                                                                                                                     Bryant D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LAFEVLANDPGITVDAPARLKMITALTRASGSQGWVGGQAIDLGSVGRKLTLPELENMHI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Satronaldan E., Schleich S., Schroeter R., Scoffone F., Schiguchi J., Schowska A., Servor D., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanakashi A., Tanakashi A., Tanakashi A., Tanakashi A., Tanakashi A., Vandenbol M., Vannier P., Vassarctti A., Viari A., Nambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wippat A., Yamamoto H., Yamano K., Yasumoto K., Yasumoto K., Yoshida K., Yoshikawa H.F., Zumstein B., Yoshikawa H., Danchin A., The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390:249-256(1997).
-!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate = diphosphate + trans, trans-farnesyl diphosphate.
-! = SUBCELLUIAR LOCATION: Cytoplasmic -! SUBCELLUIAR LOCATION: Cytoplasmic -! - SIMILARITY: Belongs to the PPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLPENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDBATAILAGDALQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKT----GALIRASVNLAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIEADTATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SKLKAYLTVCQERVERALDARLPAENI-LPQTLHQAMRYSVLNGGKRTRPLLTYATGQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEE-1996 (Rel. 33, Created)
01-FEE-1996 (Rel. 33, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Geranylgeranyl pyrophosphate synthetase homolog (EC 2.5.1.29) (GGPP synthetase) (Farnesyltranstransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 531; DB 1; Length 272;
Pred. No. 2.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pram; PF00348; polyprenyl synt; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
PROSITE; PS00423; POLYPRENYL SYNTHET 1; 1.
Transferaes; Isoprene biosynthesis; Complete proteome. SEQUENCE 272 AA; 29740 MW; 55A26E9A9895D67C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 GKRVGSDITNDKSTIPSLLSLEGAKHK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKTOGKDIDNDKPTYPALLGMAGAKOK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR, A69961, A69961.
Subtliat, S011714; Yqib.
InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D84432; BAA12575.1; -. EMBL; Z99116; CAB14359.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 43.48
Matches 116, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetase) (Farnes)
CRTE.
Cyanophora paradoxa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYAPA
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ID CRTE CYAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-UTEX LB 555 / Pringsheim;
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
Parley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
(In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
(In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 MEMALPTACALEMIHTMSLIHDDLPAMDNDSYRRGKPTNHIIYGEDLAILAGDALLAYAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LKAYLTVCQERVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVLANDPGITVDAPARL - - KMITALTRASGSQGMVGGQAIDLGSVGRK - LTLPELENMHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKTGALIRASVNIAALSKPDLDTCVAKKLD-----HYAKCIGLSFQVKDDILDIBADTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGKTQGKDI DNDKPTYPALLGMAGAKQKAQELHEQAVESLTGFGSEADLLRELSLYI IER
                                                                                                                                          'Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U30821, AAA8112.1; -.

PIR, T06969, T06969.

InterPro; IPR00092; Polyprenyl synt.

InterPro; IPR008949; Trpenoid synth.

PERO; PRO0348; polyprenyl synt, 1.

PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.

PROSITE; PS00733; POLYPRENYL SYNTHET 1; 1.

Photosynthesis; Carotenoid biosynthesis; Photosynthesis; Carotenoid biosynthesis; SRQUENCE 300 AA; 33008 MW; 05950D0E3BA049834 CRC64;
SEQUENCE FROM N.A.
STRAIN=UTEX LB 555 / Pringsheim;
Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I- CATALYTIC ACTIVITY: Trans-trans-farnesyl diphosphate + diphosphate = diphosphate + geranylgaranyl diphosphate.
-I- PATHWAY: Carotenoid and chlorophyll biosynthesis.
-I- SIMILARITY: Belongs to the PPP/GGPP synthetase family.
                                                                                                                                                                                      Plant Mol. Biol. Rep. 13:327-332(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 43.0%;
Matches 130; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 APACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEVLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 VISTAIEFHSYSLIHDDLPCMDNDNPRRGKISCHVKYGESTSLLAGDALQSLAFNILSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 SFWPNVSNLKRIKMISELSYSIGSSGMCMGQNLDLEAEKKDVNLSELRIINLYKTSFLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 SAVELVYPSSINIPSKSILSILDLPSISIGLAFQIQDDILDFXXDSV---KTDNKKIIK-K
                                                                                                                                                               Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 407:81-86(2000).
-!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 DPGITVDAPARLKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENMHIHKTGALIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 ASVNIAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIZADTATLGKTQGKDIDNDK
                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Geranyltranstransferase (EC 2.5.1.10) (Farnesyl-diphosphate synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 ERVERALDARL-PAENILP---QTLHQAMRYSVLNGGKRTRPLLTTATGQALGLPENVLD
                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               = diphosphate + trans,trans-farnesyl diphosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-!- SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , 6e-32;
ches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synt.
InterPro; IPR008949; Terpenoid synth.
Pram; PR008148; POLYPRENYL SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
Iransferase; Isoprene biosynthesis; Complete processes SEQUENCE 282 AA; 32331 MM; 228831A6DBCD6445 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.2%; Score 501; DB 1;
41.9%; Pred. No. 6e-32;
ive 56; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 PTYPALLGMAGAKQKAQELHEQAVESL 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP001119; BAB13162.1; -.
                                                                                                                                                                                                                                     Enterobacteriaceae, Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 112; Conservative
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                                                                                                                                                                                     symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                STRAIN=Tokyo 1998;
                                                                                                                                                                                                                                                            NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                            FROM N.A
                                                                                                                 (FPP synthase),
ISPA OR BU465.
                                                                                                                                                                                                                                                                                                                                                                                                                              Buchnera sp
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                                                                                                                                                                                                                                                                                                            SEQUENCE
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CRTE_RHOCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 IDTCVAKKIDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKDINDKPTYPALLGMAGA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KMITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENWHIHKTGALIRASVNLAALSKPD 200
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----TKNTYPLLIGLKKS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate = diphosphate + trans,trans.faranssyl diphosphate.-! = diphosphate LOCATION: Cytoplasmic (By similarity). -!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity). -!- SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPAENILPQTLHQAMRYSVINGGKRTRPLLTYATGQALGLPENVLDAPACAVEPIHVYSL
                                                                                                                                                    28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Geranyltranstransferase (BC 2.5.1.10) (Farnesyl-diphosphate synthase)
                                                                                                                                                                                                                                                               Buchrera aphidicola (subsp. Schizaphis graminum).
Bacceria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eriksson A.-S.,
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22084569; PubMed=12089438; Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S., Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.R.; "50 million years of genomic stasis in endosymbiotic bacteria."; Science 296:2376-2379 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7D7D901C7213ED0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00348; polyprenyl synt; i. PR031TE; P800723; POLYPRENYL SYNTHET 1; 1. PR051TE; P80044; POLYPRENYL SYNTHET 2; 1. Transferase; Isoprene biosynthesis; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 FSKEVLFILDKFSVSIGLAFQIQDDILDLKNDIKKLESKRNK-
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es 98;
                                                                                        294 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 33.2%; Score 501.5; Local Similarity 42.2%; Pred. No. 5.8% les 117; Conservative 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AE014121, AAM67992.1; -.
InterPro; IPR00092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid_synth.
                                                                                                                                   (Rel. 41, Created)
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                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    ISPA OR BUSG449
                                                                                                                                                                                                                                (FPP synthase)
                                                                                                                              28-FEB-2003
28-FEB-2003
10-OCT-2003
                                                                                     ISPA BUCAP
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Gaps

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Length 282;

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                                                                           {Rel. 15, Created}
{Rel. 15, Last sequence update}
244 HTYPLIIGLDESRKKIKQLHKKSFLAL 270
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STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 AAAVALELMHCASLVHDDLPAFDNADIRRGKPSLHKAYNEPLAVLAGDSLLIRGFEVLA- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 RASVNLAAL----SKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIRADTATLGKTQGK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 DPGITVDAPARLKWITALTRASGSQ-GMVGGQAIDLGSVGRKLTLPELBNMHIHKTGALI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 IAATOMGAIAAGYEAEPWFDLGMR------IGSAFÓIADDLKDALMSAEAMGKPAGO 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S KRIESALVKALSPEALGESPPLLAAALPYGVFPGGARIRPTILVSVALACGDDCPA-VTD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 ERVERALDARLPAENI -- LPQTLHQAMRYSVINGGKRIRPILITYATGQALG--LPENVLD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: Trans-trans-farnesyl diphosphate + isopentenyl diphosphate = diphosphate + geranylgeranyl diphosphate.
-!- PATEWAY: Carotenoid and chlorophyll biosynthesis.
-!- SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.4%; Score 399; DB 1; Length 289;
37.4%; Pred. No. 5.5e-24;
tive 46; Mismatches 107; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Armstrong G.A., Alberti M., Leach F., Hearst J.B.,
"Nucleotide sequence, organization, and nature of the protein
products of the carotenoid biosynthesis gene cluster of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008949; Terpenoid_synth.

Pitam, PR001348; polyprenyl synt; 1.

PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.

PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.

Photosynthesis; Chlorophyll blosynthesis; Carotenoid biosynthesis; Isoprene blosynthesis; Transferase.

Isoprene blosynthesis; Transferase.
                                                                                                                                        Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
MCBI _TaxID=1061;
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10-OCT-2003 (Rel. 42, Last annotation update)
Geranylgeranyl pyrophosphate synthetase (EC 2.5.1.29) (GGPP
synthetase) (Parnesyltranstransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF483A26ECA9C859 CRC64;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=SB1003 / St Louis, and BEC404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000092; Polyprenyl_synt.
InterPro; IPR008949; Terpenoid_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gen. Genet. 216:254-268(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89313663; PubMed=2747617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 AA; 30043 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X52291, CAA36538.1, -.
EMBL, Z11165, CAA77545.1, -.
PIR, S04407, S04407.
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Matches 108; Conservative
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Search completed: February 29, 2004, 14:44:55 Job time : 7.00562 secs

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| 1510 | 100.0 | 297 | 9 US-09-934-903-14 | Sequence 72, Appl 3 15.0 | 100.0 | 297 | 9 US-09-934-903-14 | Sequence 72, Appl 3 15.0 | 100.0 | 297 | 9 US-09-934-903-14 | Sequence 72, Appl 3 15.0 | 100.0 | 297 | 9 US-09-934-903-14 | Sequence 72, Appl 3 15.0 | 100.0 | 297 | 9 US-09-934-903-15 | Sequence 72, Appl 4 831 | 55.0 | 295 | 9 US-09-941-947A-20 | Sequence 72, Appl 5 15.0 | 295 | 9 US-09-9493-8506 | Sequence 13999, A 179.5 | 57.4 | 291 | 15 US-10-369-493-1999 | Sequence 13999, A 179.5 | 47.6 | 294 | 15 US-10-369-493-1999 | Sequence 13999, A 179.5 | 47.6 | 294 | 15 US-10-369-493-1599 | Sequence 13999, A 179 | 47.8 | 291 | 15 US-10-369-493-1549 | Sequence 15449, A 170 | 46.8 | 284 | 15 US-10-369-493-15817 | Sequence 15419, A 170 | 46.8 | 284 | 15 US-10-369-493-15817 | Sequence 16200, A 18 | 295 | 15 US-10-369-493-15817 | Sequence 16200, A 18 | 295 | 15 US-10-369-493-15817 | Sequence 10069, A 19 | 691.5 | 45.7 | 306 | 15 US-10-369-493-10187 | Sequence 10187, A 19 | 691.5 | 45.7 | 306 | 15 US-10-369-493-10187 | Sequence 10187, A 19 | 45.7 | 306 | 15 US-10-369-493-10187 | Sequence 10187, A 19 | 45.7 | 306 | 15 US-10-369-493-10187 | Sequence 10187, A 19 | 45.7 | 306 | 15 US-10-369-493-10187 | Sequence 10187, A 19 | 45.7 | 306 | 15 US-10-369-493-10187 | Sequence 10187, A 19 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.7 | 306 | 45.8 | 30.8 | 45.8 | 30.8 | 45.8 | 30.8 | 45.8 | 30.8 | 45.8 | 30.8 | 45.8 | 30.8 | 45.8 | 30.8 | 45.8 | 30.8 | 45.8 | 30.8 | 45.8

Sequence 11239, A Sequence 11239, A Sequence 17527, A Sequence 9246, Ap Sequence 21173, A Sequence 21173, A Sequence 10617, A Sequence 10617, A Sequence 18752, A Sequence 18752, A Sequence 18752, A Sequence 18752, A Sequence 159, Appl Sequence 17358, A Sequence 159, Appl Sequence 159, Appl Sequence 159, Appl Sequence 159, Appl Sequence 159, Appl Sequence 159, Appl Sequence 15949, A Sequence 16949, A Sequence 16949, A Sequence 16949, A Sequence 16949, A Sequence 16949, A Sequence 16949, A Sequence 16949, A Sequence 16949, A Sequence 16949, A Sequence 16949, A Sequence 20569, A Sequence 16949, A Sequence 16949, A Sequence 16949, A Sequence 16949, A Sequence 16949, A Sequence 20569, A Sequence 16949, A Sequence 20569, A Seque	Sequence 64, Appl Sequence 64, Appl Sequence 5239, Ap Sequence 12583, A
5 US-10-369-493-480 US-09-815-242-11239 US-10-369-493-912527 US-10-369-493-917527 US-10-369-493-91173 US-10-369-493-91173 US-10-369-493-91173 US-10-369-493-91173 US-10-369-493-10617 US-10-369-493-10617 US-10-369-493-10617 US-10-369-493-11358 US-10-369-493-11358 US-10-369-493-11358 US-10-369-493-11358 US-10-369-493-11358 US-10-369-493-11358 US-10-369-493-11358 US-10-369-493-11559 US-10-369-493-11559 US-10-369-493-11559 US-10-369-493-11559 US-10-369-493-11559 US-10-369-493-11559	US-09-925-637-64 US-10-084-205-64 US-09-815-242-523 US-09-815-242-125
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                                                   APPLICANT: Koffas, Wattheos
APPLICANT: Koffas, Wattheos
APPLICANT: Odom, J. Marthn
APPLICANT: Schenzle, Andreas J.
APPLICANT: No. US20020102690Alton, Kelley C.
APPLICANT: Tomb, Jean-Francois
APPLICANT: Picataggio, Stephen
APPLICANT: Picataggio, Stephen
APPLICANT: Picataggio, Stephen
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
FILE REFERENCE: Ci.1646 US NA
CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR PILING DATE: September 1, 2001
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
LENGTH: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSKLKAYLTVCQERVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQAL
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100.0%; Pred. No. 4.4e-152;
ative 0; Mismatches 0;
Sequence 14, Application US/09934903
Patent No. US20020102690A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 297; Conservative
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Patent No. US20020137190A1

GREEAL INFORMATION:

GREEAL INFORMATION:

APPLICANT: Roffas, Matthees

APPLICANT: Schenile, Andreas J

TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

FILE REPERENCE: CLISS6 US NA

CURRENT APPLICATION NUMBER: US/09/934,868

PRIOR RELING DATE: 2000-09-01

PRIOR PILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 81

SOPTWARE: Microsoft Office 97

SEQ ID NO 72

FENOM: APPLICATION OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPERTY OFFICE PROPE
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US-09-934-868-72
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100.0%; Pred. No. 4.4e-152;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Methylomonas 16a
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Matches 297; Conservative
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US-09-934-868-72
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Sequence 20, Application US/08941947A
Publication No. US20030003528A1
GENERAL INFORMATION:
APPLICANT: Brzestowicz, Patricia C.
APPLICANT: Cheng, Qiong
APPLICANT: DiCosimo, Deana J.

US-09-941-947A-20

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APPLICANT: Gdom, J. Martin

APPLICANT: Ocdom, J. Martin

APPLICANT: Picataggio, Stere

APPLICANT: Rouviere, Pierre E.

TITLE OP INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE

FILE APPLICATION NUMBER: US/09/941,947A

CURRENT APPLICATION NUMBER: US/09/941,947A

CURRENT FILING DATE: 2001-09-01

PRIOR PILING DATE: 2000-09-01

PRIOR PILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Microsoft Office 97

LENGTH: 297
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Factor No. US/2020061569A1

GRNERAL INFORMATION:
FAPPLICANT: Haselbeck, Robert
APPLICANT: Grien, Kazi L.
APPLICANT: Wall, Daniel
FAPPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Vamanoro, Robert T.
APPLICANT: Vamanoro, Robert T.
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PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLILICATION NUMBER: 60/242,578
PRIOR PLILICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/25,625
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Best Local Similarity 100.
Matches 297; Conservative
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; Sequence 4670, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei; APPLICANT: Hinkle, Gregory J.; APPLICANT: Stater, Steven C.; APPLICANT: Stater, Steven C.; APPLICANT: Coldman, Barry S.; APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13999, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 56.9
Matches 168, Conservative
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US-10-369-493-13999
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Publication No. US20030233675A1
BENERAL INFORMATION:
APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Galdman, Barry S.
APPLICANT: Galdman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: ELANTS MITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 ENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAF 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IAAYQARCQARVDAALDALFVAPREELQRLYEAMRYSVMNGGKRVRPLLAYAACBALGGA 61
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Best Local Similarity 57.8%; Pred. No. 1.3e-75;
Matches 163; Conservative 37; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                             83; Indels
                                                                                                                                                                                                                                                                                                             55.0%; Score 831; DB 9;
60.3%; Pred. No. 8.6e-80;
iive 33; Mismatches 83;
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 11971
LENGTH: 295
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                                                                                                                                                                                                             TYPE: PRT ORGANISM: Pseudomonas aeruginosa S-09-815-242-11971
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.39
Matches 176; Conservative
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)
CURRENT PILING NATE: 2003-02-28
PRIOR PLILING DATE: 2003-02-28
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13999
LENGTH: 295
                                     134 VDAPARLKWITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENMHIHKTGALIRASVNL 193
                                                                                                                                       194 AALSKPOLDTCVAKKLDHYAKCIGLSFQVKDDILDIBADTATKKTQGKDIDNDKPTYPA 253
                                                                                                                                                                                                       191 GALC-GNIDQAGLVALDRYAAAVGLAPQVVDDILDVTADTATLGKTAGKDAANDKPTYVS 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.8%; Score 782; DB 15; Length 295; 56.9%; Pred. No. 1.4e-74; cive 36; Mismatches 85; Indels 6
                                                                                                                                                                                                                                                                               254 LLGWAGAKQKAQELHEQAVESLTGFGSEADLLRELSLYIIER 295
                                                                                                                                                                                                                                                                                                                                               250 LIGLDAARELAAQLRTDAHEALEGFGTRAGRLAELADLIVLR 291
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES PLIE REFREENCE: 38-10(52052)8

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-2

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 4670 COCGANISM: Burkholderia fungorum US-10-369-493-4670 TYPE: PRT

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75 ALEMIHVYSLVHDDMPCMDDDALRRGKPTVHVKYDEATALLVGDALQSQAFVALTSD---TVDAPA-RLKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPBLENMHIHKTGALIRASV

> 13 ERVERALDARLPAENILPOTILHQAMRYSVINGGKRIRPLLITYATGQALGLPENVLDAPAC 72 Query Match
> Best Local Similarity 53.2%; Pred. No. 6.3e-68;
> Matches 151; Conservative 38; Mismatches 90; Indels 5;

15 BRVETALDHYLPGBATEPATLHBAMRYAVLGGGKRVRPLLCHAAGBLTGARABCLDAAAA 74

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73 AVEFIHVYSLIHDDLPAMDNDDLRRGKPICHKAYDEATAILAGDALQALAFBVLANDPGI 132

133 TVDAPA-RLKMITALTRASGSQGWVGGQAIDLGSVGRKLTLPELENMHIHKTGALIRASV 191

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Sequence 7429, Application US/10369493
; Sequence 7429, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TILE OF INVENTION NUMBER: US/0520,493
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7429 US-10-369-493-7429

TYPE: PRT CRGANISM: Burkholderia cepacia US-10-369-493-7429

Ouery Match 47.6%; Score 719.5; DB 15; Length 294; Best Local Similarity 53.2%; Pred. No. 6.3e-68; Matches 151; Conservative 38; Mismatches 90; Indels 5;

AVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEVLANDPGI 132

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cac, Yongwei
APPLICANT: Slater, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE REPRESENCE: 38-1015-052)B
FILE REPRESENCE: 38-1015-052)B
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER: OF SEQ ID NOS: 47374
SEQ ID NOS: 47374 US-10-369-493-15449 ; Sequence 15449, Application US/10369493 ; Publication No. US20030233675A1 TYPE: PRT
CRGANISM: Xanthomonas campestris
US-10-369-493-15449

14 RVERALDARLPAENILPQTLHQAMRYSVINGGKRTRPILITYATGQALGLPENVLDAPACA 4; Gaps Query Match
Best Local Similarity 53.2%; Pred. No. 1.9e-67;
Matches 151; Conservative 35; Mismatches 94; Indels

74 VEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEVLANDPGIT 133 qq à

134 VDAPARLKMITALTRASGSQGNVGGQAIDLGSVGRKLTLPELENMHIHKTGALIRASVNL 193 쉱 ò

194 AALSKPOLDTCVAKKLDHYAKCIGLSFQVKDDILDIBADTATLGKTQGKDIDNDKPTYPA 253 셤

Sequence 15817, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Hikke, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S. RESULT 10 US-10-369-493-15817

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63 PENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALA 122
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                                                                                                                                    194 AALSKPDLDTCVAKKIDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKDIDNDKPTYPA 253
67 VELIHAYSLVHDDLPAMDDDALRRGHPTVHIAFDEATAILAGDALQARAFELLARAP---
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                                                                                                                                                                                                                                                                                                                                                          254 LLGMAGAKOKAQELHBQAVESLTGFGSEADLLRELSLYIIER 295
                                                                                                                                                                                                                                                                                                                                                                                                   of Essential Genes in
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46.7%; Score 705.5; DB 9;
Best Local Similarity, 52.7%; Pred. No. 2e-66;
Matches 156; Conservative 39; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANI: Oblean, Kari L.
APPLICANI: Oblean, Kari L.
APPLICANI: 2yskind, Judith W.
APPLICANI: Trawick, John D.
APPLICANI: Trawick, John D.
APPLICANI: Trawick, John D.
APPLICANI: Trawick, John D.
APPLICANI: Tamanoto, Robert T.
APPLICANI: Xu, H. Howard
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Donoraryotes
FILE REPERENCE: ELITZA, OllA
CURRENT APPLICATION NUMBER: 60/191, 078
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-24
PRIOR PLING DATE: 2000-05-24
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PRIOR PLING DATE: 2000-05-24
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
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PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
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PRIOR PLING DATE: 2001-02-3
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-27
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PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING 
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US-09-815-242-14084
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APPLICANT: Cao, Yongwei
APPLICANT: Slacer, Steven C.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPRENCE: 38-10(52052)8
CURRENT PELLOATION NUMBER: US. 60/360,039
PRIOR APPLICATION NUMBER: US. 60/360,039
PRIOR APPLICANTON NUMBER: US. 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 16200
LENGTH: 284
          APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR PILING DATE: 2003-02-28
PRIOR PELING DATE: 2002-02-21
SEQ ID NO 15817
LENGTH: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 VDAPARLKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENMHIHKTGALIRASVNL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 VEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDBATAILAGDALQALAFEVLANDPGIT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 VEFIHVYSLIHDDLPPAMDNDDLRRGKPTCHKAYDBATAILAGDALQALAFBVLANDPGIT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 AALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKDIDNDKPTYPA 253
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46.8%; Score 707; DB 15; Length 284;
Best Local Similarity 53.2%; Pred. No. 1.3e-66;
Matches 150; Conservative 35; Mismatches 93; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 46.8%; Score 707; DB 15; Length 2 Best Local Similarity 53.2%; Pred. No. 1.3e-66; Matches 150; Conservative 35; Mismatches 93; Indels
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Publication No. US20030233675A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Xanthomonas campestris S-10-369-493-15817
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NVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFE 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 DIDNDKPTYPALLGMAGAKOKAQELHEQAVESLTGFGSBA---DLLRELSLYIIER 295
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APPLICANT: Construction of Section Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tanamoto, Robert T.
APPLICANT: Van H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPRENCE: Elitara, 011.A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: US/09/815,242
FRIOR PRING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
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45.8%; Score 691.5; DB 9;
Best Local Similarity 52.0%; Pred. No. 6.2e-65;
Matches 153; Conservative 36; Mismatches 96;
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PRIOR PELLOR DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELLOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2010-12-22
PRIOR PILING DATE: 2010-12-22
PRIOR PILING DATE: 2010-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PSELSEQ FOI WINDOWS VEFSION 4.0
SELENGTH: 299
                                                                                                                                                                                                                                        Sequence 10069, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                               APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Escherichia coli
US-09-815-242-10069
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                 US-09-815-242-10069
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: ALALE, Gregory J.
APPLICANT: Slater, Grewn C.
APPLICANT: Slater, Grewn C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REPERENCE: 38-10(52052)8
FURBRY PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 732
LENGTH: 299
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APPLICANT: AINCHE, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: ENPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052)B
FURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2002-02-21
SEQ ID NO 10187
LENGTH: 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LEACVKQANQALSRFIAPLPFQN---TPVVETWQYGALLGGKRLRPFLVYATGHMFGVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 VLANDPGITVDAPARLKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPBLENMHIHKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 ALIRASVNLAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 DNDKPTYPALLGMAGAKQKAQELHEQAVESLTGFGSEA---DLLRELSLYIIER 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
45.8%; Score 691.5; DB 1
Best Local Similarity 52.0%; Pred. No. 6.2e-65;
Matches 153; Conservative 36; Mismatches 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 10187, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                            Application US/10369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-369-493-732
                            Sequence 732, Applic
Publication No. US2
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-369-493-10187
JS-10-369-493-732
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Query Match 45.7%; Score 690; DB 15; Length 306;
Best Local Similarity 52.2%; Pred. No. 9.3e-65;
Matches 157; Conservative 36; Mismatches 94; Indels 14; Gaps 5;
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297 H 297

¹⁶⁰ IHKTGALIRASVNLAAL---SKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIBADTATL 236

³⁰⁶ H 306 32 sarch completed: February 29, 2004, 15:27:46 35 time : 22.7191 secs

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HKTGALIRASVNILAALSKPDIDTCVAKKIDHYAKCIGLSFQVKDDILDIEADTATIGKTQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Amino acid sequences encoded by ORF7 US-09-934-903-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Methylomonas 16a
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Best Local Similarity 100.
Matches 297; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-934-903-14
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Sequence 26387, A
Sequence 5908, Ap
Sequence 12733, A
Sequence 4190, Ap
                                                                                                                                      ; Search time 9.02528 Seconds (without alignments)
1698.885 Million cell updates/sec
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1510
1 MSKIKAYLIVCQERVERALD.......FGSEADLIRELSLYIIERTH 297
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Sequence 1
Sequence 1
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/cgn2_6/ptodata/2/jaa/5B_COWB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COWB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COWB.pep:*
/cgn2_6/ptodata/2/jaa/PoTUS_COWB.pep:*
/cgn2_6/ptodata/2/jaa/PoTUS_COWB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-26387
US-09-543-601A-26387
US-09-543-601A-5908
US-09-187-050-14
US-09-187-050-14
US-09-187-050-14
US-09-187-050-20
US-09-187-050-20
US-09-187-050-20
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US-09-187-050-31
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US-09-101-126-3
US-09-367-528A-5
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        February 29, 2004, 14:35:44
                                                                                           - protein search, using sw model
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length: 2000000000
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3171, Ap
2612, Ap
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6724, Ap
2, Appli
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GENERAL INFORMATION:
APPLICANT: Koffes, Mattheos
APPLICANT: Odon, J. Mattin
APPLICANT: Odon, J. Mattin
APPLICANT: Schenzle, Andreas J.
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Rouviere, Pierre
APPLICANT: Cheng, Qiong
TITLE OF INVENITOR: Gene Involved in Isoprenoid Compounds Production
FILE REFERENCE: Clid46 US NA
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 05/09/934,903
CURRENT FILING DATE: September 1, 2001
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 297
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ALIGNMENTS
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Patent No. 6660507
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Sequence 1273, Application US/09489039A.

Sequence 1273, Application US/09489039A.

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: GAY Breton et. al
APPLICANT: ATTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA.

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS.

PILLE REPRESENCE: 2709.2004001

CURRENT APPLICATION NUMBER: 2000-01-27

PRIOR RPLICATION NUMBER: US 60/117,747

PRIOR PILLING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                             73 AVEFIHVYSLIHDDILPAMDNDDIRRGKPTCHKAYDEATAIIAGDALQALAFEVLANDPGI 132
                                                                                                                                                                                                                                                                            133 TVDAPARLKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPBLENWHIHKTGALIRASVN 192
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                                                                                                        20 QRVDEALNQALQTLPPSDMPLSQAMRYGALLGGKRLRPFLVYAVGEMFNVPVANLDVPAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 45.9%; Score 693.5; DB 4; Length Best Local Similarity 51.2%; Pred. No. 2e-63; Matches 149; Conservative 38; Mismatches 101; Indels
  Indels
97;
  36; Mismatches
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US-09-489-039A-12733
     Conservative
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Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIOR PRILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5908
TENDRAL 3073
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TENDRAL 3073
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Patent No. 6551795
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREUOTINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AREUOTINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 EVLADTRRNPQEHAVCLEMLTRLARAAGSAGWVGGQAIDLGSVGVALDQAALEVMHHKT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 GALIEASVRIGALASGRAEPASLAALRRYAEAIGLAFQVQDDILDVESDTATLGKTQGKD 347
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241 GKDIDNDKPTYPALLGMAGAKQKAGELHEQAVESLTGFGSGSBADLLRELSLYIIERTH 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.0%; Score 831; DB 4; Length 401;
60.3%; Pred. No. 2e-77;
live 33; Mismatches 83; Indels
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 55.0%
Best Local Similarity 60.3%
Matches 176; Conservative
                                                                                                              RESULT 2
US-09-252-991A-26387
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US-09-252-991A-26387
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RESULT 5
US-09-328-352-4190
Sequence 4190, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:

Length 307;

Score 702.5; DB 4; Pred. No. 2.5e-64;

46.5%;

Query Match Best Local Similarity

ORGANISM: Proteus mirabilis

-09-543-681A-5908

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Sequence 14, Application US/09187050B
Patent No. 6043072
Patent No. 6043072
GENERAL INFORMATION,
APPLICANT: Croteau, Rodney B
APPLICANT: Hefner, Jerry
TITLE OF INVENTION: Wacleic Acids Encoding Taxus Geranylgeranyl Diphosphate
TITLE OF INVENTION: Synthase, And Methods of Use
FILE REFERENCE: WSUR12423
CURRENT APPLICATION UNDERS: US/09/187,050B
CURRENT PILLIG DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 393
                                                     230 PSDRTLRVISELGKTIGSQGLVGGQVVDITSEGDANVDLKTLEWIHIHKTAVLLECSVVS 289
                                                                                                                                                                75 BFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDBATAILAGDALQALAFEVLANDPGITV 134
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                            135 DAPARLKMITALTRASGSQGWVGGQAIDLGSVG-RKLTLPELENMHIHKTGALIRASVNL 193
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                                                                                                                                 194 AALSKPDLDTCVAKKLDHYAKCIGLSPQVKDDILDIBADTATLGKTQGKDIDNDKPTYPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , LOUATION: (1)..(393)
; OTHER INFORMATION: Computer-generated Taxus GGPP synthase protein
; OTHER INFORMATION: variant
US-09-187-050-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 393;
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                                                                                                                                                                                                                                          254 LLGMAGAKOKAQELHEQAVESLTGFGS-EADLLRELSLYIIER 295
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; Sequence 16, Application US/09187050B
; Patent No. 6043072
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
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ORGANISM: Artificial Sequence
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US-09-187-050-14
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APPLICANT: Gary L. Breton et al. Title OF THE SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOREDACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 QDNP-NFAAARAAVAVELIHCYSLAHDDIPCYDNDLIRRGQPTCHVAFGEDFALLAGDI 126
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APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Norther,
JETTLE OF INVENTION: Nucleic Acids Encoding Taxus Geranylgeranyl Diphosphate
FITLE OF INVENTION: Synthase, And Methods of Use
FILE REFERENCE: WSUR12423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQALAFEVLA----NDPGITVDAPARLKMITALTRASGSQGWVGGQAIDLGSVGRKLTLP 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELENIHENKTGALIQAALMMGAVTIFSGTDQAIPKIRQYGQAIGLAFQVQDDILDITSST 244
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                                                                                                                                                                                                                                                                                                                                             Query Match
40.1%; Score 605.5; DB 4;
Best Local Similarity 47.0%; Pred. No. 2.6e-54;
Matches 143; Conservative 50; Mismatches 100;
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CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 2
LENGTH: 393
                                                                                                  CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Patent No. 6043072
                                                                                                                                                                                                                                                                ORGANISM: Acinetobacter baumannii
-09-328-352-4190
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ORGANISM: Taxus canadensis
S-09-187-050-2
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Best Local Similarity
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S-09-187-050-2
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US-09-187-050-18
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APPLICANT: Croteau, Rodney B
APPLICANT: Hefner, Jerry
TITLE OF INVENTION: Nucleac Acids Encoding Taxus Geranylgeranyl Diphosphate
TITLE OF INVENTION: Synchase, And Methods of Use
FILE REFERENCE: WSUR12423
CURRENT APPLICATION NUMBER: US/09/187,050B
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 393
        APPLICANT: Hefner, Jerry
TITLE OF INVENTION: Nucleic Acids Encoding Taxus Geranylgeranyl Diphosphate
TITLE OF INVENTION: Synthase, And Methods of Use
FILE REPERSUCE: WSUR12423
CURRENT APPLICATION NUMBER: US/09/187,050B
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 393
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LOCATION: (1)..(393)
OTHER INFORMATION: Computer-generated Taxus GGPP synthase protein
OTHER INFORMATION: variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT

LOCATION: (1)...(1)...(2)...(2)...(1)...(1)...(1)...(1)...(1)...(2)...(1)...(2)...(3)...(1)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rothey B
APPLICANT: Groteau, Jerry
TITLE OF INVENTION: Nucleic Acids Encoding Taxus Geranylgeranyl Diphosphate
TITLE OF INVENTION: Synthase, And Methods of Use
TITLE OF INVENTION: Synthase, And Methods of Use
TITLE OF INVENTION: 1998-11-05
CURRENT APPLICATION NUMBER: US/09/187,050B
CURRENT PILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
SEQ ID NO 20
TYPE: PRT
CORRANISM: Artificial Sequence
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                                                                                                                             75 BFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEVLANDPGITV 134
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                                               Gaps
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NAME/KEY: VARIANT
LOCATION: (1)..(393)
LOCATION: (2)..(393)
OTHER INFORMATION: Computer-generated Taxus GGPP synthase protein
OTHER INFORMATION: variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Taxus GGPP OTHER INFORMATION: synthase protein variant
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Length 393;
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39.0%; Score 588.5; DB 3; Length 46.6%; Pred. No. 2.2e-52; ive 45; Mismatches 101; Indels
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Patent No. 6043072
                          Best Local Similarity 46.6
Matches 132; Conservative
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SOFTWARE: Patentin Ver. 2.0
                          SEQ ID NO 24
LENGTH: 393
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Sequence 24, Application US/09187050B
Datent No. 6043072
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Hefner, Jerry
TITLE OF INVENTION: Synthase, And Methods of Use
FILE REFERENCE: WSUR12433
CURRENT APPLICATION NUMBER: US/09/187,050B
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                      APPLICANT: Croceau, Rodney B
APPLICANT: Croceau, Rodney B
APPLICANT: Hefner, Jerry
TITLE OF INVENTION: Nucleic Acids Encoding Taxus Geranylgeranyl Diphosphate
TITLE OF INVENTION: Nucleic Acids Encoding Taxus Geranylgeranyl Diphosphate
TITLE OF INVENTION: Synthase, And Methods of Use
FILE REPRESENCE: WSUR12433
CURRENT APPLICATION NUMBER: US/09/187,050B
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
ESEQ ID NO 22
LENGTH: 393
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LOCATION: (1)...(393)
OTHER INFORMATION: Computer-generated Taxus GGPP synthase protein
OTHER INFORMATION: variant
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                                                       254 LIGMAGAKOKAQELHEQAVESLIGFGS-EADLIRELSLYIIER 295
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                                                                                         349 LWGLEXAKEFAABLATRAKEBLSSFDOIKAAPLIGLADYIAFR 391
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Sequence 22, Application US/09187050B
Patent No. 6043072
CENERAL INFORMATION:
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US-09-187-050-26
US-09-187-050-26
Sequence 26, Application US/09187050B
Sequence 26, Application US/09187050B
Sequence 26, Application US/09187050B
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Hefner, Jerry
TITLE OF INVENTION: Nucleic Acids Encoding Taxus Geranylgerany! Diphosphate
FILE REFERENCE: WSUR12423
CURRENT APPLICATION NUMBER: US/09/187,050B
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
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NAME/KEY: VARIANT
LOCATION: (1)...(393)
COTHER INFORMATION: Computer-generated Taxus GGPP synthase protein
CTHER INFORMATION: variant
US-09-187-050-24
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Taxus GGPP
OTHER INFORMATION: synthase protein variant
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; OTHER INFORMATION: Computer-generated Taxus GGPP synthase protein
; OTHER INFORMATION: variant
US-09-187-050-26
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46.6%; Pred. No. 2.2e-52;
tive 45; Mismatches 101; Indels S
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39.0%; Score 588.5; DB 3; Length
Best Local Similarity 46.6%; Pred. No. 2.2e-52;
Matches 132; Conservative 45; Mismatches 101; Indels
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Best Local Similarity 46.65
Matches 132; Conservative
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NAME/KEY: VARIANT
LOCATION: (1)..(3
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NAME/KEY: VARIANT
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                       US-09-187-050-28
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APPLICANT: Croteau, Rodney B
APPLICANT: Hefrer, Jerry
TITLE OF INVENTION: Synchase, And Methods of Use
TITLE OF INVENTION: Synchase, And Methods of Use
FILE REPREDEUR: WSUR12423
CURRENT APPLICATION NUMBER: US/09/187,050B
CURRENT FILE DEFENCE: 1998-11-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                    230 PSDRTLRVISELGKTIGSQGLVGGQVVDITSEGDANVDLKTLEWIHIHKTAVILLECSVVS 289
                                                                                                                                                                                                                           DAPARLKMITALTRASGSQGMVGGQAIDLGSVG-RKLTEPRLENMHIHKTGALIRASVNL 193
                                                                                                                               135 DAPARLKMITALTRASGSOGWVGGQAIDLGSVG-RKLTLPELENMHIHKTGALIRASVNL 193
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OTHER INFORMATION: Computer-generated Taxus GGPP synthase protein OTHER INFORMATION: variant
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46.6%; Pred. No. 2.2e-52;
tive 45; Mismatches 101;
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Best Local Similarity 46.6<sup>1</sup>
Matches 132; Conservative
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LENGTH: 39
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Pageince 26, Application US/09187050B

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GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B

APPLICANT: Croteau, Rodney B

APPLICANT: Croteau, Rodney B

APPLICANT: Croteau, Rodney B

APPLICANT: Croteau, Rodney B

APPLICANT: Weinsylver, Jerry

TITLE OF INVENTION: Synthase, And Methods of Use

FILE REPERBNCE: WSUR12423

CURRENT APPLICATION NUMBER: US/09/187,050B

CURRENT PILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 28

SEQ ID NO 28
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OTHER INFORMATION: Computer-generated Taxus GGPP synthase protein
OTHER INFORMATION: variant
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39.0%; Score 588.5; DB 3;
Best Local Similarity 46.6%; Pred. No. 2.2e-52;
Matches 132; Conservative 45; Mismatches 101;
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February 29, 2004, 14:26:38; Search time 35.1152 Seconds (without alignments) 2389.754 Million cell updates/sec
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1586107 segs, 282547505 residues

earched:

1586107

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; farnesyl diphosphate synthetase; IspA. Methylomonas 16a sp. farnesyl diphosphate synthetase (IspA) enzyme. AAE22308 standard; protein; 297 AA (revised)
(first entry) 07-AUG-2003 25-JUL-2002 AAE22308; RESULT 1

Methylomonas sp. WO200218617-A2. 07-MAR-2002 04-SEP-2001; 2001WO-US027420. 01-SEP-2000; 2000US-0229858P. 01-SEP-2000; 2000US-0229907P. BS: Miller Koffas M, Dicosimo DJ, Rouviere PE; à Brzostowicz PC, Cheng Q, Odom JM, Picataggio SK,

(DUPO) DU PONT DE NEMOURS & CO Z I.

WPI; 2002-351711/38. N-PSDB; AAD35506.

کر: تا Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon substrates.

Claim 35; Page 125-126; 156pp; English.

The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule conciding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by

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using microorganism having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Methylmonas is des go. geranyltransferase or farnesyl diphosphate synthetese [16ph], enzyme used in the invention. (Updated on 97-AUG-2003 to correct 05 field.)
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100.0%; Pred. No. 7.3e-140;
ive 0; Mismatches 0;
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Matches 297; Conservative
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N-PSDB; ABK83265.
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New high growth methanotrophic bacterial strain, useful for producing

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The invention relates to a high growth methanotrophic bacterial strain, which grows on a CI carbon substrate e.g. methane and methanol, and comportises a functional Embdenn Meyerhof carbon flux pathway comprising a gene coding a pyrophosphate dependent phosphofrutoxinase enzyme or a 165 RNA. The bacterial strain is useful for the production of single cell protein and for the biotransformation of a nitrogen-containing compound, or a mamonia, nitrate, nitrite or nitrogen. It is also useful for the production of a feed product comprising a protein, carbohydrates and a pigment and for reducing oxygen demand, for removing nitrates and intrites in methane-containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are present; The bacterial strain of the invention can be used as a carbon oxide with methane or methanol as a carbon source. It is also used in the production of biomass including proteins, carbohydrates and a wide production of biomass including proteins, carbohydrates and a wide compounds, useful as pigments and as monomers in polymeric materials and compounds, useful as pigments and as monomers in polymeric materials and in production of terpenoid and carotemoid compounds, useful as pigments and as monomers in polymeric materials and in production of expoplysaccharides at high levels. Sequences ABG61551-ABG61590 represent high growth methanotrophic bacrerial strain proteins of the invention. (Updated on 07-AUG-2003 to correct OS field.)
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comprises a
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  single cell proteins, grows on a Cl carbon substrate, and
functional gene encoding in Embden-Meyerhof carbon pathway
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100.0%; Pred. No. 7.3e-140;
ive 0; Mismatches 0;
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                                                                  11; Page 147-148; 157pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Trawick JD,

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Zyskind JW,

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Ohlsen I Xu HH;

2000US-0191078P. 2000US-020648P. 2000US-0207278P. 2000US-0242578P. 2000US-0253625P. 2000US-0253625P.

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Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa cellular proliferation protein #368.
                                                                                                                                                                                                                                                                                 AAU36378 standard; protein; 295
                                          WPI; 2002-383051,
N-PSDB; ABK50087
                                                                                                                                                Sequence 297 AA;
                                                                                                                                                                                                                                                                                                  14-FBB-2002
                                                                                                                                                                                             61
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New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                               21-MAR-2001; 2001WO-US009180
                                                                                                                                                                                                                                                                                                            (BLIT-) ELITRA PHARM INC
Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                              WPI, 2001-611495/70
                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS54237
                                     WO200170955-A2
                                                                                                                                                                   23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                       16-FEB-2001;
                                                                                                                                                                                                                                                      22-DEC-2000;
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Yamamoto RT,
                                                                          27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                 isopremoid biosynthetic enzyme isolated from Methylomonas 16a. The invention is useful for obtaining a nucleic acid molecule encoding an invention is useful for obtaining a nucleic acid molecule encoding an observation compound biosynthetic enzyme, and for the microbial production of isopremoid compounds. The molecules of the invention are also useful for regulating isopremoid biosynthesis in an organism and for producting nucleic acid is also useful for feed additive, for the producting keratemoids and their derivatives, isopremoid intermediates, and as pure products useful as pigments, flavours and fragrances. The present amino encid sequence represents the Methylomonas 16a open reading frame 7 (OR??) ispA (geranyltranferase or farmersyl diphosphate synthase enzyme) protein of the invention, as described above
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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                                                                                                                                                                                                                                                                                                                                                                        present invention relates to a new nucleic acid molecule encoding an
                                                                                                                                                                                                                                                  Novel nucleic acid molecule encoding a isoprenoid biosynthetic enzyme, isolated from Methylomonas 16a, useful for the production of isoprenoid compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKDIDNDKPTYPALLGMAGAKOKAOELHEQAVESLTGFGSEADLLRELSLYIIERTH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKDIDNDKPTYPALLGMAGAKOKAQELHEQAVBSLTGFGSEADLLRELSLYIIERTH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSKLKAYLTVCQERVERALDARIPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLPENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HKTGALIRASVNLAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIBADTATLGKTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLPENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQA
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                                                                                                                                    Picataggio SK;
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100.0%; Pred. No. 7.3e-140;
tive 0; Mismatches 0;
                                                                                                                                  Odom JM,
                                                                                           (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                     Tomb J.
                                                                                                                                                                                                                                                                                                                             Claim 4; Page 76-77; 84pp; English
                                                                                                                                Cheng Q, Koffas M, Norton KC,
Rouviere PE, Schenzle A, Tomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 297; Conservative 0
                                                       01-SEP-2000; 2000US-0229907P.
                  29-AUG-2001; 2001WO-US026852.
                                                                                                                                                                                          2002-383051/41.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, Berughonnas and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the express these proteins, and to obtain antibodies capable of binding to the express these proteins. The proteins continued and sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed appecification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 PQRADAAACAVELIHAYSLVHDDLPAMDDDDLRRGQPTTHRAFDBATAILAADGLQALAF 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 EVLADTRRNPQEHAVCLEMLTRLARAAGSAGMVGGQAIDLGSVGVALDQAALBVMHRHKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 IDNDKPTYPALLGMAGAKQKAQELHEQAVESLTGFGSBADLLRELSLYIIER 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.0%; Score 831; DB 4; Length 295; 60.3%; Pred. No. 4.7e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 60.3
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The invention relates to an isolated mucies and compitating any one of the 6113 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid modelic acid a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation of the gene product or that has an activity against a biological pathway in which a proliferation required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or gene on which the test compound that inhibits proliferation of an organism. The antisense nucleic acids required for which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits acids acids and strains; or (13) identifying the target of a compound that inhibits acids required for proliferation in cells other than S. aureus, S. typhimurium, X. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target profaration in cells other than S. aureus, S. typhimurium, a pattent did not form the directly fram NIPO at the sequence of a contraction of an electronic format directly fram NIPO at the sequence of the privated pot the privated pot the privated pot the privated pot the
                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                 Protein encoded by Prokaryotic essential gene #24192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 66589; 1766pp; English
ABU38665 standard; protein; 295 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
06-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                            21-MAR-2002; 2002WO-US009107
                                                                                      (first entry)
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                                                                                                                                                                                                                          Pseudomonas aeruginosa
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-029926/02.
N-PSDB; ACA42535.
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                                                                                      19-JUN-2003
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Wall D,
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screening

Zyskind JW; Xu HH;

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Ohlsen Forsyth F

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123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promerer operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense
                                                                                      63
                                                                                                               19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    design.
                                                                                                                                                                                                                                                                                       2 IAAYQARCQARVDAALDALFVAPREELQRLYBAMRYSVM:GGKRVRPLLAYAACRALGGA
                                                                                                                                                                                                            124 EVLANDPGITVDAPARIKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENMHIHKT
                                                                                     4 LKAYLTVCQBRVERALDARLPAENILPOTLHQAMRYSVLNGGKRTRPLLTYATGQALGEP
                                                                                                                                                64 ENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDBATAILAGDALQALAF
                                                                                                                                                                62 PQRADAAACAVELIHAYSLVHDDLPAMDDDDLRRGQPTTHRAFDBATAILAADGLQALAF
                                                                                                                                                                                                                           184 GALIRASVNIAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKD
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                    S42 QAHNKPTYPALLGLEAAKGYALEIRDLALAALDGPPPSADPIRQIARYIVER 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; prokaryotic essential gene, cell proliferation; drug
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                                                                                                                                                                                                                                                                                                                                  244 IDNDKPTYPALLGMAGAKQXAQBLHEQAVESLTGFGSEADLLRELSLYIIBR
                          Length 295;
                                                       Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #25568
                                                         83
                        55.0%; Score 831; DB 6; 60.3%; Pred. No. 4.7e-73; ive 33; Mismatches 83
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 68065; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU40141 standard; protein; 295
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Carr GJ,
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96-SEP-2001, 2001US-0094893.

25-COT-2001, 2001US-0342923P.

08-FEB-2002, 2002US-00072851.

06-MAR-2002, 2002US-0362699P.
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                                       Best Local Similarity 60.3 Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
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Trawick JD,
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N-PSDB; ACA44011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas putida
Sequence 295 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2002
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                           Query Match
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Wall D,
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nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the activated; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway in cequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) decernaining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the strains; or product of an organism. The antisense nucleic acids required to contain proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. preumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent din not form part of the printed specification, but was obtained in electronic format directly from Wipo at firm printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences
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Sequence 295 AA;

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67 LDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEVL 126
                                                                                                                                                                                                                                       127 ANDPGIT--VDAPARLKWITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENMHIHKTG 184
                                                                                                                                                                                                                                                                                                                                                                 125 L-DPCLSPQIDS-IRLAMVQVLAKAAGPAGMVGGQAIDLGSVGQKLDQQALEFWHRHKTG 182
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                                                                                                      7 YLTVCQERVERALDARLPAENILPQTIHQAMRYSVINGGKRTRPLLTYATGQALGLPENV 66
                                                                                                                                                          64
                                                                                                                                                       5 YOASCOARVDAALEPLFIAPSKELERLYAAMRYSVMNGGKRVRPLLAYAACBALGAPAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                     ALIRASVNIAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEDKPTYPALLGLEAAKAYAIELRDQALAAIQGFGEKAEPLRALARYIVER 293
  Length 295;
                                                    80; Indels
53.7%; Score 811; DB 6;
58.8%; Pred. No. 4.3e-71;
iive 36; Mismatches 80;
Query Match
Best Local Similarity 58.8%
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183
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Protein encoded by Prokaryotic essential gene #27032. ABU41505 standard; protein; 295 AA. (first entry) 19-JUN-2003 ABU41505; ESULT 7 BU41505

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Pseudomonas syringae.

03-OCT-2002

WO200277183-A2

21-MAR-2002; 2002WO-US009107.

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the invertion trainers to an isolated muctate acid compilating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid enoding a polypeptide whose expression is inhibited by the antisense comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated conflicted by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular or proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation of the paper product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity, (11) a culture comprising strains in which the gene or value activity, (11) a culture comprising strains in which the gene compound's activity, (11) a culture comprising strains in which the gene conflicteration of an organism. The antisense nucleic acids required for proliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids for redining a required for proliferation and the present seminates and serior of a cempound is energied by propiement or parameters and the serior of the required for proliferation and the present seminates and the proper serior or parameters and the serior of the required for proliferation of an organism. The artisens and the serior of the serior of the serior of the serior of the serior of the serior 
                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                        Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                        Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                        Haselbeck R,
                                                                                                                                                                                                                                                                     Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claim 25; SEQ ID NO 69429; 1766pp; English.
                                                                                                                                                                                                                                        Malone C,
                                                                                                                                                                                                                                                                     Carr GJ,
                    21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00372851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                       (BLIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                        Zamudio C,
Trawick JD,
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N-PSDB; ACA45375.
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Wall D,
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63 4 LKAYLTVCQBRVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLP 0; Gaps 52.4%; Score 791; DB 6; Length 295; 56.8%; Pred. No. 4e-69; ive 36; Mismatches 91; Indels Best Local Similarity 56.88 Matches 167; Conservative Query Match

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64 ENVLDAPACAVEPIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAF 123

181 124 EVLANDPGITVDAPARLKMITALTRASGSQGMVGGQAIDLGSVGRKETLPPELENMHIHKT

184 GALIRASVNLAALSKPDLDTCVAKKLDHYAKCIGLSFQVIDDILDIEADTATLGKTQGKD 243

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Neisseria gonorrhoeae
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Best Local Similarity
Matches 152; Conserv
                                                                standard;
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GALIEASVRLGALASGQADQARLDALQVYARAVGLAFQVQDDILDVESDTATLGKRQGAD 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 LKAWQQRAQAQTELLLERFLPSGNEIPHTLHEAMRYAALDGGKRLRPMLVLAASELGGAM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
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DVLSRP--TZIPAARQLAMLSVLAKAGGSAGMAGGQAIDLANVGKQMVQADLERMHSLKT
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                                   IDNDKPIYPALLGMAGAKQKAQELHEQAVESLIGFGSEADLLRELSLYIIERTH 297
                                                                                                                                                                                                                                                                                                                                                                                                  New protein from Neisseria gonorrheae, useful for the manufacture medicament for treating or preventing N. gonorrheae infection.
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                                                                                                                                                                 gonorrhoeae amino acid sequence SEQ
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                                                                                                 protein; 298
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                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New protein from Neisseria gonorrheae, useful for the manufacture medicament for treating or preventing N. gonorrheae infection.
ADNDKPTYVKLMGLEAARSYAHKLVAEAVALLEPFGDKALRIRQLAEFAVARKX
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51.7%; Pred. No. 2.1e-63;
iive 44; Mismatches 96
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screening
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Xu HH;
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for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
                                                                                                                                                                                           Protein encoded by Prokaryotic essential gene #22743.
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Yamamoto R,
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                                      ABU37216 standard; protein; 298 AA
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-CCT-2001, 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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N-PSDB; ACA41086.
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ESULT 10
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ENVLDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAF

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124 EVLANDPGITVDAPARLKMITALTRASGSQGWVGGQAIDIGSVGRKLTLPELENMHIHKT

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184 GALIRASVNIAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIEADTATLGKTQGKD

RESULT 11 ABU38181

LKAWQQRAQAQTELLLERFLPSGNEIPHTLHEAMRYAALDGGKRLRPMLVLAASSLGGAM 66 4 LKAYLTVCQBRVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLP 63

Length 298;

96; Indels

48.5%; Score 733; DB 6; 51.7%; Pred. No. 2,1e-63; ive 44; Mismatches 96

152; Conservative

Similarity

Query Match Best Local 8 Matches

standardise OS field!

Sequence 298 AA;

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183

184

123

243 244

The invention relates to an isolated nucleic acid comprising any one of

The invention relates to an isolated nucleic acid comparising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that thinbits cellular proliferation; (7) identifying a compound that inhibits proliferation of an activity of a gene in an operon required for proliferation or that inhibits proliferation of an activity of a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overaxpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational days is scorening or screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimutium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in the procession of the strains of the target proliferation or the present seq

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

claim 25; SEQ ID NO 66105; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid

Antisense; prokaryotic essential gene; cell proliferation; drug design. Zyskind JW; Xu HH; Oblsen KL, Forsyth RA, Protein encoded by Prokaryotic essential gene #23708 Haselbeck R, Yamamoto R, ABU38181 standard; protein; 298 AA. Malone C, Carr GJ, 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 21-MAR-2002; 2002WO-US009107. 08-FEB-2002; 2002US-00072851. (first entry) (BLIT-) BLITRA PHARM INC. Neisseria meningitidis Zamudio C, Trawick JD, WPI; 2003-029926/02. N-PSDB; ACA42051. WO200277183-A2. 19-JUN-2003 03-OCT-2002. ABU38181; Wang L, Wall D,

encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated antisense nucleic acid; (4) an autibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the attisense nucleic acid; (4) an autibody capable of specifically binding the polypeptide; (5) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of required for proliferation; (7) identifying a compound that inhibits entitle activity of required for proliferation or that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation (8) identifying a gene required for cellular proliferation of the ball of a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for cellular proliferation of solute candidate molecules for required for an activity or the strains or screening for homologous nucleic acids required for an expense or the candidate molecules for actional drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at flowly. 888888888888888888888888888888888

Sequence 298 AA;

67 HEAVGQAMAAIEMIHAYSLVHDDMPAMDNDSLRRGKPTCHVRYGEATALLTGDALQTQAF 126 64 ENVLDAPACAVBFIHVYSLIHDDEPAMDNDDERRGKPTCHKAYDEATAILAGDALQALAF 123 184 GALIRASVNLAALSKPDLDTCVAKKLDHYAKCIGLSFQVKDDILDIBADTATLGKTQGKD 243 244 127 DVLSRP--TELPARQLAMLSVLAKAGSSMGMAGGQAIDLANVGKQMAQTDLEQMHSLKT 184 4 LKAYLIVCQERVERALDARLPAZNILPQTLHQAMRYSVLNGGKRTRPLLTYATGQALGLP 63 7 LKAWQQRAQAQTELLLERFILPSENEIPHTLHEAMRYAALDGGKRLRPMIVLAASELGEAV 66 124 EVLANDPGITVDAPARIKMITALTRASGSQGMVGGQAIDLGSVGRKLTLPELENMHIHKT 2; Gaps 244 IDNDKPTYPALLGMAGAKOKAQELHBQAVESLTGFGSEADLLRELSLYIIERTH 297 245 ADNDKPTYVKLMGLBAARSYAHKLVABAVALLEPFGDKALRLRQLAEFAVARKY 298 48.3%; Score 729; DB 6; Length 298; 51.4%; Pred. No. 5.2e-63; ive 44; Mismatches 97; Indels Matches 151; Conservative Best Local Similarity Query Match ò 8 D2 g 엄 ò 8 ਨੇ

Protein encoded by Prokaryotic essential gene #6917. ABU21390 standard; protein; 293 AA 19-JUN-2003 RESULT 12 ABU21390

(first entry)

Antisense; prokaryotic essential gene; cell proliferation; drug design. Burkholderia fungorum.

W0200277183-A2.

03-OCT-2002

06.SEP-2001; 2001US-00948993. 25-0CT-2001; 2001US-03429239. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 2001US-00815242 21-MAR-2002; 2002WO-US009107

(BLIT-) ELITRA PHARM INC.

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, a d Wall Wall

2003-029926/02.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. N-PSDB; ACA25260.

Claim 25; SEQ ID NO 49314; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the foll antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid containing the vector; (3) an isolated on the largement whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or the activity of a gene in an operor required by the proliferation or the activity of a gene in an operor required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; or that inhibits cellular proliferation, or that inhibits cellular proliferation of an ordanism acts; (9) manufacturing an antibiotic; (10) profiling a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity, (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for cellular proliferation to solate candidate molecules for rational driving profired for proliferation in cells of homologous nucleic acids required for equilibrial for proliferation in cells of the strains of an organism of the training for the surface of a compound of a condition of a serving of the strains of the strain of the surface of the strain of the surface of th K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 293 AA;

Length 293; Indels 47.6%; Score 719.5; DB 6; ilarity 53.2%; Pred. No. 4.3e-62; Conservative 38; Mismatches 90; Similarity Watches 151; Query Match Local

12 BRVETALDHYLPGEATEPATLHEAMRYAVLGGGKRVRPLLCHAAGELTGARAECLDAAAA 71 13 ERVERALDARLPAENILPQTLHQAMRYSVLNGGKRTRPLLTTATGQALGLPENVLDAPAC

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73 AVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEVLANDPGI 132

129 -VLAPAQQAALVRELALASGSVGKCGQAIDLASVGHTLIRTQLETWHRKTGALLRAAV 187 133 TVDAPA-RLKMITALTRASGSQGWVGGQAIDLGSVGRKLTLPELENWHIHKTGALIRASV

192 NIAALSKPDLDTCVAKKLDHYAKCIGLSFQVXDDILDIBADTATLGKTQGKDIDNDKPTY 251

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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an athibited by the nutleense nucleic acid; (4) an athibited py the confiscation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which the test compound that inhibits proliferation of an companian acts; (9) amendecturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent
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to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
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Xu HH;
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                                                                252 PALLGMAGAKOKAQELHEQAVESLTGFGSEADLLRELSLYIIER 295
                                                                                           248 VSIIGLDASRALAAQLRSDAHAALAPFGARAQRLAELADLVVNR 291
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Forsyth F
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Yamamoto R,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362859.
06-MAR-2002; 2002US-0362859P.
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Trawick JD,
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N-PSDB; ACA23611
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Wall D,
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ų,
                    K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
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required for proliferation in cells other than S. aureus, S. typhimurium
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Xu HH;
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for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                               DB 6; Length 294;
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                                                                                                                                                                                                            47.1%; Score 711; DB 6; Length 29
53.0%; Pred. No. 3e-61;
ive 41; Mismatches 87; Indels
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Forsyth RA,
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Yamamoto R,
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Carr GJ,
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25-OCT-2001; 2001US-0342923P.
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06-MAR-2002; 2002US-0362699P.
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Matches 151; Conservative
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Trawick JD,
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N-PSDB; ACA31926.
                                                                                                                                                                 Sequence 294 AA;
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Wall
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Salmonella typhi.

WO200170955-A2

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The invention relates to an isolated nucleic acid comprising any one of the invention relates to an isolated nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid containing the vector; (3) an isolated contained by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the agene product or that has an activity against a biological pathway required for proliferation, or that the inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's adivity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a proliferation of an organism of an organism. The antisense nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids are useful for intentive proliferation of an organism or screening for homologous nucleic acids required for accepting a proliferation of an organism or screening for homologous nucleic acids required for a cellular proliferation of an organism or screening for homologous nucleic acids required for a cellular proliferation of an organism or screening for homologous nucleic acids required for a cellular proliferation of an organism can enable manufacturing a captured or a cellular proliferation of an organism captured and an organism captured and an organism captured and an organism captured and an organism captured and an organism capture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.1%; Score 711; DB 6; Length 299; 54.1%; Pred. No. 3.1e-61;
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Best Local Similarity 54.1%;
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LDAPACAVEFIHVYSLIHDDLPAMDNDDLRRGKPTCHKAYDEATAILAGDALQALAFEVL 126 66 LIDAPAAAVBCIHAYSLIHDDLPAMDDDDLRRGQPTCHIKRGEANAILAGDALQTLAFSIL 125 186 187 IRASVNLAALSKPDLDTCVAKKLDHYAKCIGLSPQVKDDILDIBADTATLGKTQGKDIDN 246 186 IRSAVRLGALSAGEQGRKALPILDRYAESÍGLAFQVQDDILDVVGDTATLGKRQGADQQL 12 QERVERALDARLPAENILPQ----TIHQAMRYSVINGGKRTRPLITYATGQALGLPENV OARVVRANDAL -- RRFIAPOPFONTPLVBAMHYGALLGGKRLRPFLVYATGNMFGISDNT AND PGITYDAPARLKMITALTRASGSQGMYGGQAIDLGSYGRKLTLPELENMHIHKTGAL 247 DKPTYPALLGMAGAKOKAQELHEQAVESITGFGSEA---DLLRELSLYIIER 295 246 GKSTYPALLGLEGAQRKARDLIDDARQSINBLAAQSLDTSALEALADYIIQR 297 89; Indels 10;

prokaryotic cellular proliferation protein; antibiotic; Salmonella typhi cellular proliferation protein #382. AAU38491 standard; protein; 299 AA antibacterial; drug design (first entry) Antisense; AAU38491; RESULT 1 AAU38491 XXXXXXXXXXXXX

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, that use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas acuginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins continued in a mission of proteins used to screen compounds in rational drug discovery programmes. The autisense mucleic acid sequence is also useful to screen for homologous concentration proteins colored which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGALIRASVNIAALSKPDLDTCVAKKLDHYAKCIGLSPQVKDDILDIEADTATLGKTQGK 242
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                                                                                                                                                                                                                                                                                                 Trawick JD,
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Xu HH;
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16-FEB-2001;
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23-OCT-2000;
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Yamamoto RT,
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23-MAY-2000;
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